

CC Human NGF is useful as a reagent for study of the nervous system, and
 CC for treatment of senile dementia. The DNA encoding this fragment was
 CC derived from the human gene or is synthesized chemically.
 CC See also AA012639.

XX Sequence . 241 AA:

Query Match 99.5%: Score 1270; DB 12; Length 241;
 Best local similarity 100.0%: Pred. No. 1.3e-134;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 MSMLFTTLTAFLIGIQAEPHSESNVPAGHTIPQVHMTKLQHSIDLALRRARSAPAAIA 61
 DB 1 MSMLFTTLTAFLIGIQAEPHSESNVPAGHTIPQVHMTKLQHSIDLALRRARSAPAAIA 60
 OY 62 ARVAGOTRNITVDPRLFKKRLRSRVLFTSTOPPREAADTODLDFEYGAAPFNRTHRK 121
 DB 61 ARVAGOTRNITVDPRLFKKRLRSRVLFTSTOPPREAADTODLDFEYGAAPFNRTHRK 120
 OY 122 RSSHPPIFRGEFSVCDVSVMGDKTTATDICKKEVNLGEVINNSVKQYFFETKCR 181
 DB 121 RSSHPPIFRGEFSVCDVSVMGDKTTATDICKKEVNLGEVINNSVKQYFFETKCR 180
 OY 182 DPNPVDSCGKIDSKHNSCTTHTFVKALTMQKQAAAFRIIDPACVLSRAVNR 241
 DB 181 DPNPVDSCGKIDSKHNSCTTHTFVKALTMQKQAAAFRIIDPACVLSRAVNR 240
 OY 242 A 242
 DB 241 A 241

RESULT 2
 AAR1474
 ID AAR1474 standard; Protein; 241 AA.

XX AC AAR1474;
 XX DT 26-APR-1991 (first entry)
 XX DE Human nerve growth factor.
 XX KW NGF; senile dementia.
 XX OS Homo sapiens.
 XX FH Key
 FT Peptide 1..18
 FT Protein /label- signal sequence
 FT Protein 19..241
 FT Protein /label- pro-NGF
 FT Protein 122..241
 FT Disulfide-bond /label- mature NGF
 FT Disulfide-bond 135..202
 FT Disulfide-bond 180..230
 FT Disulfide-bond 190..232
 XX PN EP414151-A.
 XX PD 27-FEB-1991.
 XX PF 17-AUG-1990; 90EP-0115815.
 XX PR 21-AUG-1989; 89JP-0212980.
 XX PR 20-DEC-1989; 89JP-0328198.
 XX PR 13-APR-1990; 90JP-0096252.
 XX PR 07-JUN-1990; 90JP-0147392.
 XX PA (TAKE) TAKEDA CHEMICALS IND KK.
 XX PI Kakinuma A, Nakahama K, Yoshimura K, Katsuo Y, Iwan M;
 XX DR WPI; 1991-059398/09.

DR N-PSDB: AA010620.

XX Human nerve growth factor containing cysteine residues - used as
 PT reagent and therapeutic drug for senile dementia.
 XX PS Claim 1; Fig 1; 33pp; English.

XX The sequence was deduced from a clone isolated from a lambda EXB13
 CC genomic library prep. from human leukocyte DNA, using a probe
 CC synthesized based on the sequence of the known human NGF gene [A.
 CC Ullrich et al., Nature 303, 821 (1983)]. The clone, betaLN2113,
 CC isolated from the library was cleaved with SmaI and ApaI to remove
 CC a 1kb fragment contg. the gene which was then inserted into plasmid
 CC pluscript IIK to obtain pNGFp107G. The gene was sequenced from
 CC this plasmid using Sequase (Biochemical). The sequence of the
 CC protein coding region was found to be in complete agreement with
 CC that of Ullrich et al. The sequence was used to produce
 CC recombinant h-NGF for use in the prodn. of drugs for e.g. senile
 CC dementia.

XX Sequence 241 AA:

Query Match 99.5%: Score 1270; DB 12; Length 241;
 Best local similarity 100.0%: Pred. No. 1.3e-134;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 MSMLFTTLTAFLIGIQAEPHSESNVPAGHTIPQVHMTKLQHSIDLALRRARSAPAAIA 61
 DB 1 MSMLFTTLTAFLIGIQAEPHSESNVPAGHTIPQVHMTKLQHSIDLALRRARSAPAAIA 60
 OY 62 ARVAGOTRNITVDPRLFKKRLRSRVLFTSTOPPREAADTODLDFEYGAAPFNRTHRK 121
 DB 61 ARVAGOTRNITVDPRLFKKRLRSRVLFTSTOPPREAADTODLDFEYGAAPFNRTHRK 120
 OY 122 RSSHPPIFRGEFSVCDVSVMGDKTTATDICKKEVNLGEVINNSVKQYFFETKCR 181
 DB 121 RSSHPPIFRGEFSVCDVSVMGDKTTATDICKKEVNLGEVINNSVKQYFFETKCR 180
 OY 182 DPNPVDSCGKIDSKHNSCTTHTFVKALTMQKQAAAFRIIDPACVLSRAVNR 241
 DB 181 DPNPVDSCGKIDSKHNSCTTHTFVKALTMQKQAAAFRIIDPACVLSRAVNR 240
 OY 242 A 242
 DB 241 A 241

RESULT 3

AAR13858
 ID AAR13858 standard; Protein; 241 AA.

XX AC AAR13858;
 XX DT 21-NOV-1991 (first entry)
 XX DE Human nerve growth factor.
 XX KW hNGF.
 XX OS Homo sapiens.
 XX PN JP03175976-A.
 XX PD 31-JUL-1991.
 XX PR 12-DEC-1989; 89JP-0320483.
 XX PR 30-SEP-1989; 89JP-0253796.
 XX PR 15-DEC-1989; 89JP-0314860.
 XX PR 12-DEC-1989; 89JP-0320483.
 XX PA (TAKE) TAKEDA CHEMICAL IND KK.

DR WPI: 1991-269694/37.
 DR N-PSDB: AAO13397.
 PT Secretory prep. of animal protein - by culturing
 PT Schizosaccharomyces pombe which retains DNA at 3'-terminal of
 PT promoter region.
 PS Disclosure: Fig 3: 12pp; Japanese.
 CC The amino acid sequence is encoded that of human nerve growth factor
 CC (NGF). It may be expressed in Schizosaccharomyces pombe using the
 CC glyceraldehyde-3-phosphate dehydrogenase (Gld) gene promoter.
 CC
 XX Sequence 241 AA:

Query Match 99.5%; Score 1270; DB 12; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1,3e-134;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MSMLFYTLITAFILGIGIAEPHSESNVPAGHTIPQVHMTKLQHSIDTALRRASAPAAIA 61
 DB 1 MSMLFYTLITAFILGIGIAEPHSESNVPAGHTIPQVHMTKLQHSIDTALRRASAPAAIA 60
 QY 62 ARVAGOTRNITVDPLFKKRLRSPRYLSTQPPREADTODLDFVCGAAPPNRTTHSK 121
 DB 61 ARVAGOTRNITVDPLFKKRLRSPRYLSTQPPREADTODLDFVCGAAPPNRTTHSK 120
 QY 122 RSSSHPIFRHGEFSVCDVSVMVGDKTATDINGKKEVMVLGEVINNSVFKQYFETICR 181
 DB 121 RSSSHPIFRHGEFSVCDVSVMVGDKTATDINGKKEVMVLGEVINNSVFKQYFETICR 180
 QY 182 DPNPVDSCGRCIDSKHNSICTTHTFVKALTMDSKQAAFRIRIDTACVLSKAVRR 241
 DB 181 DPNPVDSCGRCIDSKHNSICTTHTFVKALTMDSKQAAFRIRIDTACVLSKAVRR 240
 QY 242 A 242
 DB 241 A 241

RESULT 4

AA077419
 ID AAR77419 standard; Protein: 241 AA.

XX AAR77419;
 AC AAR77419;
 XX 10-FEB-1996 (first entry)
 DT Human nerve growth factor.
 DE Human nerve growth factor.
 KW Nerve growth factor; neurotrophic factor; therapeutic;
 KM protein refolding; NGF.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT 123..241
 FT /note= "mature protein"
 FT 1..121
 FT /note= "pre-region"

XX W09530686-A1.
 XX 16-NOV-1995.
 PD 02-MAY-1995: 95WO-US05423.
 XX 27-JUN-1994: 94US-0266080.
 PR 09-MAY-1994: 94US-0240122.
 XX (SYNT) SYNTX-SYNERGEN NEUROSCIENCE JOINT VENTU.
 PA Bonam D, Kohno T, Lile J, Rosendahl MS;
 PI

XX WPI: 1995-404080/51.
 DR N-PSDB: AAT05437.
 XX Process for bacterial expression of recombinant neurotrophic factor
 PT - useful for promoting the survival and maintaining phenotypic
 PT differentiation of nerve and glial cells.
 XX
 PS Disclosure: Page 33-34; 57pp; English.

CC The nerve growth factor (NGF) gene is expressed in Escherichia
 CC coli cells. The recombinant protein is solubilized and
 CC sulfonated and allowed to refold in the presence of PEG and urea.
 CC Biologically active NGF, used for promoting the survival of and
 CC maintaining the phenotypic differentiation of nerve and glial cells,
 CC is isolated and purified. This method breaks incorrectly formed
 CC disulfide bonds and allows refolding of the factor into the correct
 CC tertiary structure required for maximum yield of full active protein.
 CC
 XX Sequence 241 AA:

Query Match 99.5%; Score 1270; DB 16; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1,3e-134;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MSMLFYTLITAFILGIGIAEPHSESNVPAGHTIPQVHMTKLQHSIDTALRRASAPAAIA 61
 DB 1 MSMLFYTLITAFILGIGIAEPHSESNVPAGHTIPQVHMTKLQHSIDTALRRASAPAAIA 60
 QY 62 ARVAGOTRNITVDPLFKKRLRSPRYLSTQPPREADTODLDFVCGAAPPNRTTHSK 121
 DB 61 ARVAGOTRNITVDPLFKKRLRSPRYLSTQPPREADTODLDFVCGAAPPNRTTHSK 120
 QY 122 RSSSHPIFRHGEFSVCDVSVMVGDKTATDINGKKEVMVLGEVINNSVFKQYFETICR 181
 DB 121 RSSSHPIFRHGEFSVCDVSVMVGDKTATDINGKKEVMVLGEVINNSVFKQYFETICR 180
 QY 182 DPNPVDSCGRCIDSKHNSICTTHTFVKALTMDSKQAAFRIRIDTACVLSKAVRR 241
 DB 181 DPNPVDSCGRCIDSKHNSICTTHTFVKALTMDSKQAAFRIRIDTACVLSKAVRR 240
 QY 242 A 242
 DB 241 A 241

RESULT 5

AA066688
 ID AAR66688 standard; Protein: 241 AA.

XX AAR66688;
 AC AAR66688;
 XX 23-AUG-1995 (first entry)
 DT Human nerve growth factor.
 DE Human nerve growth factor.
 KW Human nerve growth factor; hNGF; polyclonal antibody;
 KM Immunogen; enzyme immunoassay.
 XX Homo sapiens.
 OS

XX Key Location/Qualifiers
 FH Peptide 1..18
 FT /label= sig_peptide
 FT Peptide 19..121
 FT /label= pro_peptide
 FT MISC-difference 8
 FT /note= "corresponding codon TCG"
 FT MISC-difference 59
 FT /note= "corresponding codon TAT"
 FT MISC-difference 173
 FT /note= "corresponding codon TAC"
 FT Disulfide-bond 136..201

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FT Disulfide-bond 179..229
XX Disulfide-bond 189..231
XX JF06317587-A.
XX
XX 15-MOV-1994.
XX
XX 14-FEB-1991; 91JP-0021181.
XX
XX 31-AUG-1990; 90JP-0231317.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX WPI; 1995-033116/05.
XX
XX N-PSDB; AA079871.
XX
XX Polyclonal antibody against human nerve growth factor (NGF) -
XX useful to detect human NGF, for diagnosis of disease
XX
XX Example 1; Pages 31-33; 35pp; Japanese.
XX
XX AA079871 encodes AAR65688 human nerve growth factor (hNGF), the
XX protein was used as an immunogen to generate a polyclonal
XX antibody against hNGF. The polyclonal antibody can be used
XX to detect and determine hNGF pref. by enzyme immunoassay.
XX
XX Sequence 241 AA:
XX
XX Query Match 99.5%; Score 1270; DB 16; Length 241;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-134;
XX Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 2 MSMLFTLTITAFILGIAOEPHSESNVPAGHTIPQVHWTKLOHSIDTALRRARSAPAAIA 61
XX 1 MSMLFTLTITAFILGIAOEPHSESNVPAGHTIPQVHWTKLOHSIDTALRRARSAPAAIA 60
XX
XX 62 ARVAGOTRNTITVDPRLFKRRRLSPRVLESTQPREAADTODLDFEYGAAPFNTRHSK 121
XX 61 ARVAGOTRNTITVDPRLFKRRRLSPRVLESTQPREAADTODLDFEYGAAPFNTRHSK 120
XX
XX 122 RSSSHPIFRHGEFSVCDVSVMVGDKTTATDIKKEVNVLGEVNINSVKOYFEETKCR 181
XX 121 RSSSHPIFRHGEFSVCDVSVMVGDKTTATDIKKEVNVLGEVNINSVKOYFEETKCR 180
XX
XX 182 DPNPVDGCGRIGDSKHMNSCTTHTFVKALTMGKQAAAFIRIDPACVCVLSRAVRR 241
XX 181 DPNPVDGCGRIGDSKHMNSCTTHTFVKALTMGKQAAAFIRIDPACVCVLSRAVRR 240
XX
XX 242 A 242
XX
XX 241 A 241
XX
XX RESULT 6
XX AAM26237
XX ID AAM26237 standard; Protein: 241 AA.
XX
XX AAM26237:
XX
XX 16-MAR-1998 (first entry)
XX
XX Human preproNGF.
XX
XX Fusion protein: hydrophilic spacer; recombinant; expression system;
XX carboxypeptidase; preproNGF.
XX
XX Homo sapiens.
XX
XX WO9728272-A1.
XX
XX 07-AUG-1997.
XX
XX 31-JAN-1997; 97MO-US01470.

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XX
XX 31-JAN-1996; 96US-0595043.
XX
XX (TECH-) TECHNOLOGENE INC.
XX
XX Sgarlato GD;
XX
XX WPI; 1997-402624/37.
XX
XX N-PSDB; AAT80162.
XX
XX Recombinant protein expression system for fusion protein production
XX - useful for high quantity production of authentic recombinant
XX proteins
XX
XX Example 6; Page 140-141; 194pp; English.
XX
XX A novel recombinant vector has been developed which comprises a
XX nucleotide sequence encoding a fusion protein. The fusion protein
XX comprises three domains joined together in order, from N-terminus to
XX C-terminus, of a first domain comprising a protein of interest, a second
XX domain comprising a hydrophilic spacer and an affinity domain, each
XX human preproNGF, used in example 6 of the present invention. The
XX recombinant vector is used for the production of authentic recombinant
XX proteins of interest. The method of the invention is useful for the
XX expression of fusion proteins capable of isolation by affinity
XX chromatography in pro- or eukaryotic cells. This method allows
XX for the efficient cleavage and generation of authentic proteins of
XX interest that do not contain extraneous (i.e. non-naturally occurring)
XX amino acids.
XX
XX Sequence 241 AA:
XX
XX Query Match 99.5%; Score 1270; DB 18; Length 241;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-134;
XX Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 2 MSMLFTLTITAFILGIAOEPHSESNVPAGHTIPQVHWTKLOHSIDTALRRARSAPAAIA 61
XX 1 MSMLFTLTITAFILGIAOEPHSESNVPAGHTIPQVHWTKLOHSIDTALRRARSAPAAIA 60
XX
XX 62 ARVAGOTRNTITVDPRLFKRRRLSPRVLESTQPREAADTODLDFEYGAAPFNTRHSK 121
XX 61 ARVAGOTRNTITVDPRLFKRRRLSPRVLESTQPREAADTODLDFEYGAAPFNTRHSK 120
XX
XX 122 RSSSHPIFRHGEFSVCDVSVMVGDKTTATDIKKEVNVLGEVNINSVKOYFEETKCR 181
XX 121 RSSSHPIFRHGEFSVCDVSVMVGDKTTATDIKKEVNVLGEVNINSVKOYFEETKCR 180
XX
XX 182 DPNPVDGCGRIGDSKHMNSCTTHTFVKALTMGKQAAAFIRIDPACVCVLSRAVRR 241
XX 181 DPNPVDGCGRIGDSKHMNSCTTHTFVKALTMGKQAAAFIRIDPACVCVLSRAVRR 240
XX
XX 242 A 242
XX
XX 241 A 241
XX
XX RESULT 7
XX AAM48886
XX ID AAM48886 standard; Protein: 241 AA.
XX
XX AAM48886:
XX
XX 12-OCT-1998 (first entry)
XX
XX Human prepro-nerve growth factor beta chain.
XX
XX Neurotrophin; nerve growth factor; NGF; human; purification;
XX hydrophobic interaction chromatography.
XX
XX Homo sapiens.
XX
XX

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FH	Key	Location/Qualifiers
FT	Protein	1..121
FT	Protein	/label= Prepro-Region
FT	Protein	122..241
FT	Modified-site	/label= MaL-protein
FT	Region	167
FT	Region	/note= "N-glycosylated"
FT	Region	179..189
FT	Region	/note= "conserved Cys-containing region involved in Cys knot motif"
FT	Region	229..231
FT	Region	/note= "conserved Cys-containing region involved in Cys knot motif"
XX		
PN	M09822234-A2.	
XX		
PD	22-MAY-1998.	
XX		
PF	14-NOV-1997;	97MO-US21068.
PR	29-MAY-1997;	970S-0047855.
PR	15-NOV-1996;	96US-0030838.
XX		
PA	(GETH) GENENTECH INC.	
PI	Beck JT, Burton LE, Schmeizer CH;	
XX		
DR	WPI: 1998-322333/28.	
XX		
PT	Isolation of neurotrophin(s) from, e.g. mis-folded or glycosylated variant(s) - using hydrophobic interaction chromatography,	
PT	optionally in combination with high performance cation exchange chromatography	
PS	Disclosure; Fig 4; 59pp; English.	
CC	This polypeptide comprises the human nerve growth factor (NGF)	
CC	beta chain precursor. Methods are provided for large-scale purification of neurotrophins, including mature NGF, suitable for clinical use. A claimed method comprises: (1) separating the neurotrophin from the other proteins using a hydrophobic interaction chromatography resin (HICR); and optionally (2) separating the neurotrophin from a chemical variant by high performance cation exchange chromatography (HCEC). The processes can also be used for purification of e.g. mouse NGF (see AA048887), brain-derived neurotrophic factor (see AA048888), neurotrophin-4/5 (see AA048890) and neurotrophin-3 (see AA048892). The processes allow separation of neurotrophins from various undesirable misprocessed, misfolded, size-, glycosylated or charge forms. They allow selective separation from their variants and other molecules, and from other polypeptides with high pI. The processes are applicable to starting materials from various sources, including fermentation broths or lysed bacterial or mammalian cells.	
SQ	Sequence	241 AA:
	Query Match	99.5%; Score 1270; DB 19; Length 241;
	Best local similarity	100.0%; Pred. No. 1,3e-134;
	Matches 241; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	2 MSMLFYLTIAFLIGIOAPHSSESNVPAGHTIPQVHYTKKLDHSLDTPLRRASAPAAATA	61
Db	1 MSMLFTLTIAFLIGIOAPHSSESNVPAGHTIPQVHYTKKLDHSLDTPLRRASAPAAATA	60
OY	62 ARVAGOTRNITVDPLRFKKRLRSFRVLSTQPREEAADODDLEFGAAPPNRTRSK	121
Db	61 ARVAGOTRNITVDPLRFKKRLRSFRVLSTQPREEAADODDLEFGAAPPNRTRSK	120
OY	122 RSSSHPIFHNGEFSVCDSSVMVGOKTATATIKNGEVNWGEVINNSVKOFEEFKCR	181
Db	121 RSSSHPIFHNGEFSVCDSSVMVGOKTATATIKNGEVNWGEVINNSVKOFEEFKCR	180
OY	182 DPAIVDSGGRGIDSKRMNSICTTTTFYKALTDMGOKAMREIRTDACVCVLSRAVR	241

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Db      161 DPNPVDSCRCIDSKHNNSTCTTHFFVNAKLTIDGQAMRRIRIDTACVLSKAVRR 240
OY      242 A 242
Db      241 A 241

RESULT 8
AAV07303
ID      AAY07303 standard: Protein; 241 AA.
XX
AC      AAY07303;
XX
DT      06-JUL-1999 (first entry)
XX
DE      Human nerve growth factor beta protein.
XX
KV      Cerebrospinal; axon; growth; mammal; spinal cord injury; lesion; NGF;
KV      expression vector; neurotrophin; nerve growth factor 2; neurotrophin 3;
KV      Nf3; voluntary motor function.
XX
XX      Homo sapIens.
OS
XX      MO9900148-A2.
XX
PD      07-JAN-1999.
XX
PF      30-JUN-1998; 98MO-US13778.
XX
PR      30-JUN-1997; 97US-0051255.
XX
PA      (REGC ) UNIV CALIFORNIA.
XX
XX      Gage FH, Gfill R, Tuszyński NH;
XX      WPI; 1999-095478/08.
XX      N-PSDB; AAX34366.
XX
PT      Treating spinal cord injuries in a mammal - by inducing growth of
PT      cerebrospinal projection axons using a recombinant vector for
PT      expressing CST neurotrophin
XX
XX      Disclosure: Fig 6; 49pp; English.
XX
XX      The invention relates to a method of inducing cerebrospinal projection
XX      (CST) axon growth in a mammal with a spinal cord injury that involves
XX      a CST lesion by delivering a recombinant expression vector for CST
XX      neurotrophin, such as this sequence - nerve growth factor beta. The
XX      method is used to induce partial recovery of voluntary motor function
XX      in a mammal after disruption of corticospinal projections in the spinal
XX      cord.
XX
XX      Sequence 241 AA:
XX
Query Match 99.5%; Score 1270; DB 20; Length 241;
Best Local Similarity 100.0%; Pred. No. 1,3e-134;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      2 MSMFTTLTAFLTAFLIGIOAPHSSESNVPAGHITIPQVHNTKLQHSIDTALRRASAPAAATA 61
Db      1 MSMFTTLTAFLTAFLIGIOAPHSSESNVPAGHITIPQVHNTKLQHSIDTALRRASAPAAATA 60
OY      62 ARAVAGOTRNTYDPRLEFKKRLRSRVLESTOPPREADODDLEFVGGAAPFNKTRSK 121
Db      61 ARAVAGOTRNTYDPRLEFKKRLRSRVLESTOPPREADODDLEFVGGAAPFNKTRSK 120
OY      122 RSSSHHIFHRGEFSVCDYSVAVGDKTATDICKGEVAVLGEVNIINSVEKQYFFETKCR 181
Db      121 RSSSHHIFHRGEFSVCDYSVAVGDKTATDICKGEVAVLGEVNIINSVEKQYFFETKCR 180
OY      182 DPNPVDSCRCIDSKHNNSTCTTHFFVNAKLTIDGQAMRRIRIDTACVLSKAVRR 241

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Db 181 DPNPVDSCGCKIDSKHMNSYCTTHTFVKALTMDCQQAAMRFTRIDACVLSRAKAVR 240
OY 242 A 242
Db 241 A 241

RESULT 9

AAB66929

ID AAB66929 standard; Protein: 241 AA.

AC AAB66929;

DT 17-APR-2001 (first entry)

DE Human NGF.

KM Human: neuroprotective; neuronal factor; NF; neurotrophin-3; NT-3;
KW neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
KW Huntington's chorea; nerve damage; nerve growth factor; NGF.

OS Homo sapiens.

PN US6174701-B1.

PD 16-JAN-2001.

PE 31-MAY-1995; 95US-0455741.

PR 15-MAR-1990; 90US-0494024.

PR 31-JAN-1995; 95US-0381030.

PR 12-DEC-1989; 89US-0449811.

PA (GETH) GENENTECH INC.

PI Rosenthal A, Winslow JM;

DR WPI: 2001-201803/20.

PT New nucleic acid encoding a neuronal factor (rat precursor
PT neurotrophin-3; NT-3), useful in the recombinant preparation of NT-3,
PT which is useful for enhancing the survival of nerve cells and treating
PT neurodegenerative diseases
PS Disclosure: Fig 3; 18pp; English.

CC The present invention relates to neuronal factor (NF; also known as
CC neurotrophin-3/NT-3; see AAF55829-AAF55830 and AAB66927-AA66928). NF
CC is useful in treating neurodegenerative diseases, e.g. Alzheimer's
CC disease, Parkinson's disease, Huntington's chorea and other conditions
CC characterised by necrosis or loss of neurons. NF is also useful for
CC treating damaged nerves, e.g. nerves damaged by traumatic conditions such
CC as burns or wounds. The present sequence is human nerve growth factor
CC (NGF), which was used in a sequence homology alignment with human NF
CC protein.

SQ Sequence 241 AA;

Query Match 99.5%; Score 1270; DB 22; Length 241;

Best Local Similarity 100.0%; Pred. No. 1.3e-134; Indels 0; Gaps 0;

Matches 241; Conservative 0; Mismatches 0;

OY 2 MSMLFTTLTAFLIGIOAEPHSESNVPAGHTIPVHNTKLOHSIDTLARRARSAAPAAATA 61
Db 1 MSMLFTTLTAFLIGIOAEPHSESNVPAGHTIPVHNTKLOHSIDTLARRARSAAPAAATA 60
OY 62 ARVAGOTRNTITVDPRLFFKKRLRSRVLESTOPPREADTODLDFEYGAAPFNRTHRSK 121
Db 61 ARVAGOTRNTITVDPRLFFKKRLRSRVLESTOPPREADTODLDFEYGAAPFNRTHRSK 120
OY 122 RSSNHPFRGSEFVCDSSVWVGDKTATDIDKEVNVGSEVNNINSVFKOYFEETKCR 181
Db 121 RSSNHPFRGSEFVCDSSVWVGDKTATDIDKEVNVGSEVNNINSVFKOYFEETKCR 180

OY 182 DPNPVDSCGCKIDSKHMNSYCTTHTFVKALTMDCQQAAMRFTRIDACVLSRAKAVR 241
Db 181 DPNPVDSCGCKIDSKHMNSYCTTHTFVKALTMDCQQAAMRFTRIDACVLSRAKAVR 240
OY 242 A 242
Db 241 A 241

RESULT 10

AAE18904

ID AAE18904 standard; Protein: 241 AA.

AC AAE18904;

DT 21-MAY-2002 (first entry)

DE Human beta nerve growth factor (NGF) protein.

KM Human: nerve growth factor; NGF; neurotrophin; cholinergic neuron;
KW gene therapy; neuroprotective; Alzheimer's disease; Parkinson's disease;
KW neurodegenerative condition; ALS; amyotrophic lateral sclerosis.

OS Homo sapiens.

PN WO200207774-A2.

PD 31-JAN-2002.

PE 17-MAY-2001; 2001WO-US16122.

PR 19-JUL-2000; 2000US-0620174.

PA (REGC) UNIV CALIFORNIA.

PI Tuszyński MH;

DR WPI: 2002-195846/25.

DR N-PSDB: AAD30144.

PT Delivering therapeutic neurotrophin to targeted defective, diseased or
PT damaged cholinergic neurons, useful for treating neurodegenerative
PT disease, comprises administering a neurotrophin encoding transgene into
PT the brain
PS Example 1; Fig 2; 38pp; English.

CC The invention relates to a method for delivering therapeutic neurotrophin
CC to targeted defective, diseased or damaged cholinergic neurons in
CC the mammalian brain. The method comprises delivering a neurotrophic
CC composition comprising a neurotrophin encoding transgene into one or more
CC delivery sites within a region of the brain containing targeted neurons.
CC The method is useful for treating neurodegenerative conditions such as
CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis
CC (ALS) in primates by stimulating the growth of neurons thus recovering
CC neurological function. The present sequence is human nerve growth factor
CC (NGF-2) protein which is a neurotrophin.

SQ Sequence 241 AA;

Query Match 99.5%; Score 1270; DB 23; Length 241;

Best Local Similarity 100.0%; Pred. No. 1.3e-134; Indels 0; Gaps 0;

Matches 241; Conservative 0; Mismatches 0;

OY 2 MSMLFTTLTAFLIGIOAEPHSESNVPAGHTIPVHNTKLOHSIDTLARRARSAAPAAATA 61
Db 1 MSMLFTTLTAFLIGIOAEPHSESNVPAGHTIPVHNTKLOHSIDTLARRARSAAPAAATA 60
OY 62 ARVAGOTRNTITVDPRLFFKKRLRSRVLESTOPPREADTODLDFEYGAAPFNRTHRSK 121
Db 61 ARVAGOTRNTITVDPRLFFKKRLRSRVLESTOPPREADTODLDFEYGAAPFNRTHRSK 120

OY 122 RSSHPHFHGRGEFVSVDVSVWGDKTATDINGKEVNVLGEVINNSVFKOYFEETKCR 181
DB 121 RSSHPHFHGRGEFVSVDVSVWGDKTATDINGKEVNVLGEVINNSVFKOYFEETKCR 180
OY 182 DPNPVDSCRGIDSKHMNSYCTTHTFVKALTMGKQAAAFRIRIDTACVLSRAVRR 241
DB 181 DPNPVDSCRGIDSKHMNSYCTTHTFVKALTMGKQAAAFRIRIDTACVLSRAVRR 240
OY 242 A 242
DB 241 A 241

RESULT 11
ABB04994
ID ABB04994 standard; Protein: 241 AA.
AC ABB04994;
DE 19-MAR-2002 (first entry)
DT Human beta nerve growth factor protein.
XX
XX Human: nerve growth factor 2; beta nerve growth factor; NGF-2; NT-3;
XX neurotrophin-3; nervous system growth factor; neuronal atrophy;
XX aging; brain; axonal growth; neuron; neurotrophic; neuroprotective;
XX anti-aging; cholinergic neuron growth stimulator; gene therapy.
XX Homo sapiens.
XX OS
XX US2001043920-A1.
XX PN
XX 22-NOV-2001.
XX PD
XX 05-DEC-2000; 2000US-0730790.
XX PE
XX 15-APR-1998; 98US-0060543.
XX PR
XX (TUSZ/) TUSZYNSKI M H.
XX PA (BLES/) BLESCH A.
XX PI Tuszynski MH, Blesch A;
XX DR WPI: 2002-105567/14.
XX DR N-PSDB; ABA92503.
XX PT Ameliorating neuronal atrophy and loss of accompanying normal aging
XX comprises delivering a transgene encoding a growth factor to a
XX mammalian brain to stimulate axon growth in cholinergic neurons -
XX PS Disclosure; Fig 6 1-2; 18pp; English.
XX
XX The present invention describes a method for ameliorating neuronal
XX atrophy and loss of accompanying normal aging in the mammalian brain.
XX The method comprises delivering a growth factor (GF)-encoding transgene
XX to preselected delivery sites in the brain, so that the encoded GF is
XX expressed in the brain and stimulates axonal growth in targeted
XX Gf-receptive neurons. The growth factor has neurotrophic, neuroprotective
XX and anti-aging activities, and can be used as a cholinergic neuron
XX growth stimulator and in gene therapy. The method is used to
XX ameliorating neuronal atrophy and loss of accompanying normal aging, in
XX the human brain. The present sequence represents human beta nerve growth
XX factor, which is given in the exemplification of the present invention.

SO Sequence 241 AA:
Query Match 99.5%; Score 1270; DB 23; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.3e-134;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 MSMLFTTLTAFLIGIOAEPRHSESNVPAGHTIPQVHMTKLOHSLDTALRRARSAPAAIA 61
DB 1 MSMLFTTLTAFLIGIOAEPRHSESNVPAGHTIPQVHMTKLOHSLDTALRRARSAPAAIA 60

OY 62 ARVAGOTRNTITVDPRLFKRRRLRSRVLFESTOPPREADTODLDFEYGAAPFNRTHRSK 121
DB 61 ARVAGOTRNTITVDPRLFKRRRLRSRVLFESTOPPREADTODLDFEYGAAPFNRTHRSK 120
OY 122 RSSHPHFHGRGEFVSVDVSVWGDKTATDINGKEVNVLGEVINNSVFKOYFEETKCR 181
DB 121 RSSHPHFHGRGEFVSVDVSVWGDKTATDINGKEVNVLGEVINNSVFKOYFEETKCR 180
OY 182 DPNPVDSCRGIDSKHMNSYCTTHTFVKALTMGKQAAAFRIRIDTACVLSRAVRR 241
DB 181 DPNPVDSCRGIDSKHMNSYCTTHTFVKALTMGKQAAAFRIRIDTACVLSRAVRR 240
OY 242 A 242
DB 241 A 241

RESULT 12
AAP40038
ID AAP40038 standard; Protein: 245 AA.
AC AAP40038;
DE 25-JAN-1992 (first entry)
DT Sequence encoded by portion of human beta-nerve growth factor
XX (NGF) chromosomal gene which includes an exon.
XX DE
XX Nerve damage; therapy.
XX KW
XX Homo sapiens.
XX OS
XX EP121338-A.
XX FN
XX 10-OCT-1984.
XX PD
XX 02-MAR-1984; 84EP-0301377.
XX PE
XX 03-MAR-1983; 83US-0471962.
XX PR
XX (GETH) GENENTECH INC.
XX PA Gray AM, Ullrich A;
XX PI WPI: 1984-251909/41.
XX DR N-PSDB; AAN40033.
XX DR Human beta-nerve growth factor free from other proteins - obtd.
XX PT by recombinant DNA techniques for treating nerve damage
XX PS Example; Fig 5; 42pp; English.
XX
XX The inventors claim human beta-nerve growth factor (NGF) free from
XX other proteins of human origin. Also claimed are the DNA sequence
XX encoding human beta-NGF operably linked with a DNA sequence capable
XX of effecting its expression in a recombinant host cell; a replicable
XX expression vector contg. the DNA; and host cells transformed with
XX the vector. The plasmid claimed is plasmid ph-beta-NGF trp 1. Using
XX CC the plasmid, larger amounts of pure beta-NGF are obtainable than by
XX CC extn. of natural materials, see e.g. EP-2139.
XX CX

SO Sequence 245 AA:
Query Match 99.5%; Score 1270; DB 5; Length 245;
Best Local Similarity 100.0%; Pred. No. 1.4e-134;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 MSMLFTTLTAFLIGIOAEPRHSESNVPAGHTIPQVHMTKLOHSLDTALRRARSAPAAIA 61
DB 5 MSMLFTTLTAFLIGIOAEPRHSESNVPAGHTIPQVHMTKLOHSLDTALRRARSAPAAIA 64
OY 62 ARVAGOTRNTITVDPRLFKRRRLRSRVLFESTOPPREADTODLDFEYGAAPFNRTHRSK 121

Db 65 ARVAGOTRNTITVDPRLFKRRRLSPRVLFSTQPPREADTDLDPEVGGAAFPNKRTHRSK 124
 Qy 122 RSSSHPIFRHGEFSCVDSVSWVGGDKTTATDICKGEVNLGEVNIINNSVFQYFEETKCR 181
 Db 125 RSSSHPIFRHGEFSCVDSVSWVGGDKTTATDICKGEVNLGEVNIINNSVFQYFEETKCR 184
 Qy 182 DPNPVDSCGCGIDSKHNSYCTTHTFEVKALTMDCQKAAAFRITDTCACVLSRKAAYR 241
 Db 185 DPNPVDSCGCGIDSKHNSYCTTHTFEVKALTMDCQKAAAFRITDTCACVLSRKAAYR 244
 Qy 242 A 242
 Db 245 A 245

RESULT 13
 AAR45241
 ID AAR45241 standard; Protein: 307 AA.
 AC AAR45241;
 DT 20-JUN-1994 (first entry)
 DE Human pre-pro nerve growth factor.
 KM Mature: beta-nerve growth factor; pre-pro portion;
 expression; NGF; hNGF; treatment; Alzheimer's Disease.
 OS Homo sapiens.
 FH Key
 FT Peptide 1..187
 FT /note="signal peptide"
 FT Peptide 188..307
 FT /note="mature peptide"
 PN US372063-A.
 PD 21-DEC-1993.
 PF 20-JUN-1989; 89US-0383118.
 PR 22-NOV-1988; 88US-0274878.
 PR 20-JUL-1989; 89US-0383118.
 PA (SYNT) SYNTEX USA INC.
 PI Baecher PA, Barnett JW, Burszky-Petlegrew H, Chan HM, Nguyen BT;
 PI Ward C;
 DR WPI: 1993-413401/51.
 DR N-PSDB: AA054283.
 PT Prodn. of active mature human beta-nerve growth factor in insect
 PT cells - using baculovirus expression system, and potential use of
 PT recombinant hNGF in treatment of Alzheimer's disease
 XX Disclosure: fig 1; 23pp; English.
 CC The sequence is that of human pre-pro nerve growth factor
 CC which was used in a method of producing biologically active
 CC mature human beta-nerve growth factor in insect cells.
 SO Sequence 307 AA;
 Qy Query Match 99.2%; Score 1267; DB 14; Length 307;
 Db Best Local Similarity 99.6%; Pred. No. 4.2e-134;
 Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 62 ARVAGOTRNTITVDPRLFKRRRLSPRVLFSTQPPREADTDLDPEVGGAAFPNKRTHRSK 121
 Db 127 ARVAGOTRNTITVDPRLFKRRRLSPRVLFSTQPPREADTDLDPEVGGAAFPNKRTHRSK 186
 Qy 122 RSSSHPIFRHGEFSCVDSVSWVGGDKTTATDICKGEVNLGEVNIINNSVFQYFEETKCR 181
 Db 187 RSSSHPIFRHGEFSCVDSVSWVGGDKTTATDICKGEVNLGEVNIINNSVFQYFEETKCR 246
 Qy 182 DPNPVDSCGCGIDSKHNSYCTTHTFEVKALTMDCQKAAAFRITDTCACVLSRKAAYR 241
 Db 247 DPNPVDSCGCGIDSKHNSYCTTHTFEVKALTMDCQKAAAFRITDTCACVLSRKAAYR 306
 Qy 242 A 242
 Db 307 A 307

RESULT 14
 AAB67865
 ID AAB67865 standard; Protein: 241 AA.
 AC AAB67865;
 DT 29-JUN-2001 (first entry)
 DE Amino acid sequence of a human polypeptide designated PTMA-8.
 KM PTMA: immune deficiency; infection; autoimmune disorder; wound closure;
 KM connective tissue disease; multiple sclerosis; rheumatoid arthritis;
 KM systemic lupus erythematosus; autoimmune pulmonary inflammation; ulcer;
 KM Guillain-Barre syndrome; autoimmune thyroiditis; myasthenia gravis;
 KM insulin dependent diabetes mellitus; graft-versus-host disease;
 KM autoimmune inflammatory eye disease; gut protection; gut regeneration;
 KM fibrosis; reperfusion injury; systemic cytokine damage.
 OS Homo sapiens.
 PN WO200123572-A2.
 PD 05-APR-2001.
 PF 29-SEP-2000; 2000WO-US41035.
 PR 30-SEP-1999; 99US-0156745.
 PR 06-OCT-1999; 99US-0158947.
 PR 13-OCT-1999; 99US-0158248.
 PR 06-DEC-1999; 99US-0169344.
 PR 29-JUN-2000; 2000US-0215048.
 PA (CURA-) CURAGEN CORP.
 PI Prayaga SK, Vernet C, Shinkets RA, Burgess C, Spletter KA;
 DR WPI: 2001-273512/28.
 DR N-PSDB: AAF80462.
 PT Novel polypeptides termed PTMA, and nucleic acids encoding PTMA,
 PT useful for detecting and treating diseases caused immune deficiencies -
 XX Claim 1: Page 20-22: 128pp; English.
 CC The present sequence represents a PTMA-8 (not defined) polypeptide. The
 CC sequence is derived from clone A1049825. The polypeptide is 26958.5
 CC daltons. PTMA polynucleotides and polypeptides are used in the
 CC manufacture of a medicament for treating a syndrome associated with a
 CC human disease, the disease selected from a pathology associated with
 CC PTMA. They may be useful in the treatment of various immune deficiencies
 CC and disorders. These immune deficiencies may be genetic or caused by
 CC viral as well as bacterial or fungal infections or may result from
 CC autoimmune disorders. Autoimmune disorders which may be treated using
 CC PTMA include, for example, connective tissue disease, multiple sclerosis,
 CC systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary

CC inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin
 CC dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease
 CC and autoimmune inflammatory eye disease. Additionally PTMA may also be
 CC useful to promote better or faster closure of non-healing wounds,
 CC including pressure ulcers, ulcers associated with vascular insufficiency,
 CC surgical and traumatic wounds. Furthermore, PTMA may also be useful for
 CC gut protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissue, and conditions resulting from
 CC systemic cytokine damage.

XX Sequence 241 AA:

Query Match 99.18; Score 1266; DB 22; Length 241;
 Best Local Similarity 99.68; Pred. No. 3.8e-134;
 Matches 240; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 MSMLFYTLITAFILGIOAEPSHESNVPAGHTIPQVHHTKLQHSLODALARASAPAAIA 61
 DB 1 MSMLFYTLITAFILGIOAEPSHESNVPAGHTIPQVHHTKLQHSLODALARASAPAAIA 60
 OY 62 ARVAGQTRNITVDPRLFKKRLRSRVLFTSTOPPREAADTQDDFEVGAAPFNRTNRSK 121
 DB 61 ARVAGQTRNITVDPRLFKKRLRSRVLFTSTOPPREAADTQDDFEVGAAPFNRTNRSK 120
 OY 122 RSSHPHIFHGEFSVCDVSVMVGDKTTATDINGKKEVNLGGEVNNINSVFKOYFETKCR 181
 DB 121 RSSHPHIFHGEFSVCDVSVMVGDKTTATDINGKKEVNLGGEVNNINSVFKOYFETKCR 180
 OY 182 DPNPVDSCGCGIDSKHNSCTTHTFVKALITMDGKQAMRFIRIDTACVCLSKRAVR 241
 DB 181 DPNPVDSCGCGIDSKHNSCTTHTFVKALITMDGKQAMRFIRIDTACVCLSKRAVR 240
 OY 242 A 242
 DB 241 A 241

RESULT 15

AAR37799
 ID AAR37799 standard; Protein: 307 AA.

XX AAR37799;
 XX 29-SEP-1993 (first entry)

XX Human NGF.

XX Chimeric; human; prepro; NGF; brain-derived neurotrophic factor;
 KW BDNF; chimera; fusion; mouse; nerve growth factor; peripheral;
 KW central; precursor; nervous system.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Region 1..187

XX Protein /note="Prepro region"

XX 188..307

XX /note="Mature NGF"

XX MO9310150-A.

XX 27-MAY-1993.

XX 13-NOV-1992: 92MO-US09792.

XX 14-NOV-1991: 91US-0792492.

XX (AMGE-) AMGEN.

XX (REG-) REGENERON PHARM INC.

XX Giles D, Hu SS, Ip N, Squinto SP, Yancopoulos GD;

XX WPI: 1993-182492/22.

DR N-PSDB; AAQ42571.

XX Eukaryotic expression of neurotrophins - using prepro region of a
 PT different neurotrophin for more efficient post-translational
 PT processing

XX Disclosure; fig 4: 80pp; English.

XX This sequence represents human nerve growth factor (NGF). The protein
 CC encoded by this sequence promotes the development of the peripheral
 CC nervous system and also influences the development and maintenance of
 CC specific populations of neurons in the central nervous system. Two
 CC major transcripts from the NGF gene result in a "long" and "short" NGF
 CC prepeptide. The "short" precursor contains a conventional signal
 CC sequence at the N-terminus which flanks the pro-region. The "long"
 CC precursor contains an additional "pro-region" at its N-terminal. No
 CC functional distinction has been elucidated between the "long" and
 CC "short" forms. Characteristics of NGF, such as isoelectric point and
 CC primary structure, are very similar to brain derived neurotrophic
 CC factor (BDNF). The NGF coding sequence may be used in the
 CC construction of a chimeric nucleic acid molecule to encode a prepro-
 CC NGF/BDNF chimera (see also AAQ42568-69).

XX Sequence 307 AA:

Query Match 99.18; Score 1266; DB 14; Length 307;
 Best Local Similarity 99.68; Pred. No. 5.5e-134;
 Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 MSMLFYTLITAFILGIOAEPSHESNVPAGHTIPQVHHTKLQHSLODALARASAPAAIA 61
 DB 67 MSMLFYTLITAFILGIOAEPSHESNVPAGHTIPQVHHTKLQHSLODALARASAPAAIA 126
 OY 62 ARVAGQTRNITVDPRLFKKRLRSRVLFTSTOPPREAADTQDDFEVGAAPFNRTNRSK 121
 DB 127 ARVAGQTRNITVDPRLFKKRLRSRVLFTSTOPPREAADTQDDFEVGAAPFNRTNRSK 186
 OY 122 RSSHPHIFHGEFSVCDVSVMVGDKTTATDINGKKEVNLGGEVNNINSVFKOYFETKCR 181
 DB 187 RSSHPHIFHGEFSVCDVSVMVGDKTTATDINGKKEVNLGGEVNNINSVFKOYFETKCR 246
 OY 182 DPNPVDSCGCGIDSKHNSCTTHTFVKALITMDGKQAMRFIRIDTACVCLSKRAVR 241
 DB 247 DPNPVDSCGCGIDSKHNSCTTHTFVKALITMDGKQAMRFIRIDTACVCLSKRAVR 306
 OY 242 A 242
 DB 307 A 307

Search completed: December 2, 2002, 15:08:37
 Job time : 50.2298 secs

GenCore version 5.1.3
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OM protein - protein search, using SW model

Run on: December 2, 2002, 15:05:43 : Search time 19.2919 Seconds
(Without alignments)
1205.921 Million cell updates/sec

Title: US-10-072-681-1

Sequence: 1 PMSMFTLTITAFILIGIAOE.....FIRIDPACVCLSRRAVRA 242

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR.*
2: PIR1.*
3: PIR2.*
4: PIR3.*
5: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1370	99.5	286 1	NGHUBM
2	1124	88.0	229 2	I46614
3	1107	86.7	245 2	I56570
4	1096	85.8	307 1	NGMSMG
5	1092	85.5	241 2	JL0097
6	1073	84.0	303 1	NGRTBA
7	788.5	61.7	243 2	A26311
8	773	60.5	235 2	S14481
9	675.5	52.9	243 2	I51193
10	658	51.5	125 2	A26312
11	649	50.8	246 2	A39218
12	484	37.9	117 2	I51709
13	481.5	37.7	194 2	I51709
14	481.5	37.7	257 2	C40304
15	472	37.0	258 2	S09155
16	471.5	36.9	257 2	I50400
17	471	36.9	282 2	I50400
18	455.5	35.4	116 2	NGNXTI
19	446.5	35.1	116 2	A38566
20	426	33.4	286 2	S50855
21	365	28.6	247 2	A40304
22	364	28.5	249 2	B40304
23	360	28.2	249 2	S12555
24	358.5	28.1	252 2	A30361
25	348.5	27.3	248 2	JC6183
26	343	26.9	236 2	JH0287
27	337.5	26.4	210 2	A42587
28	335	26.2	269 2	I51708
29	330.5	25.9	209 2	B42687

30	323.5	25.3	114 2	I84765	brain-derived neur
31	316.5	24.8	114 2	I50606	brain-derived neur
32	307.5	24.1	114 2	I51599	brain-derived neur
33	84.5	6.6	5126 2	S40450	ryanidine receptor
34	83	6.5	397 2	S52783	aspartic proteinase
35	80	6.3	835 2	C97322	probable alpha-ara
36	79.5	6.2	749 2	E86774	hypothetical prote
37	79	6.2	807 2	A53225	ecdysone-induced p
38	79	6.2	1095 2	T24061	hypothetical prote
39	78.5	6.1	513 2	A12555	hypothetical prote
40	78.5	6.1	701 2	T52384	hypothetical prote
41	78.5	6.1	742 2	T43520	condensin complex
42	78.5	6.1	1076 2	D82083	carbamoyl phosphat
43	78.5	6.1	1084 2	B64088	hemoglobin-binding
44	78.5	6.1	1609 2	E87243	probable cation tr
45	78	6.1	323 2	S69647	hypothetical prote

ALIGNMENTS

RESULT 1

nerve growth factor beta chain precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 18-Jun-1999
C:Accession: A01399; S10253
R:Ullrich, A.; Gray, A.; Berman, C.; Dull, T.J.
Nature 303, 821-825, 1983
A:Title: Human beta-nerve growth factor gene sequence highly homologous to that of mo
A:Reference number: A93305; MUID:83244969; PMID:6688123
A:Accession: A01399
A:Molecule type: DNA
A:Residues: 1-286 <B0R>
R:Berzani, G.; Pizzutti, A.; Ruggeri, E.I.; Fallini, A.; Sillani, V.; Sidoli, A.; Scarla
Nucleic Acids Res. 18, 4020, 1990
A:Title: cDNA sequence of human beta-NGF.
A:Reference number: S10253; MUID:90326556; PMID:2374737
A:Accession: S10253
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 46-286 <B0R>
A:Cross-references: EMBL:X52599; NID:929476; PIDN:CNA36832.1; PID:929477
C:Comment: Nerve growth factor is found in submaxillary gland in large quantities and
nic sensory ganglia in vivo and in vitro and to increase cellular neurotubule levels
C:Genetics:
A:Gene: GDB:NGFB
A:Cross-references: GDB:120233; OMIM:162030
A:Map position: 1p13.1-1p13.1
C:Complex: nerve growth factor is composed of two alpha chains, two beta chains, and
C:Subfamily: nerve growth factor beta chain
C:Keywords: glycoprotein; growth factor; submandibular gland
F:1-166/Domain: signal sequence and propeptide (fragment) #status predicted <SIG>
F:167-284/Product: nerve growth factor beta chain #status predicted <MAP>
F:26,114,159,211/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:181-246,224-274,234-276/Disulfide bonds: #status predicted

Query Match 99.5%; Score 1270; DB 1; Length 286;
Best local similarity 100.0%; Pred. No. 6, 2e-112;

Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	2	MSMFTLTITAFILIGIAOE	PHSESNVPA	GHITIPV	HTKLOHSLD	TALRA	SAPAA	AA	61
DB	46	MSMFTLTITAFILIGIAOE	PHSESNVPA	GHITIPV	HTKLOHSLD	TALRA	SAPAA	AA	105
QY	62	ARVAGTNRITITDPR	LFKKRLRS	PRVLF	STQPREA	ADTOD	LFVGA	APNR	121
DB	106	ARVAGTNRITITDPR	LFKKRLRS	PRVLF	STQPREA	ADTOD	LFVGA	APNR	165
QY	122	RSSSHPIFRGFSV	CDVSVM	GDCKTAT	DIKKEV	YVGEV	INNSV	KOVFE	181
DB	166	RSSSHPIFRGFSV	CDVSVM	GDCKTAT	DIKKEV	YVGEV	INNSV	KOVFE	225

F:135,180/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:202,267,245-295,255-297/Disulfide bonds: #status experimental
F:332/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 85.8%; Score 1096; DB 1; Length 307;
Best Local Similarity 85.0%; Pred. No. 1,7e-95;
Matches 204; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

OY 2 MSMLFYLITLAFILGIAEPHSESNVPAGHTIPQVHMTKLQHSIDLALRRASAPAAATA 61
DB 67 MSMLFYLITLAFILGIAEPHSESNVPAGHTIPQVHMTKLQHSIDLALRRASAPAAATA 126
OY 62 ARVAGOTRNTITVDPRFLFKRRRLSPRYLFTSTOPPREAADTODLDFEYGAAPFNTRHSK 121
DB 127 ARVAGOTRNTITVDPRFLFKRRRLSPRYLFTSTOPPREAADTODLDFEYGAAPFNTRHSK 186
OY 122 RSSSHPIFRHGEFSVCDSSVWVGDKTTATDIDKGEVNVGAEVNNINSVKOFEEFKCR 181
DB 187 RSSSHPIFRHGEFSVCDSSVWVGDKTTATDIDKGEVNVGAEVNNINSVKOFEEFKCR 246
OY 182 DPNPVDGCRGIDSKHNSCTTHTFVKALITMDGQAAMRFIRIDTACVLSRAKAVR 241
DB 247 ASNPVSGCRGIDSKHNSCTTHTFVKALITMDGQAAMRFIRIDTACVLSRAKAVR 306

RESULT 5

nerve growth factor beta chain precursor - guinea pig
C:Species: *Cavia porcellus* (guinea pig)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 15-Mar-1996

C:Accession: J10097
R:Schwarz, M.A.; Fisher, D.; Bradshaw, R.A.; Isackson, P.J.
J. Neurochem. 52, 1203-1209, 1989

A:Title: Isolation and sequence of a cDNA clone of beta-nerve growth factor from the guinea pig
A:Reference number: J10097; MUID:89177243; PMID:2926597

A:Accession: J10097
A:Molecule type: mRNA
A:Residues: 1-241 <SCH>
A:Note: the authors translated the codon GCU for residue 214 as Asp

C:Gene: *Beta-MGF*
C:Superfamily: nerve growth factor beta chain
C:Keywords: glycoprotein; growth factor; hormone
F:1-121/Domain: propeptide #status predicted <PRO>
F:122-241/Product: nerve growth factor beta chain #status predicted <MAT>
F:146-154/Region: receptor binding #status predicted
F:169,114/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 85.5%; Score 1092; DB 2; Length 241;
Best Local Similarity 86.2%; Pred. No. 2,9e-95;
Matches 207; Conservative 10; Mismatches 23; Indels 0; Gaps 0;

OY 2 MSMLFYLITLAFILGIAEPHSESNVPAGHTIPQVHMTKLQHSIDLALRRASAPAAATA 61
DB 1 MSMLFYLITLAFILGIAEPHSESNVPAGHTIPQVHMTKLQHSIDLALRRASAPAAATA 60
OY 62 ARVAGOTRNTITVDPRFLFKRRRLSPRYLFTSTOPPREAADTODLDFEYGAAPFNTRHSK 121
DB 61 ARVAGOTRNTITVDPRFLFKRRRLSPRYLFTSTOPPREAADTODLDFEYGAAPFNTRHSK 120
OY 122 RSSSHPIFRHGEFSVCDSSVWVGDKTTATDIDKGEVNVGAEVNNINSVKOFEEFKCR 181
DB 121 RSSSHPIFRHGEFSVCDSSVWVGDKTTATDIDKGEVNVGAEVNNINSVKOFEEFKCR 180
OY 182 DPNPVDGCRGIDSKHNSCTTHTFVKALITMDGQAAMRFIRIDTACVLSRAKAVR 241
DB 181 DPNPVDGCRGIDSKHNSCTTHTFVKALITMDGQAAMRFIRIDTACVLSRAKAVR 240

RESULT 6

nerve growth factor beta chain precursor - multimammate rat (*Mastomys natalensis*)
C:Species: *Mastomys natalensis*

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 18-Jun-1999
C:Accession: J10343
R:Fahnestock, M.; Bell, R.A.

Gene 69, 257-264, 1988
A:Title: Molecular cloning of a cDNA encoding the nerve growth factor precursor from *Mastomys natalensis*
A:Reference number: J10343; MUID:89172070; PMID:3234767

A:Accession: J10343
A:Molecule type: mRNA
A:Residues: 1-303 <FAH>
A:Cross-references: GB:M22748; NID:9202514; PIDN:AAA40599.1; PID:9202515
A:Note: It is uncertain whether Met-1 or Met-63 is the initiator
C:Superfamily: nerve growth factor beta chain
C:Keywords: glycoprotein; growth factor; homodimer; submaxillary gland
F:144-301/Product: nerve growth factor beta chain #status predicted <MAT>
F:131,176,228/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:198-263,241-291,251-293/Disulfide bonds: #status predicted

Query Match 84.0%; Score 1073; DB 1; Length 303;
Best Local Similarity 83.3%; Pred. No. 2,4e-93;
Matches 200; Conservative 17; Mismatches 23; Indels 0; Gaps 0;

OY 2 MSMLFYLITLAFILGIAEPHSESNVPAGHTIPQVHMTKLQHSIDLALRRASAPAAATA 61
DB 63 MSMLFYLITLAFILGIAEPHSESNVPAGHTIPQVHMTKLQHSIDLALRRASAPAAATA 122
OY 62 ARVAGOTRNTITVDPRFLFKRRRLSPRYLFTSTOPPREAADTODLDFEYGAAPFNTRHSK 121
DB 123 ARVAGOTRNTITVDPRFLFKRRRLSPRYLFTSTOPPREAADTODLDFEYGAAPFNTRHSK 182
OY 122 RSSSHPIFRHGEFSVCDSSVWVGDKTTATDIDKGEVNVGAEVNNINSVKOFEEFKCR 181
DB 183 RSSSHPIFRHGEFSVCDSSVWVGDKTTATDIDKGEVNVGAEVNNINSVKOFEEFKCR 242
OY 182 DPNPVDGCRGIDSKHNSCTTHTFVKALITMDGQAAMRFIRIDTACVLSRAKAVR 241
DB 243 ARNPVSGCRGIDSKHNSCTTHTFVKALITMDGQAAMRFIRIDTACVLSRAKAVR 302

RESULT 7

nerve growth factor beta chain precursor - chicken (fragment)
C:Species: *Gallus gallus* (chicken)
C:Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 21-Jul-2000

C:Accession: A26311; A24857; S00127; S12532
R:Ebdendal, T.; Larhammar, D.; Persson, H.
EMBO J. 5, 1483-1487, 1986

A:Title: Structure and expression of the chicken beta nerve growth factor gene.
A:Reference number: A26311; MUID:86300646; PMID:3017695
A:Accession: A26311

A:Molecule type: mRNA
A:Residues: 1-243 <EBE>
A:Cross-references: GB:X04003; NID:963697; PIDN:CAA27633.1; PID:91334740
R:Ylton, D.; Perret, C.; Frechlin, N.; Keller, A.; Behar, G.; Brechet, P.; Aufferay, C.
FEBS Lett. 203, 82-86, 1986
A:Title: Molecular cloning of the avian beta-nerve growth factor gene: transcription
A:Reference number: A24857; MUID:86248129; PMID:3720959
A:Accession: A24857

A:Molecule type: DNA
A:Residues: 118-243 <NIO>
A:Cross-references: GB:D00010; GB:N00010; GB:X04067; NID:9222840; PIDN:BA000008.1; PI
R:Weller, R.; Becker-Andre, M.; Goeltz, R.; Heumann, R.; Shaw, A.; Thoenen, H.
EMBO J. 5, 1489-1493, 1986
A:Title: Molecular cloning of bovine and chick nerve growth factor (NGF): delineation
A:Reference number: A26312; MUID:86300647; PMID:2427334
A:Accession: S00127

A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 121-243 <KEI>
A:Cross-references: GB:M26810; NID:9212446; PIDN:AAA48984.1; PID:9212447
R:Idanez, C.F.; Hallböök, F.; Ebdendal, T.; Persson, H.
EMBO J. 9, 1477-1483, 1990
A:Title: Structure-function studies of nerve growth factor: functional importance of
A:Reference number: S12532; MUID:90228346; PMID:2328722

A:Molecule type: DNA
A:Residues: 1-257 <ON>
A:Cross-references: GB:M37763; NID:9189300; PIDN:AAA5953.1; PID:9189301
R:Koselthel, A.; Goeddel, D.V.; Nguyen, T.; Lewis, M.; Shih, A.; Laramee, G.R.; Nikolic
Neuron 4, 767-773, 1990
A:Title: Primary structure and biological activity of a novel human neurotrophic factor
A:Reference number: JH0141; MUID:90265727; PMID:2344409
A:Accession: JH0141
A:Molecule type: DNA
A:Residues: 1-257 <ROS>
R:Malonpierre, P.C.; Le Beau, M.M.; Esplinoza III, R.; Ip, N.Y.; Belluscio, L.; de la Mc
Genomics 10, 558-568, 1991
A:Title: Human and rat brain-derived neurotrophic factor and neurotrophin-3: gene struc
A:Reference number: A40304; MUID:91365361; PMID:1889806
A:Accession: C40304
A:Molecule type: DNA
A:Residues: 1-257 <MAI>
A:Cross-references: GB:M61380; NID:9189302; PIDN:AAA63231.1; PID:9189303
R:Kishino, Y.; Yoshimura, K.; Nakahama, K.
FEBS Lett. 286, 187-191, 1990
A:Title: Cloning and expression of a cDNA encoding a novel human neurotrophic factor.
A:Reference number: S10719; MUID:90306351; PMID:2365067
A:Accession: S10719
A:Molecule type: mRNA
A:Residues: 1-257 <KAI>
R:Fanopoulos, G.D.; Malonpierre, P.C.; Ip, N.Y.; Aldrich, T.H.; Belluscio, L.; Boulton
Cold Spring Harb. Symp. Quant. Biol. 55, 371-379, 1990
A:Title: Neurotrophic factors, their receptors, and the signal transduction pathways the
A:Reference number: A60536; MUID:9111157; PMID:1966766
A:Accession: C60536
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-73, 'Q', '75-77', 'R', '79-108', 'T', '110-257' <YAN>
C:Genetics:
A:Gene: GDB:125917
A:Cross-references: GDB:125917; OMIM:162660
A:Map position: 12p13-12p13
C:Superfamily: nerve growth factor beta chain
C:Keywords: glycoprotein
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-138/Domain: propeptide #status predicted <PRO>
F:139-257/Product: neurotrophin-3 #status predicted <MAT>
F:131/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 37.7%; Score 481.5; DB 2; Length 257;
Best local similarity 40.7%; Pred. No. 1e-37;
Matches 107; Conservative 37; Mismatches 88; Indels 31; Gaps 6;
OY 2 MSNLFYTLTAFLIGIOAEPSSESNVPAGHTIPQV-----JMTKIDHSID 46
DB 1 MSILFYIFLAIKRGIOGNSMDORSLEPDSLNSLILKIDQADILKKNLSKOMVDKENVQ 60
OY 47 TALRNA-----RSAPPAALAAAVAGOTRNITVDPRLFK-KRRLSRPSVLESTOPREAA 98
DB 61 STLPKAEAPREPERGCPAKSAFOV-----IAMDTELLROQRVNSPVLSDSTPLEP 114
OY 99 ADTODLDEFGAAPPFNFTBRSKRSSHPIFHGSEFVSQSVWYCGDKTTATDIXGKEY 158
DB 115 PPLYLIMEDYVGSPPVYANNTSRKRYAEHK-SHREYSVCDSSESLWYTDKSSAIDIRGHQV 173
OY 159 MVLGEVNIINSVFOYFEETKCRDPNPVDSGCRGIDSKHNSYCTTHTFVKALTMW-GK 217
DB 174 TVLGEITKIGNSPVKQYFEYTRCKEARPVKNGCRGIDDKHNSQCKTSQTYVALTSNNK 233
OY 218 QAAMRFIRIDTACVCSVRKAVR 240
DB 234 LVGNRMIRIDTSCVCAUSKRIGR 256

RESULT 15
S09155
neurotrophin-3 precursor - mouse

C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999
A:Accession: S09155; S11179
R:Hohn, A.; Leibrock, J.; Bailey, K.; Barde, Y.A.
Nature 344, 339-341, 1990
A:Title: Identification and characterization of a novel member of the nerve growth fa
A:Reference number: S09155; MUID:90190865; PMID:2314473
A:Accession: S09155
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-258 <HOH>
A:Cross-references: GB:X53257; NID:953451; PIDN:CAA37348.1; PID:953452
R:Kolbeck, R.; Jungbluth, S.; Barde, Y.A.
Eur. J Biochem 225, 995-1003, 1994
A:Title: Characterization of neurotrophin dimers and monomers.
A:Reference number: S11179; MUID:95045576; PMID:7957235
A:Accession: S11179
A:Status: preliminary
A:Molecule type: protein
A:Residues: 140-152 <KOL>
C:Superfamily: nerve growth factor beta chain
C:Keywords: glycoprotein
F:1-18/Domain: signal sequence #status predicted <SIG>
F:140-258/Product: neurotrophin-3 #status predicted <MAT>
F:131/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 37.0%; Score 472; DB 2; Length 258;
Best local similarity 41.9%; Pred. No. 8e-37;
Matches 108; Conservative 33; Mismatches 97; Indels 20; Gaps 5;
OY 2 MSNLFYTLTAFLIGIOAEPSSESNVPAGH-----TIPQVHTKIDHSIDRAL----- 49
DB 1 MSILFYIFLAIKRGIOGNSMDORSLEPDSLNSLILKIDQADILKKNLSKOMVDKENVQ 60
OY 50 -----RRASAPPAALAAAVAGOTRNITVDPRLFKRRLSRPSVLESTOPREAAOTD 104
DB 61 STLPKAEAPREPERGCPAKSAFOV-----IAMDTELLROQRVNSPVLSDSTPLEP 120
OY 105 DFEVGAAPPNFTN-RSKRSSHPFIHGEFVSQSVWYCGDKTTATDIXGKEYAVLGE 163
DB 121 EDYVGNPVYANNTSRKRYAEHK-SHREYSVCDSSESLWYTDKSSAIDIRGHQVVLGE 179
OY 164 VNINSVFOYFEETKCRDPNPVDSGCRGIDSKHNSYCTTHTFVKALTMW-GKQAAVR 222
DB 180 IXTGNSPVKQYFEYTRCKEARPVKNGCRGIDDKHNSQCKTSQTYVALTSNNKLVGR 239
OY 223 FIRIDTACVCSVRKAVR 240
DB 240 WIRIDTSCVCAUSKRIGR 257

Search completed: December 2, 2002, 15:13:57
Job time: 20.2919 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 2, 2002, 15:05:43 ; Search time 9.92966 seconds

(without alignments)
1010.837 Million cell updates/sec

Title: US-10-072-681-1

Perfect score: 1277

Sequence: 1 PMSMLFTTLTAFLIGIOAE.....FTRIDACVLSRKAVARA 242

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1270	99.5	241	NGF_HUMAN
2	1124	88.0	229	NGF_PIG
3	1107	86.7	241	NGF_RAT
4	1106	86.6	231	NGF_BOVIN
5	1096	85.8	241	NGF_MOUSE
6	1092	85.5	241	NGF_CAVPO
7	1073	84.0	241	NGF_PRANA
8	788.5	61.7	243	NGF_CHICK
9	773	60.5	231	NGF_XENLA
10	675.5	52.9	243	NGF_XENLA
11	484	37.9	117	NGF_DABRR
12	481.5	37.7	194	NGF_XIPMA
13	481.5	37.7	257	NT3_HUMAN
14	474	37.1	260	NT3_XENLA
15	473.5	37.1	257	NT3_FELCA
16	472	37.0	258	NT3_MOUSE
17	471.5	36.9	257	NT3_CHICK
18	471	36.9	258	NT3_RAT
19	459.5	36.0	233	NT3_BRARE
20	449.5	35.2	116	NGF_NAJNA
21	445.5	34.9	116	NGF_NAJAT
22	372.5	29.2	140	NT7_CYPCA
23	365	28.6	247	BDNF_HUMAN
24	365	28.5	249	BDNF_RAT
25	364	28.4	255	BDNF_CAVPO
26	364	28.3	247	BDNF_PROLO
27	364	28.3	247	BDNF_URSAR
28	361	28.3	247	BDNF_URSAR
29	360	28.2	249	BDNF_MOUSE
30	358.5	28.1	247	BDNF_PIG
31	350	27.4	247	BDNF_FELCA
32	348.5	27.3	248	BDNF_BOVIN
33	347.5	27.2	246	BDNF_CHICK

34	343	26.9	236	NT4_XENLA	P24727 xenopus lae
35	338.5	26.5	270	BDNF_CYPCA	090332 cyprinus ca
36	337.5	26.4	210	NT5_HUMAN	P34130 homo sapien
37	335	26.2	269	BDNF_XIPMA	002133 xiphophorus
38	330.5	25.9	209	NT5_RAT	P25432 xenopus lae
39	323.5	25.3	114	BDNF_MACMU	006225 macaca mula
40	307.5	24.1	114	BDNF_XENLA	P25432 xenopus lae
41	230	18.0	257	NT6B_HUMAN	P34133 homo sapien
42	227	17.8	257	NT6A_HUMAN	P34132 homo sapien
43	225	17.6	186	NT6G_HUMAN	P34132 homo sapien
44	190	14.9	42	NGF_VIPLE	P25428 vipera lebe
45	136	10.6	154	NT3_CEREL	095150 cervus elap

ALIGNMENTS

```

RESULT 1
NGF_HUMAN
ID NGF_HUMAN STANDARD: PRT: 241 AA.
AC P01138:
DT 21-JUL-1986 (rel. 01, Created)
DT 01-JAN-1990 (rel. 13, Last sequence update)
DT 16-OCT-2001 (rel. 40, Last annotation update)
DE beta-nerve growth factor precursor (Beta-NGF).
GN NGF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83244963; PubMed=6688123;
RA Ullrich A., Gray A., Berman C., Dull T.J.;
RT "Human beta-nerve growth factor gene sequence highly homologous to
RL that of mouse."
RL Nature 303:821-825(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=84206565; PubMed=6327169;
RA Ullrich A., Gray A., Berman C., Coussens L., Dull T.J.;
RT "Sequence homology of human and mouse beta-NGF subunit genes."
RL Cold Spring Harb. Symp. Quant. Biol. 48:435-442(1983).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RX MEDLINE=90326556; PubMed=2374737;
RA Borsani G., Pizutti A., Ruggeri E.I., Fallini A., Silani V.,
RT "cdna sequence of human beta-NGF."
RL Nucleic Acids Res. 18:4020-4020(1990).
RN [4]
RP SEQUENCE OF 178-219 FROM N.A.
RX TISSUE=Leukocyte;
RX MEDLINE=9122573; PubMed=2025430;
RA Hallboeek F., Ibanez C.F., Persson H.;
RT "Evolutionary studies of the nerve growth factor family reveal a
RL novel member abundantly expressed in Xenopus ovary."
RN Neuron 6:845-856(1991).
RN [5]
RP FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
EMBRYONIC SENSORY NEURONS.
RN [6]
RP SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
RN [7]
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CC EMBL: V01511; CA224755.1; -
DR EMBL: M21062; AAA5931.1; -
DR EMBL: X52595; CA36832.1; -
DR PIR: A01399; NGHUBM.
DR PIR: S10253; S10253.
DR HSSP: P01139; 1BET.
DR Genew: HGNC:7808; NGFB.
DR MIM: 162030; -.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF_1.
DR PRINTS: PR00268; NGF.
DR ProDom: PD02052; NGF_1.
DR SMART: SM00140; NGF_1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS50270; NGF_2; 1.
DR Growth factor; Signal.
KW Growth factor; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT PROPEP 19 121
FT CHAIN 122 241 BETA-NERVE GROWTH FACTOR.
FT DISULFID 136 201 BY SIMILARITY.
FT DISULFID 179 229 BY SIMILARITY.
FT DISULFID 189 231 BY SIMILARITY.
FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 241 AA; 26987 MW; CFIDB4DC6B736B0F CRC64;

Query Match 99.5%; Score 1270; DB 1: Length 241;
Best Local Similarity 100.0%; Pred. No. 3e-113;
Matches 241: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 MSMLTYTLTFLIGIOAEPSHESNVPAHTIPQVHTKQLQHSLSLDPALRRASAPAAATA 61
DB 1 MSMLTYTLTFLIGIOAEPSHESNVPAHTIPQVHTKQLQHSLSLDPALRRASAPAAATA 60
OY 62 ARVAGOTRTNVDPPLFKRRRLSPRVLFSTOPPREAADODLDFEYGAAPNRTHRK 121
DB 61 ARVAGOTRTNVDPPLFKRRRLSPRVLFSTOPPREAADODLDFEYGAAPNRTHRK 120
OY 122 NSSSPPIHRRGEFSVCDVSVMGDKTTATDIDKGEVNLGEVINNSVFKOFFETKCR 181
DB 121 NSSSPPIHRRGEFSVCDVSVMGDKTTATDIDKGEVNLGEVINNSVFKOFFETKCR 180
OY 182 DNPVDSGCRGIDSKHNSYCTTHTTFVKALTMDSKQAAAFRTIDTACVLSRAVRA 241
DB 181 DNPVDSGCRGIDSKHNSYCTTHTTFVKALTMDSKQAAAFRTIDTACVLSRAVRA 240
OY 242 A 242
DB 241 A 241

RESULT 2
NGF_PIG STANDARD: PRT: 229 AA.
ID NGF_PIG
AC Q29074;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Beta-nerve growth factor precursor (Beta-NGF) (fragment).
GN NGFB.
OS Sus. scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Large white; TISSUE=Blood;
RX MEDLINE=94313891; PubMed=8039422;
RA Labib-Mansals T., Mellink C., Yezle M., Gellin J.;
RT "A new marker (NGFB) on pig chromosome 4, isolated by using a
RL cytogenet. Cell Genet. 67:120-125(1994).

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CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS.
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC
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CC
DR EMBL: L31898; AAA1301.1; -
DR HSSP: P01139; 1BET.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF_1.
DR ProDom: PD02052; NGF_1.
DR SMART: SM00140; NGF_1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS50270; NGF_2; 1.
DR Growth factor; Signal.
FT MON_TER 1 1
FT SIGNAL <1 6 POTENTIAL.
FT PROPEP 7 109 BETA-NERVE GROWTH FACTOR.
FT CHAIN 110 229 BY SIMILARITY.
FT DISULFID 124 189 BY SIMILARITY.
FT DISULFID 167 217 BY SIMILARITY.
FT DISULFID 177 219 BY SIMILARITY.
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 229 AA; 25275 MW; FE8890771CBA3189 CRC64;

Query Match 88.0%; Score 1124; DB 1: Length 229;
Best Local Similarity 92.6%; Pred. No. 2e-99;
Matches 212: Conservative 4; Mismatches 13; Indels 0; Gaps 0;

OY 14 LIGIOAEPSHESNVPAHTIPQVHTKQLQHSLSLDPALRRASAPAAATAARVAGOTRTNV 73
DB 1 LIGIOAEPSHESNVPAHTIPQVHTKQLQHSLSLDPALRRASAPAAATAARVAGOTRTNV 60
OY 74 DPLFKRRRLSPRVLFSTOPPREAADODLDFEYGAAPNRTHRKSSSPPIHRRGE 133
DB 61 DPLFKRRRLSPRVLFSTOPPREAADODLDFEYGAAPNRTHRKSSSPPIHRRGE 120
OY 134 FSVCDVSVMGDKTTATDIDKGEVNLGEVINNSVFKOFFETKCRDNPVDSGCRGI 193
DB 121 FSVCDVSVMGDKTTATDIDKGEVNLGEVINNSVFKOFFETKCRDNPVDSGCRGI 180
OY 194 DSKHNSYCTTHTTFVKALTMDSKQAAAFRTIDTACVLSRAVRA 242
DB 181 DSKHNSYCTTHTTFVKALTMDSKQAAAFRTIDTACVLSRAVRA 229

RESULT 3
NGF_RAT STANDARD: PRT: 241 AA.
ID NGF_RAT
AC P25427;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Beta-nerve growth factor precursor (Beta-NGF).
GN NGFB.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89037223; PubMed=3184206;

```

RA Whittemore S.R., Friedman P.L., Larhammar D.G., Persson H.,
 RA Gonzalez-Carvajal M., Holets V.R.,
 RT "Rat beta-nerve growth factor sequence and site of synthesis in the
 RT adult hippocampus.",
 RL J. Neurosci. Res. 20:403-410(1998).
 RM (2)
 RP SEQUENCE OF 178-219 FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE-Liver;
 RX MEDLINE-9122573; PubMed-2025430;
 RA Hallboeok F., Ibanez C.F., Persson H.,
 RT "Evolutionary studies of the nerve growth factor family reveal a
 RT novel member abundantly expressed in Xenopus ovary.",
 RL Neuron 6:845-858(1991).
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 CC EMBRYONIC SENSORY NEURONS.
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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 CC -----
 DR EMBL: M35589; AAA41697.1; ALT_INIT.
 DR HSSP: P01139; 1BET.
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF; 1.
 DR PRINTS: PR00268; NGF.
 DR PRODOM: PD002052; NGF; 1.
 DR SMART: SM00140; NGF; 1.
 DR PROSITE: PS00248; NGF_1; 1.
 DR PROSITE: PS00270; NGF_2; 1.
 KM Growth factor; Signal.
 FT SIGNAL 1 16
 FT PROPEP 19 121 POTENTIAL.
 FT CHAIN 122 241 BETA-NERVE GROWTH FACTOR.
 FT DISULFID 136 201 BY SIMILARITY.
 FT DISULFID 179 229 BY SIMILARITY.
 FT DISULFID 189 231 BY SIMILARITY.
 FT CARBOHYD 69 69 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHYD 114 114 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAc...) (POTENTIAL).
 SQ SEQUENCE 241 AA; 27009 MW; 665f42371563213D CRC64;
 Query Match 86.7%; Score 1107; DB 1; Length 241;
 Best Local Similarity 85.8%; Pred. No. 8.7e-98;
 Matches 206; Conservative 14; Mismatches 20; Indels 0; Gaps 0;
 Oy 2 MSMLFTLTITAFITGIAOEPHSESNVPAHGRTIPQVHTKLOHSDTALRRARSAAPAAIA 61
 Db 1 MSMLFTLTITAFITGIAOEPHSESNVPAHGRTIPQVHTKLOHSDTALRRARSAAPAAIA 60
 Oy 62 ARVAGOTRNITVDPRLFKRRRLSPRVLFSTOPPREADTODLDFEYGAAPFNRTKRSK 121
 Db 61 ARVAGOTRNITVDPRLFKRRRLSPRVLFSTOPPREADTODLDFEYGAAPFNRTKRSK 120
 Oy 122 RSSSHPIFRGSESVCDSSVAVGDKTATDIDKKEVAVGAEVAVINSVVKOFEETKCR 181
 Db 121 RSSSHPIFRGSESVCDSSVAVGDKTATDIDKKEVAVGAEVAVINSVVKOFEETKCR 180
 Oy 182 DPPVDSGCGIDSKHMSVCTTHTFVKALJMDGKQAMRFIDPACVLSRKAAR 241
 Db 181 APPVDSGCGIDSKHMSVCTTHTFVKALJMDGKQAMRFIDPACVLSRKAAR 240
 RESULT 4
 NGF_BOVIN
 ID NGF_BOVIN STANDARD: PRF: 231 AA.

AC P13600; O18969;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Beta-nerve growth factor precursor (beta-NGF) (fragment).
 GN NGF.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RX (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE-Blood;
 RX MEDLINE-97430845; PubMed-9284944;
 RA Eldique C., Laurent P., Hayes H., Rodellar C., Levezuel H.,
 RT "Assignment of the beta-nerve growth factor (NGF) to bovine
 RT chromosome 3 band q23 by in situ hybridization.",
 RL Cytogenet. Cell Genet. 77:306-307(1997).
 RM (2)
 RP SEQUENCE OF 107-231 FROM N.A.
 RX MEDLINE-86300647; PubMed-2427334;
 RA Meller R., Becker-Andre M., Gotz R., Heumann R., Shaw A., Thoenen H.,
 RT "Molecular cloning of bovine and chick nerve growth factor (NGF):
 RT delineation of conserved and unconserved domains and their
 RT relationship to the biological activity and antigenicity of NGF.",
 RL EMBO J. 5:1489-1493(1986).
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 CC EMBRYONIC SENSORY NEURONS.
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: Y09566; CA170759.1; -
 DR EMBL: M26809; AAA30666.1; -
 DR PIR: A26312; A26312.
 DR HSSP: P01139; 1BET.
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF; 1.
 DR PRODOM: PD002052; NGF; 1.
 DR SMART: SM00140; NGF; 1.
 DR PROSITE: PS00248; NGF_1; 1.
 DR PROSITE: PS00270; NGF_2; 1.
 KM Growth factor; Signal.
 FT SIGNAL 1 8
 FT PROPEP 9 111 POTENTIAL.
 FT CHAIN 112 231 BETA-NERVE GROWTH FACTOR.
 FT DISULFID 126 191 BY SIMILARITY.
 FT DISULFID 169 219 BY SIMILARITY.
 FT DISULFID 179 221 BY SIMILARITY.
 FT CARBOHYD 156 156 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHYD 118 118 L -> F (IN REF. 2).
 FT CONFLICT 161 161 L -> K (IN REF. 2).
 FT CONFLICT 230 231 AP -> RA (IN REF. 2).
 SQ SEQUENCE 231 AA; 25437 MW; 0160509291A118C CRC64;
 Query Match 86.6%; Score 1106; DB 1; Length 231;
 Best Local Similarity 90.7%; Pred. No. 1e-97;
 Matches 205; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
 Oy 12 AFIGIOAEPHSESNVPAHGRTIPQVHTKLOHSDTALRRARSAAPAAIAARVAGOTRNT 71
 Db 11 AFIGIOAEPHSESNVPAHGRTIPQVHTKLOHSDTALRRARSAAPAAIAARVAGOTRNT 71

DB 1 AFLIGIOAAPHESNVPAGHAIPQAMRIKLOHSLDTVLRRAHSAAGIARVAGQTHNI 60
 OY 72 TVDRLEFKRRRLSPVLESTOPPREADDTODLDFEYGAAPFNTRHRSKSSHPFHR 131
 DB 61 TVDPKLEFKRRRLSPVLESTOPPREADDTODLDFEAGAGASSFNTRHRSKSSHPVLHR 120
 OY 132 GEFVCSDSVWVGDKTATADIRKGEVNYLGVNINNSVEFQYFETCRDPNPDVSGCR 191
 DB 121 GEFVCSDSVWVGDKTATADIRKGEVNYLGVNINNSVEFQYFETCRDPNPDVSGCR 180
 OY 192 GIDSKHNSCTTHTTFVAKLTMDCNOAMNRFIRDTACVCLSRK 237
 DB 181 GIDAKHNSCTTHTTFVAKLTMDCNOAMNRFIRDTACVCLSRK 226
 RESULT 5
 NGF_MOUSE
 ID NGF_MOUSE STANDARD: PRT: 241 AA.
 AC POL139: 063864.
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Beta-nerve growth factor precursor (Beta-NGF).
 GN NGFB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID:10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-83167518; PubMed-6336309;
 RA Scott J., Selby M.J., Urdan M.S., Quiroga M., Bell G.I., Rutter W.J.;
 RT "Isolation and nucleotide sequence of a cDNA encoding the precursor
 RL of mouse nerve growth factor.";
 NL Nature 302:538-540(1983).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-83244969; PubMed-6688123;
 RA Ullrich A., Gray A., Berman C., Dull T.J.;
 RT "Human beta-nerve growth factor gene sequence highly homologous to
 RL that of mouse.";
 NL Nature 303:821-825(1983).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-84206565; PubMed-6327169;
 RA Ullrich A., Gray A., Berman C., Coussens L., Dull T.J.;
 RT "Sequence homology of human and mouse beta-NGF subunit genes.";
 RL Cold Spring Harb. Symp. Quant. Biol. 48:435-442(1983).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6; TISSUE-Submaxillary gland;
 RX MEDLINE-88038655; PubMed-3670303;
 RA Selby M.J., Edwards R., Sharp F., Rutter W.J.;
 RT "Mouse nerve growth factor gene: structure and expression.";
 RL Mol. Cell. Biol. 7:3057-3064(1987).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-93264919; PubMed-1284621;
 RA Yamamoto T., Yamakuni T., Okabe N., Amano T.;
 RT "Production and secretion of nerve growth factor by clonal striated
 RL muscle cell line, G8-1.";
 RL Neurochem. Int. 21:251-258(1992).
 RN [6]
 RP SEQUENCE OF 122-239.
 RX MEDLINE-73075048; PubMed-4566923;
 RA Angeletti R.H., Hermodson M.A., Bradshaw R.A.;
 RT "Amino acid sequences of mouse 2.5S nerve growth factor. II.
 RT Isolation and characterization of the thermolabile and peptic peptides
 RL and the complete covalent structure.";
 RL Biochemistry 12:100-115(1973).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE-92065986; PubMed-1956407;

RA McDonald N.O., Lapatto R., Murray-Rust J., Gunning J., Wlodaver A.,
 RA Blundell T.L.;
 RT "New protein fold revealed by a 2.3-A resolution crystal structure of
 RT nerve growth factor.";
 RL Nature 354:411-414(1991).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE-94260545; PubMed-8201620;
 RA Holland D.R., Coussens L.S., Meng W., Matthews B.W.;
 RT "Nerve growth factor in different crystal forms displays structural
 RT flexibility and reveals zinc binding sites.";
 RL J. Mol. Biol. 239:385-400(1994).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (3.15 ANGSTROMS) OF 7S COMPLEX.
 RC STRAIN-Swiss Webster; TISSUE-Submaxillary gland;
 RX MEDLINE-98035451; PubMed-9351801;
 RA Bax B., Blundell T.L., Murray-Rust J., McDonald N.O.;
 RT "Structure of mouse 7S NGF: a complex of nerve growth factor with
 RT four binding proteins.";
 RL Structure 5:1275-1285(1997).
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSOR NERVOUS SYSTEMS. IT
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 CC EMBRYONIC SENSOR NEURONS.
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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 CC -----
 DR EMBL: M35075; AAA39818.1; ALT_INIT.
 DR EMBL: V00836; CAA24221.1; ALT_INIT.
 DR EMBL: K01759; AAA39820.1; ALT_INIT.
 DR EMBL: M14805; AAA39821.1; ALT_INIT.
 DR EMBL: M17298; AAA37687.1; ALT_INIT.
 DR EMBL: M17296; AAA37687.1; JOINED.
 DR EMBL: M17297; AAA37687.1; JOINED.
 DR EMBL: S62089; CAB32081.2; ALT_SEQ.
 DR PIR: A01400; NCMSG.
 DR PDB: 1BET; 31-MAY-94.
 DR PDB: 1BTG; 08-MAR-96.
 DR PDB: 1SGF; 27-MAY-98.
 DR MGD; MGI:97321; NGFB.
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF; 1.
 DR PRINTS; PR00268; NGF.
 DR PRODOM; PD002052; NGF; 1.
 DR SMART; SM00140; NGF; 1.
 DR PROSITE; PS00248; NGF; 1.
 DR PROSITE; PS50270; NGF_2; 1.
 DR Growth factor; Signal; 3D-structure.
 FT SIGNAL; 1-18
 FT PROPEP; 19-121
 FT CHAIN; 122-241 BETA-NERVE GROWTH FACTOR.
 FT DISULFID; 136-201
 FT DISULFID; 179-229
 FT DISULFID; 189-231
 FT CARBOHYD; 69-69
 FT CARBOHYD; 114-114
 FT CONFLICT; 233-241
 FT SEQUENCE; 241 AA; 27076 MW; 164465E1DC550081 CRC64;
 Query Match 85.8%; Score 1096; DB 1; Length 241;
 Best Local Similarity 85.0%; Pred. No. 9,6e-97;
 Matches 204; Conservative 14; Mismatches 22; Indels 0; Gaps 0;
 2 MSALFTLTITAFILGIOAAPHESNVPAGHAIPQAMRIKLOHSLDTALRARSAPAAIA 61
 ||||||||||||||||||| : : : |||||||||||||||||||

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Db 1 MSMLFTYLTAFILGVAQEPYDSNVPEGSVPEAHMTKLQNSLDLTALRRASAPATA 60
OY 63 ARVACQTANITVDPRLEFKRRRLSPRVLFSTOPPREAATDODDFEVGGAAPFNTRHSK 121
DB 61 ARVGTQTNITVDPRLEFKRRRLSPRVLFSTOPPREAATDODDFEVGGAAPFNTRHSK 120
OY 122 RSSHPHFHNGEFSVCDVSVMVADKTATDIDKGEVNLGAEVNNINSVFOYFFETKCR 181
DB 121 RSSHPHFHNGEFSVCDVSVMVADKTATDIDKGEVNLGAEVNNINSVFOYFFETKCR 180
OY 182 DPNPVDSCGRCIDSKHNSYCTTHTFEKALTMDGKQAAARFRIDTACVLSRAVAR 241
DB 181 ASNPVSCGRCIDSKHNSYCTTHTFEKALTMDGKQAAARFRIDTACVLSRAVAR 240

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RESULT 6

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NGF_CAVPO STANDARD; PRT; 241 AA.
ID NGF_CAVPO
AC P19093;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Beta-nerve growth factor precursor (Beta-NGF).
GN NGFB.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.
OX NCBI_TaxID=101141;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=89177243; PubMed=2926397;
RX Schwarz M.A., Fisher D., Bradshaw R.A., Isackson P.J.;
RT "Isolation and sequence of a cDNA clone of beta-nerve growth factor
RT from the guinea pig prostate gland."
RL J. Neurochem. 52:1203-1209(1989).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS.
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
DR PIR: J10097; J10097.
DR HSSP: P01139; 1BET.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF.
DR PRINTS: PR00268; NGF.
DR PRODOM: PD002052; NGF.
DR SMART: SM00140; NGF.
DR PROSITE: PS00248; NGF_1;
DR PROSITE: PS02070; NGF_2; 1.
KW Growth factor; Signal.
FT SIGNAL 1 18
FT PROPEP 19 121
FT CHAIN 122 241
FT DISULFID 136 201
FT DISULFID 179 229
FT DISULFID 189 231
FT CARBOHYD 69 69
FT CARBOHYD 114 114
SQ SEQUENCE 241 AA; 26821 MW; 2FAE26B197804B84 CRC64;

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Query Match 85.5%; Score 1092; DB 1; Length 241;
Best Local Similarity 86.2%; Pred. No. 2,3e-96;
Matches 207; Conservative 10; Mismatches 23; Indels 0; Gaps 0;

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OY 2 MSMLFTYLTAFILGVAQEPHSESNVPAGHTIPQVHTKLOHSIDTLARRASAPATA 61
DB 1 MSMLFTYLTAFILGVAQEPHSESNVPAGHTIPQVHTKLOHSIDTLARRASAPATA 60
OY 62 ARVACQTANITVDPRLEFKRRRLSPRVLFSTOPPREAATDODDFEVGGAAPFNTRHSK 121
DB 61 ARVGTQTNITVDPRLEFKRRRLSPRVLFSTOPPREAATDODDFEVGGAAPFNTRHSK 120

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OY 122 RSSHPHFHNGEFSVCDVSVMVADKTATDIDKGEVNLGAEVNNINSVFOYFFETKCR 181
DB 121 RSSHPHFHNGEFSVCDVSVMVADKTATDIDKGEVNLGAEVNNINSVFOYFFETKCR 180
OY 182 DPNPVDSCGRCIDSKHNSYCTTHTFEKALTMDGKQAAARFRIDTACVLSRAVAR 241
DB 181 DPNPVDSCGRCIDSKHNSYCTTHTFEKALTMDGKQAAARFRIDTACVLSRAVAR 240

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RESULT 7

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NGF_PRANA STANDARD; PRT; 241 AA.
ID NGF_PRANA
AC P20675;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Beta-nerve growth factor precursor (Beta-NGF).
GN NGFB.
OS Praomys natalensis (African soft-furred rat) (Mastomys natalensis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
OC Mastomys.
OX NCBI_TaxID=10112;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=89172070; PubMed=3234767;
RX Fahnestock M., Bell R.A.;
RT "Molecular cloning of a cDNA encoding the nerve growth factor
RT precursor from Mastomys natalensis."
RL Gene 69:257-264(1988).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS.
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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CC -----
DR EMBL: M22748; AAA40599.1; AL1_INIT.
DR PIR: J10343; NGFTRA.
DR HSSP: P01139; 1BET.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF.
DR PRINTS: PR00268; NGF.
DR PRODOM: PD002052; NGF.
DR SMART: SM00140; NGF.
DR PROSITE: PS00248; NGF_1;
DR PROSITE: PS02070; NGF_2; 1.
KW Growth factor; Signal.
FT SIGNAL 1 18
FT PROPEP 19 121
FT CHAIN 122 241
FT DISULFID 136 201
FT DISULFID 179 229
FT DISULFID 189 231
FT CARBOHYD 69 69
FT CARBOHYD 114 114
SQ SEQUENCE 241 AA; 27035 MW; 8BFB207A1FB2E7 CRC64;

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Query Match 84.0%; Score 1073; DB 1; Length 241;
Best Local Similarity 83.3%; Pred. No. 1.5e-94;
Matches 200; Conservative 17; Mismatches 23; Indels 0; Gaps 0;

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OY 2 MSMLFTYLTAFILGVAQEPHSESNVPAGHTIPQVHTKLOHSIDTLARRASAPATA 61

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RA Hallboeck F., Ibanez C.F., Persson H.:
 RT "Evolutionary studies of the nerve growth factor family reveal a
 RL novel member abundantly expressed in Xenopus ovary.";
 CC Nucleic Acids Res. 1991;19(19):5845-5858.
 CC
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 CC SENSORY NEURONS.
 CC
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
 CC
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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 CC
 CC EMBL: X55716; CAA39249.1; ALT_INIT.
 CC PIR: S14481; S14481.
 CC
 CC HSP: P01139; 1BE7.
 CC InterPro: IP002072; NGF.
 CC Pfam: PF00243; NGF; 1.
 CC PRINTS: PR00268; NGF.
 CC PRODOM: PD002052; NGF; 1.
 CC SMART: SM00140; NGF; 1.
 CC PROSITE: PS00248; NGF_1; 1.
 CC PROSITE: PS50270; NGF_2; 1.
 CC Growth factor; Signal.
 CC
 CC SIGNAL 1 18
 CC PROPEP 19 114 POTENTIAL.
 CC CHAIN 115 231 NERVE GROWTH FACTOR.
 CC DISULFID 128 193 BY SIMILARITY.
 CC DISULFID 171 221 BY SIMILARITY.
 CC DISULFID 181 223 BY SIMILARITY.
 CC CARBOHYD 63 63 N-LINKED (GLCNAc...) (POTENTIAL).
 CC CARBOHYD 107 107 N-LINKED (GLCNAc...) (POTENTIAL).
 CC CARBOHYD 158 158 N-LINKED (GLCNAc...) (POTENTIAL).
 CC SEQUENCE 231 AA; 26416 MW; 72A04E7D00B858C5 CRC64;
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 Query Match 60.5%; Score 773; DB 1; Length 231;
 Best Local Similarity 63.6%; Pred. No. 3.9e-66;
 Matches 154; Conservative 27; Mismatches 41; Indels 20; Gaps 6;
 Oy 2 MSMLFYTLITAFILGIAEPHSESNVPAGHT---IP-QVHWTK-LQHSLSLTALRRANSA 55
 Db 1 MSMLFYTLITAFILGIAEPHSESNVPAGHT---IP-QVHWTK-LQHSLSLTALRRANSA 55
 Oy 56 PAALIAAVAGOTRNTITVDPLFLFKRRRLSPRYLSTOPPREAADTODLDFEYGAAPFN 115
 Db 50 -HGKLEAKESYFRNVTVDPLFLFKRRRLSPRYLSTOPPREAADTODLDFEYGAAPFN 115
 Oy 116 RTHSKSSSSHPFRHGEFVSCDSVWVGDKTTATIDIKGEVNLGVNINSVFOYF 175
 Db 108 KTIKAKR-TYHPVLHKGELSVSCDSVWVGDKTTATIDIKGEVNLGVNINSVFOYF 166
 Oy 176 EETKCRDPNVDSCGRGIDSKHNSYCTTTFVKALTDGKQAAKRFIRIDTACVLSR 236
 Db 167 EETKCRDPNVDSCGRGIDSKHNSYCTTTFVKALTDGKQAAKRFIRIDTACVLSR 236
 Oy 236 RK 237
 Db 227 RK 228
 RESULT 10
 NGF_BUNNU STANDARD: PRT: 243 AA.
 AC P34128;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Nerve growth factor precursor (NGF).
 OS Bungarus multicinctus (Many-banded krait).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Lophosaurops; Squamata; Serpentes; Colubroidea;
 CC Elapidae; Bungarinae; Bungarus.
 CC NCBI_TaxID=8616;
 CC
 CC [1]
 CC
 CC SEQUENCE FROM N.A.
 CC TISSUE=Venom gland;
 CC MEDLINE=93192074; PubMed=7916740;
 CC Danse J.M., Garner J.M.;
 CC "Molecular cloning of a cDNA encoding a nerve growth factor precursor
 CC from the krait, Bungarus multicinctus.";
 CC Growth Factors 8:77-86(1993).
 CC
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 CC SENSORY NEURONS.
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 CC -1- SUBUNIT: HOMODIMER.
 CC
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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 CC
 CC EMBL: S56212; AA25729.1; -
 CC HSP: P01139; 1BE7.
 CC InterPro: IP002072; NGF.
 CC Pfam: PF00243; NGF; 1.
 CC PRINTS: PR00268; NGF.
 CC PRODOM: PD002052; NGF; 1.
 CC SMART: SM00140; NGF; 1.
 CC PROSITE: PS00248; NGF_1; 1.
 CC PROSITE: PS50270; NGF_2; 1.
 CC Growth factor; Signal.
 CC
 CC SIGNAL 1 18 POTENTIAL.
 CC PROPEP 19 125 NERVE GROWTH FACTOR.
 CC CHAIN 126 243 BY SIMILARITY.
 CC DISULFID 139 204 BY SIMILARITY.
 CC DISULFID 182 232 BY SIMILARITY.
 CC DISULFID 192 234 BY SIMILARITY.
 CC SEQUENCE 243 AA; 27514 MW; E3F64B142179A08 CRC64;
 SO
 Query Match 52.9%; Score 675.5; DB 1; Length 243;
 Best Local Similarity 56.8%; Pred. No. 7.4e-57;
 Matches 137; Conservative 30; Mismatches 67; Indels 7; Gaps 4;
 Oy 2 MSMLFYTLITAFILGIAEPHSESNVPAGHT---HTIPQVHWTKLQHSLSLTALRRANSA 57
 Db 1 MSMLFYTLITAFILGIAEPHSESNVPAGHT---HTIPQVHWTKLQHSLSLTALRRANSA 57
 Oy 58 PAALIAAVAGOTRNTITVDPLFLFKRRRLSPRYLSTOPPREAADTODLDFEYGAAPFN 116
 Db 61 PAKSDDELGSAAANITVDPLFLFKRRRLSPRYLSTOPPREAADTODLDFEYGAAPFN 116
 Oy 117 THRSKSSSSHPFRHGEFVSCDSVWVGDKTTATIDIKGEVNLGVNINSVFOYF 176
 Db 120 NIMA-NNENHNVHNGEHSVSCDSVWVGDKTTATIDIKGEVNLGVNINSVFOYF 178
 Oy 177 EETKCRDPNVDSCGRGIDSKHNSYCTTTFVKALTDGKQAAKRFIRIDTACVLSR 236
 Db 179 EETKCRDPNVDSCGRGIDSKHNSYCTTTFVKALTDGKQAAKRFIRIDTACVLSR 238
 Oy 237 K 237
 Db 239 K 239

```

RESULT 11
NGF_DABRR STANDARD: PRT: 117 AA.
ID NGF_DABRR
AC P3094:
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Nerve growth factor (NGF).
OS Dabolia russelli russelli (Russell's viper) (Vipera russelli russelli).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubridae;
OC Viperidae; Viperinae; Dabolia.
OX NCBI_TaxID=31159;
RN [1]
RP SEQUENCE.
RC Tissue-Venom: PubMed-1477101;
RA MEDLINE-93120151; Inoue S., Ikeda K., Hayashi K.;
RT Koyama J.-I., Inoue S., Ikeda K., Hayashi K.;
RT "Purification and amino-acid sequence of a nerve growth factor from
RT the venom of Vipera russelli russelli."
RL Blochm. Biophys. Acta 1160:287-292(1992).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
CC NEURONS IN THE BRAIN.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC PIR: S28161; S28161.
CC HSSP: P01139; 1BET.
CC InterPro: IPR002072; NGF.
CC Pfam: PF00243; NGF.
CC PRINTS: PR00268; NGF.
CC PRODOM: PD002052; NGF.
CC SMART: SM00140; NGF.
CC PROSITE: PS00248; NGF.
CC PROSITE: PS0270; NGF.
CC Glycoprotein; Growth factor.
KM DISULFID 12 77 BY SIMILARITY.
FT DISULFID 55 105 BY SIMILARITY.
FT DISULFID 65 107 BY SIMILARITY.
FT CARBOHYD 21 21 N-LINKED (GLCNAC...)
SQ SEQUENCE 117 AA; 13283 MW; A64559C5FEC11F66 CRC64;

Query Match 37.9%; Score 484; DB 1; Length 117;
Best Local Similarity 74.1%; Pred. No. 4,4e-39;
Matches 83; Conservative 19; Mismatches 10; Indels 0; Gaps 0;

OY 126 HFFHRCESVCDVSVMWGDKTTATDIDKGEVNVGLGVNINNSVFKOYFEETKCRDPNP 185
DB 1 HPHMGGEFSCDVSVMWVANKTTATDIDKGVNVVAVDYNINNVYQYFEETKCRNP 60

OY 186 VDSGCGIDSKHNNSTCTTHTFVKALTMDCQAAWRFIRIDTACVCVLSRK 237
DB 61 VPSGCGIDAKHNNSTCTTDTFVALTMERNQASWREIRINTACVCVLSRK 112

RESULT 12
NGF_XIPMA STANDARD: PRT: 194 AA.
ID NGF_XIPMA
AC P34129;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Nerve growth factor precursor (NGF).
OS Xiphophorus maculatus (Southern platyfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Atherinomorpha;
OC Caprinodontiformes; Poeciliidae; Xiphophorus.
OX NCBI_TaxID=8083;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RA MEDLINE-92333301; PubMed-1629719;
RA Goltz R., Raulf F., Scharf M.;
RT "Brain-derived neurotrophic factor is more highly conserved in
RT structure and function than nerve growth factor during vertebrate
RT evolution."
RL J. Neurochem. 59:432-442(1992).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
CC NEURONS IN THE BRAIN.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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CC or send an email to license@sdb-eb.ch).
CC EMBL: X59941; CAA42566.1;
CC HSSP: P01139; 1BET.
CC InterPro: IPR002072; NGF.
CC Pfam: PF00243; NGF.
CC PRINTS: PR00268; NGF.
CC PRODOM: PD002052; NGF.
CC SMART: SM00140; NGF.
CC PROSITE: PS00248; NGF.
CC PROSITE: PS0270; NGF.
CC Growth factor; Signal.
KM SIGNAL 1 30 POTENTIAL.
FT PROPEP 31 79 NERVE GROWTH FACTOR.
FT CHAIN 80 194 BY SIMILARITY.
FT DISULFID 90 155 BY SIMILARITY.
FT DISULFID 133 183 BY SIMILARITY.
FT DISULFID 143 185 BY SIMILARITY.
SQ SEQUENCE 194 AA; 21596 MW; 0369E0FA51147AE CRC64;

Query Match 37.7%; Score 481.5; DB 1; Length 194;
Best Local Similarity 58.9%; Pred. No. 1,4e-38;
Matches 99; Conservative 13; Mismatches 39; Indels 17; Gaps 3;

OY 72 TVDPRLFKRRRLSPVLESTQPPREADYDOLDFE-VGGAAPNRHRRSSSHIF 130
DB 40 TVDPKLFKRRRLSPVLESTQPP-----DAEPAGGQGVSKRRRQPO-----H 83

OY 131 RGEFSVCDVSVMWGDKTTATDIDKGEVNVGLGVNINNSVFKOYFEETKCRDPNPVDSGC 190
DB 84 RGVSVCEVSVMWGNKXTATDISGREVTVLPYVININNVKKQYFEETKCHSPSGSRC 143

OY 191 RGISKHNSTCTTHTFVKALTMDCQAAWRFIRIDTACVCVLSRK 238
DB 144 LGIDARRHNSHCTSHTEFVALTSENQVAMRLIRINACVCVLSRK 191

RESULT 13
NT3_HUMAN STANDARD: PRT: 257 AA.
ID NT3_HUMAN
AC P20783;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (HDNF)
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

```

RA MEDLINE-90263277; PubMed-2344409;
 RA Rosenthal A., Goeddel D.V., Nguyen T., Lewis M., Shih A.,
 RA Laramee G.R., Nikolic K., Winslow J.W.;
 RT "Primary structure and biological activity of a novel human
 RT neurotrophic factor.";
 RL Neuron 4:767-773(1990).
 RM
 RP
 RP SEQUENCE FROM N.A.
 RX MEDLINE-91045937; PubMed-2236018;
 RA Jones K.R., Reichardt L.F.;
 RT "Molecular cloning of a human gene that is a member of the nerve
 RT growth factor family.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8060-8064(1990).
 RM
 RM
 RP SEQUENCE FROM N.A.
 RX MEDLINE-90306351; PubMed-2365067;
 RA Katsuo Y., Yoshimura K., Nakahama K.;
 RT "Cloning and expression of a cDNA encoding a novel human neurotrophic
 RT factor.";
 RL FEBS Lett. 266:187-191(1990).
 RM
 RM
 RP SEQUENCE FROM N.A.
 RX MEDLINE-91365361; PubMed-1899806;
 RA Maisonnier P.C., Le Beau M.M., Espinosa R. III, Ip N.Y.,
 RA Belluscio L., de la Monte S.M., Squinto S., Furch M.E.,
 RA Yancopoulos G.D.;
 RT "Human and rat brain-derived neurotrophic factor and neurotrophin-3:
 RT gene structures, distributions, and chromosomal localizations.";
 RL Genomics 10:558-568(1991).
 RM
 RM
 RP SEQUENCE OF 194-236 FROM N.A.
 RC TISSUE=Leukocyte;
 RX MEDLINE-9122573; PubMed-2025430;
 RA Hallboeck F., Ibanez C.F., Persson R.;
 RT "Evolutionary studies of the nerve growth factor family reveal a
 RT novel member abundantly expressed in xenopus ovary.";
 RL Neuron 6:845-858(1991).
 RM
 RM
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RA MEDLINE-95217877; PubMed-7703225;
 RA Robinson R.C., Radziejewski C., Stuart D.I., Jones E.Y.;
 RT "Structure of the brain-derived neurotrophic factor/neurotrophin 3
 RT heterodimer.";
 RL Biochemistry 34:4139-4146(1995).
 RM
 RM
 RP VARIANT GLU-76.
 RX MEDLINE-95251647; PubMed-7733919;
 RA Hattori M., Nanko S.;
 RT "Association of neurotrophin-3 gene variant with severe forms of
 RT schizophrenia.";
 RL Biochem. Biophys. Res. Commun. 209:513-518(1995).
 RM
 RM
 RP VARIANT GLU-76.
 RX MEDLINE-96253892; PubMed-8925252;
 RA Arinami T., Takekoshi K., Itokewa M., Hamaguchi H., Toru M.;
 RT "Failure to find associations of the CA repeat polymorphism in the
 RT first intron and the G1y-63/Glu-63 polymorphism of the neurotrophin-3
 RT gene with schizophrenia.";
 RL Psychiatr. Genet. 6:13-15(1996).
 RM
 RM
 RP FUNCTION: SEEMS TO PROMOTES THE SURVIVAL OF VISCERAL AND
 CC PROPRIOCEPTIVE SENSORY NEURONS.
 CC
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC
 CC -1- TISSUE SPECIFICITY: BRAIN AND PERIPHERAL TISSUES.
 CC
 CC -1- POLYMORPHISM: Variant Glu-76 (frequently reported as Glu-63) was
 CC thought to be associated with severe forms of schizophrenia. This
 CC does not seem to be the case.
 CC
 CC
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
 CC
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DR EMBL: X53655; CAA37703.1;
 DR EMBL: M37763; AAA59553.1;
 DR EMBL: M61180; AAA63231.1;
 DR PIR: JH0141; JH0141.
 DR PIR: A36208; A36208.
 DR PIR: S10719; S10719.
 DR PIR: C40304; C40304.
 DR PDB: 1BND; 04-APR-96.
 DR PDB: 1B8K; 09-FEB-99.
 DR Genew: HGNC:8023; NTF3.
 DR MIM: 162660;
 DR InterPro: IPR002400; GF_cysknob.
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF.1.
 DR PRINTS: PR00438; GRCYSKNOT.
 DR PRINTS: PR00268; NGF.
 DR PRODOM: PD002052; NGF; 1.
 DR SMART: SM00140; NGF; 1.
 DR PROSITE: PS00248; NGF_1; 1.
 DR PROSITE: PS00270; NGF_2; 1.
 KW Growth factor; Signal; Polymorphism; 3D-structure.
 FT SIGNAL 1 16
 FT PROPEP 17 138
 FT CHAIN 139 237 NEUROTROPHIN-3.
 FT DISULFID 152 217
 FT DISULFID 195 246
 FT DISULFID 205 248
 FT CARBOHYD 131 131
 FT VARIANT 76 76
 SO SEQUENCE 257 AA; 29354 MW; 39A5B5328E25E03 CRC64;
 Query Match 37.7%; Score 481.5; DB 1; Length 257;
 Best Local Similarity 40.7%; Pred. No. 2e-38;
 Matches 107; Conservative 37; Mismatches 88; Indels 31; Gaps 6;
 2 MSNLFYTLTAFLIGIOAEPHSESNVPAGHTIPQV-----HRTKQHSID 46
 1 MSILFVIFALTRKQCNNDONSLEPDSLSLITLIDADLKLRKSKOVAVENKIO 60
 47 TALRRA-----KSAPAAIAIARVAGOTRNITVDPLRF-KRLNLSPVLFSTOPREA 98
 61 SLFPAEAPREEREGCPAKSAFOV-----IANDTELROQRVNSPVLISDSTPLEP 114
 99 ADTODLFEVGAAPFNTRHSKRSSSHPIFRGCEFSVDSVWVGDDTTATDRIKGEY 158
 115 PLYLMEDEVGSPVYVANTSRKRYAEK-SHREYEVCSDESLSVMTDKSSAIDIRGNOY 173
 159 NVLGEVNTNNSYFKRYFETCRDPNPYDSCGRIDSKHNSCTTHTFVALTMD-GK 217
 174 TVLGEIKGNSFVKQYFETRCRARPKNKCGRIDKIDKHNSSCKTSQTYVALTSNNK 233
 218 QAAMFRIDRTACVLSRKAAR 240
 234 LVGMWRIRIDTSCVCAISRKRGR 256
 RESULT 14
 NT3_XENLA
 ID NT3_XENLA STANDARD: PRT; 260 AA.
 AC P25435;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Neurotrophin-3 precursor (NT-3) (neurotrophic factor) (HNF) (nerve
 DE growth factor 2) (NGF-2).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodinae; Xenopus.


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OX NCBI_TaxID=8355;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97252639; PubMed=9096131;
RA Xie K., Wang T., Olafsson P., Mizuno K., Lu B.;
RT "Activity-dependent expression of NT-3 in muscle cells in culture:
RL implications in the development of neuromuscular junctions.";
RN (2)
RP SEQUENCE OF 197-217 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=9122573; PubMed=1025430;
RA Hallboeck F., Ihanez C.F., Persson H.;
RT "Evolutionary studies of the nerve growth factor family reveal a
RL novel member abundantly expressed in Xenopus ovary.";
RX Neuron 6:845-858(1991).
CC -1- FUNCTION: SEEMS TO PROMOTES THE SURVIVAL OF VISCERAL AND
CC PROPRIOCEPTIVE SENSORY NEURONS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE NCF-BETA FAMILY.
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CC -----
DR EMBL: U27576; AAB17723.1; -.
DR HSP: P20783; 188K.
DR InterPro: IPR002400; GF_cysknob.
DR InterPro: IPR002072; NCF.
DR Pfam: PF00243; NCF; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRODOM: PD002052; NCF; 1.
DR SMART: SM00140; NCF; 1.
DR PROSITE: PS00248; NCF_1; 1.
DR PROSITE: PS50270; NCF_2; 1.
DR Growth factor; Signal.
KW SIGNAL.
FT PROPEP 17 141
FT CHAIN 142 260
FT DISULFID 155 220
FT DISULFID 198 249
FT DISULFID 208 251
FT CARBOHYD 134 134
SQ SEQUENCE 260 AA; 30022 MW; FFB8507A5EA93CC5 CRC64;

Query Match 37.18; Score 474; DB 1; Length 260;
Best Local Similarity 41.58; Pred. No. 1e-37;
Matches 108; Conservative 36; Mismatches 94; Indels 22; Gaps 7;

OY 2 MSMLFTLLTAFLIGIOAEPHSESNVPAQH-----TIPQVHMTK---LDHSLDTALRRA 52
DB 1 MSILFTVMEFLPYCGIHATNMKRLPENSNLSLEFKILQADLKNKISKQVDTENHQ 60
OY 53 RSAPAAIAIARVAGOTRN-----ITVDPRLF---KRRRLSRPVLFSOTPREADQ 102
DB 61 STLPKQIILLDGDNDNMKQDPVIVSLAEALVKQKQNRKSPVLLSDLPLEPPPLX 120
OY 103 DLDFEVCAGAPF-NRTHRSKRSSHPIFHGRFESVCDVSVWGDKTATADINKREVMVL 161
DB 121 LMDVYIGHSTVNNKTSRRKRAEHR-GHREGYSVCDSESLAVTDKMAIDIRGHOTVTL 179
OY 162 GEVNNINSVEKQYFETFCRDPNPVDSGCGIDSKHNSYCTTHTFPKALIND-GKQAA 220
DB 180 GEIKTGSPPVKYFETTRCKEARPVKNGCGIDKHNMSCKTSOTYVRALDTSNNKMG 229
OY 221 WRIRIDTACVCLSRKAVR 240

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DB 240 WRIRIDTSCVCLSRKIGR 259

RESULT 15
ID NCBI_TaxID STANDARD: PRT: 257 AA.
AC 09PST2;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (HDNF)
DE (Nerve growth factor 2) (NGF-2).
GN NT-3.
OS Fells silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Fells.
OX NCBI_TaxID=9685;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=10211727; PubMed=10745216;
RA Iain E.S., Hohn A., Shatz C.J.;
RT "Dynamic regulation of BDNF and NT-3 expression during visual system
RL development.";
RX J. Comp. Neurol. 420:1-18(2000).
CC -1- FUNCTION: SEEMS TO PROMOTES THE SURVIVAL OF VISCERAL AND
CC PROPRIOCEPTIVE SENSORY NEURONS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE NCF-BETA FAMILY.
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CC -----
DR EMBL: AF192538; AAF03424.1; -.
DR HSP: P20783; 188K.
DR InterPro: IPR002072; NCF.
DR Pfam: PF00243; NCF; 1.
DR PRINTS: PR00268; NCF.
DR PRODOM: PD002052; NCF; 1.
DR SMART: SM00140; NCF; 1.
DR PROSITE: PS00248; NCF_1; 1.
DR PROSITE: PS50270; NCF_2; 1.
DR Growth factor; Signal.
KW SIGNAL.
FT PROPEP 17 138
FT CHAIN 139 257
FT DISULFID 152 217
FT DISULFID 195 246
FT DISULFID 205 248
FT CARBOHYD 131 131
SQ SEQUENCE 257 AA; 29403 MW; EB53F7E59C51138A CRC64;

Query Match 37.18; Score 473.5; DB 1; Length 257;
Best Local Similarity 40.18; Pred. No. 1e-37;
Matches 103; Conservative 40; Mismatches 95; Indels 19; Gaps 5;

OY 2 MSMLFTLLTAFLIGIOAEPHSESNVPAQHITPQV-----HMTLQHSLO 46
DB 1 MSILFTVMEFLPYCGIHATNMKRLPENSNLSLEFKILQADLKNKISKQVDTENHQ 60
OY 47 TALRRASAPAAIAIARVAGOTRNIT-VDPRLFK-KRRRLSRPVLFSOTPREADQDL 104
DB 61 STLPKQIILLDGDNDNMKQDPVIVSLAEALVKQKQNRKSPVLLSDLPLEPPPLX 120
OY 105 DFEVGAAPFNKTHRSKRSSHPIFHGRFESVCDVSVWGDKTATADINKREVMVL 164
DB 121 EDVYGSPVAANRTSRRKRAEHR-SHREGYSLCDSESLAVTDKSAIDIRGHOTVGEI 179
OY 165 NINNSVFKQYFETFCRDPNPVDSGCGIDSKHNSYCTTHTFPKALIND-GKQAA 223

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Db 180 KSGNSPVKQYFETRCKEARPYKNGCRGIDKHNNSOCKTSQTYVRALTSNNKLYGRM 239
QY 224 IRIDTACVCLSRRAVR 240
Db 240 IRIDTSCVCLSRKIGR 256

Search completed: December 2, 2002, 15:12:42
Job time : 10.9297 secs

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OW protein - protein search, using sw model

Run on: December 2, 2002, 15:05:42 ; Search time 37.449 Seconds
(without alignments)
1331.501 Million cell updates/sec

Title: US-10-072-681-1

Perfect score: 1377

Sequence: 1 PMSMLFTTLTAFLICIOAE.....FTRIDTACVCYLKRAVRA 242

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP_RMBL_21:*
2: SP_Archaea:*
3: SP_Bacteria:*
4: SP_Fungi:*
5: SP_Human:*
6: SP_Invertebrate:*
7: SP_Mammal:*
8: SP_Pbhc:*
9: SP_Organelle:*
10: SP_Pbhc:*
11: SP_Pbhc:*
12: SP_Pbhc:*
13: SP_Virus:*
14: SP_Virus:*
15: SP_Virus:*
16: SP_Virus:*
17: SP_Virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1265	99.1	241	4	09UKL8
2	1265	99.1	241	4	09P208
3	1258	98.5	241	4	08P650
4	1249	97.8	241	6	09N2F0
5	1248	97.7	241	6	09N2F1
6	1247	97.7	241	6	09N2E9
7	1132	88.6	217	6	09N183
8	1038	81.3	294	11	09N184
9	713	55.8	241	13	09DE29
10	709	55.5	241	13	09QW38
11	462	36.2	87	4	09P2C3
12	459	35.9	87	4	09P2C4
13	449.5	35.2	132	11	09W015
14	426.5	33.4	241	6	09N182
15	426	33.4	286	13	091988
16	363	28.4	247	6	097759

17	360	28.2	249	11	08VNH4	08vnh4 mus musculus
18	342.5	26.8	246	13	08OC74	08qg74 cyclophilops
19	341.5	26.7	246	13	08OC76	08qg76 japaalura sp
20	339.5	26.6	270	13	09YH42	09y42 brachydania
21	335.5	26.3	246	11	08OC75	08qg75 phrynoceph
22	334.5	26.2	153	11	09CYL3	09cy13 mus musculus
23	331.5	26.0	177	13	09RIL2	09r12 poephille gu
24	319	25.0	247	13	08OC77	08qg77 tylocroctito
25	294.5	23.1	101	6	09P2C2	09p22 macaca fusc
26	293	22.9	324	13	09X95	09x95 lampetra fl
27	291	22.8	186	11	09S09	09s09 fowlpox vir
28	282	21.0	52	6	09N1V4	09n1v4 equus caball
29	226	17.7	85	6	002790	002790 macropus fu
30	224	17.5	42	6	002802	002802 trichosurus
31	220	17.2	85	6	013114	013114 isodon mac
32	220	17.2	85	6	013122	013122 tarsipes ro
33	220	17.2	85	6	002795	002795 orlithorbyn
34	220	17.2	85	6	002798	002798 petaurus br
35	220	17.2	85	6	013104	013104 ceratetus
36	220	17.2	85	6	002792	002792 notoryctes
37	220	17.2	85	6	013105	013105 dasyuroides
38	220	17.2	85	6	002801	002801 techylosu
39	219	17.1	85	6	002803	002803 trichosurus
40	211	16.5	42	6	002794	002794 orlithorbyn
41	209	16.4	42	6	002800	002800 tachylosu
42	178.5	14.0	186	6	09BFI4	09bf14 lemur calca
43	178.5	14.0	186	6	09BFI1	09bf1 castor cana
44	176.5	13.8	186	6	09BFI7	09bf7 ochotona hy
45	175	13.7	185	6	09BFI6	09bf6 calpa alai

ALIGNMENTS

RESULT 1

09UKL8 ID 09UKL8 PRELIMINARY; PRT: 241 AA.

AC 09UKL8; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Nerve growth factor B.

GN NGFB

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-9925629; PubMed-10322959;

RA Tong Y., Wang H., Chen W.,

RT Cloning and sequencing of the gene for premature beta nerve growth

factor.

RL Chung Kuo Ying Yung Sheng Li Hsueh Tsa Chih 13:316-318(1997).

RN [2]

RP SEQUENCE FROM N.A.

RA Tong Y., Wang H.,

RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF15960; AAD5975.1; -.

DR HSSP; P01139; 1BE7.

DR InterPro; IPR02072; NGF.

DR Pfam; PF00243; NGF; 1.

DR PRINTS; PR00268; NGF.

DR ProDom; PD002052; NGF; 1.

DR SMART; SM00140; NGF; 1.

DR SMART; PS00248; NGF; 1.

DR PROSITE; PS00270; NGF; 2; 1.

DR PROSITE; PS00270; NGF; 2; 1.

SO SOURCE

241 AA; 26959 MW; 619DFC65EB3BD671 CRC64;

Query Match

Best Local Similarity 99.1%; Score 1265; DB 4; Length 241;

Matches 240; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
OY 2 MSMLFTLTITAFILGIGIOAEPHSESNVPAAGHTIPQVHMTKLOHSLDTALRRARSAAPAAATA 61
DB 1 MSMLFTLTITAFILGIGIOAEPHSESNVPAAGHTIPQVHMTKLOHSLDTALRRARSAAPAAATA 60
OY 62 ARVAGOTRNTITVDPRLFKKRLRSLPRVLFSTQPREAADTODLDFEYVGAAPFNRTHRSK 121
DB 61 ARVAGOTRNTITVDPRLFKKRLRSLPRVLFSTQPREAADTODLDFEYVGAAPFNRTHRSK 120
OY 122 RSSSHPIFRHGEFSCVDSVSWVWGDKTTATDIDKKEVNWLCGEVNNINSVFQYFFETKCR 181
DB 121 RSSSHPIFRHGEFSCVDSVSWVWGDKTTATDIDKKEVNWLCGEVNNINSVFQYFFETKCR 180
OY 182 DPNPVDGCGIGIDSKHNSYCTTHTFVKALTMDCQAAMRFIRIDTACVLSRKAARR 241
DB 181 DPNPVDGCGIGIDSKHNSYCTTHTFVKALTMDCQAAMRFIRIDTACVLSRKAARR 240
OY 242 A 242
DB 241 A 241
```

```
RESULT 2
O9P208 PRELIMINARY: PRT: 241 AA.
AC O9P208:
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Beta-nerve growth factor (Fragment).
GN BETA-NGF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kitanu T., Kobayakawa H., Saitou N.;
RT "Silver Project";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DB EMBL: AB037519; BAA90437.1; -.
DR HSSP: P01139; 1BET.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF. 1.
DR PRINTS: PR00268; NGF. 1.
DR ProDom: PD002052; NGF. 1.
DR SMART: SM00140; NGF. 1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS00270; NGF_2; 1.
FT NON_TER 241
SQ SEQUENCE 241 AA: 26998 MW: D5531ED825D96C14 CRC64:
```

Query Match 99.1%; Score 1265; DB 4; Length 241;
Best Local Similarity 99.6%; Pred. No. 8,3e-117;
Matches 240; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 241 A 241

```
RESULT 3
O96P60 PRELIMINARY: PRT: 241 AA.
AC O96P60:
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Nerve growth factor beta.
GN NGF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Zhang B., Zhou Y., Peng X., Yuan J., Qiang B.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DB EMBL: AF11526; AAI05874.1; -.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF. 1.
DR ProDom: PD002052; NGF. 1.
DR PROSITE: PS00248; NGF_1; UNKNOWN_1.
DR PROSITE: PS00270; NGF_2; 1.
SQ SEQUENCE 241 AA: 26964 MW: 745216485C21E558 CRC64:
```

Query Match 98.5%; Score 1258; DB 4; Length 241;
Best Local Similarity 98.8%; Pred. No. 4.1e-116;
Matches 238; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
OY 2 MSMLFTLTITAFILGIGIOAEPHSESNVPAAGHTIPQVHMTKLOHSLDTALRRARSAAPAAATA 61
DB 1 MSMLFTLTITAFILGIGIOAEPHSESNVPAAGHTIPQVHMTKLOHSLDTALRRARSAAPAAATA 60
OY 62 ARVAGOTRNTITVDPRLFKKRLRSLPRVLFSTQPREAADTODLDFEYVGAAPFNRTHRSK 121
DB 61 ARVAGOTRNTITVDPRLFKKRLRSLPRVLFSTQPREAADTODLDFEYVGAAPFNRTHRSK 120
OY 122 RSSSHPIFRHGEFSCVDSVSWVWGDKTTATDIDKKEVNWLCGEVNNINSVFQYFFETKCR 181
DB 121 RSSSHPIFRHGEFSCVDSVSWVWGDKTTATDIDKKEVNWLCGEVNNINSVFQYFFETKCR 180
OY 182 DPNPVDGCGIGIDSKHNSYCTTHTFVKALTMDCQAAMRFIRIDTACVLSRKAARR 241
DB 181 DPNPVDGCGIGIDSKHNSYCTTHTFVKALTMDCQAAMRFIRIDTACVLSRKAARR 240
OY 242 A 242
DB 241 A 241
```

```
RESULT 4
O9N2F0 PRELIMINARY: PRT: 241 AA.
AC O9N2F0:
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Beta-nerve growth factor (Fragment).
GN BETA-NGF.
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-GORILLA-01;
RA Kitanu T., Kobayakawa H., Saitou N.;
RT "Silver Project";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DB EMBL: AB037519; BAA90439.1; -.
DR
```

DR HSSP: P01139; 1BET.
DR InterPro: IPR002072; NCF.
DR Pfam: PF00243; NCF; 1.
DR PRINTS: PR00268; NCF; 1.
DR PRODOM: PD002052; NCF; 1.
DR SMART: SM00140; NCF; 1.
DR PROSITE: PS00248; NCF_1; 1.
DR PROSITE: PS00270; NCF_2; 1.
DR NON_TER 241 241
SQ SEQUENCE 241 AA; 26915 MW; 6F5AD163C84BB34 CRC64;

Query Match 97.8%; Score 1249; DB 6; Length 241;
Best Local Similarity 98.8%; Pred. No. 3.1e-115;
Matches 238; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 MSMLFTLTATLTAFLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAATA 61
DB 1 MSMLFTLTATLTAFLIGIOAEHSESNVPAGHTIPQAHMTKLOHSLDTALRRASAPAAATA 60
OY 62 ARVAGOTRNITVDPRLEFKRRRLSPRVLESTOPPREAADTODLDFEVGAAPFNRTHSK 121
DB 61 ARVAGOTRNITVDPRLEFKRRRLSPRVLESTOPPREAADTODLDFEVGAAPFNRTHSK 120
OY 122 RSSHPHFHGFSEVCDVSVMVGDKTATDIDKEVMVLGEVINNSVFOYFEETKCR 181
DB 121 RSSHPHFHGFSEVCDVSVMVGDKTATDIDKEVMVLGEVINNSVFOYFEETKCR 180
OY 182 DPNPVDSCGCGIDSKHNSYCTTHTFVKALTMGKQAAAFRIRIDTACVLSRAVRR 241
DB 181 DPNPVDSCGCGIDSKHNSYCTTHTFVKALTMGKQAAAFRIRIDTACVLSRAVRR 240
OY 242 A 242
DB 241 A 241

RESULT 5

ID 09N2F1 PRELIMINARY; PRT; 241 AA.
AC 09N2F1.
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Beta-nerve growth factor (Fragment).
GN BETA-NGF.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CHMP-220;
RA Kitano T., Kobayakawa H., Saitou N.;
RT "Silver Project."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB037518; BAA90438.1; -
DR HSSP: P01139; 1BET.
DR InterPro: IPR002072; NCF.
DR Pfam: PF00243; NCF; 1.
DR PRINTS: PR00268; NCF; 1.
DR PRODOM: PD002052; NCF; 1.
DR SMART: SM00140; NCF; 1.
DR PROSITE: PS00248; NCF_1; 1.
DR PROSITE: PS00270; NCF_2; 1.
DR NON_TER 241 241
SQ SEQUENCE 241 AA; 26868 MW; B39FA8912C00A0B CRC64;

Query Match 97.7%; Score 1248; DB 6; Length 241;
Best Local Similarity 98.3%; Pred. No. 3.9e-115;
Matches 237; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 MSMLFTLTATLTAFLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAATA 61
DB 1 MSMLFTLTATLTAFLIGIOAEHSESNVPAGHTIPQAHMTKLOHSLDTALRRASAPAAATA 60

DB 1 MSMLFTLTATLTAFLIGIOAEPHSESNVPAGHTIPQAHMTKLOHSLDTALRRASAPAAATA 60
OY 62 ARVAGOTRNITVDPRLEFKRRRLSPRVLESTOPPREAADTODLDFEVGAAPFNRTHSK 121
DB 61 ARVAGOTRNITVDPRLEFKRRRLSPRVLESTOPPREAADTODLDFEVGAAPFNRTHSK 120
OY 122 RSSHPHFHGFSEVCDVSVMVGDKTATDIDKEVMVLGEVINNSVFOYFEETKCR 181
DB 121 RSSHPHFHGFSEVCDVSVMVGDKTATDIDKEVMVLGEVINNSVFOYFEETKCR 180
OY 182 DPNPVDSCGCGIDSKHNSYCTTHTFVKALTMGKQAAAFRIRIDTACVLSRAVRR 241
DB 181 DPNPVDSCGCGIDSKHNSYCTTHTFVKALTMGKQAAAFRIRIDTACVLSRAVRR 240
OY 242 A 242
DB 241 A 241

RESULT 6

ID 09N2E9 PRELIMINARY; PRT; 241 AA.
AC 09N2E9.
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Beta-nerve growth factor (Fragment).
GN BETA-NGF.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ORAN-01;
RA Kitano T., Kobayakawa H., Saitou N.;
RT "Silver Project."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB037520; BAA90440.1; -
DR HSSP: P01139; 1BET.
DR InterPro: IPR002072; NCF.
DR Pfam: PF00243; NCF; 1.
DR PRINTS: PR00268; NCF; 1.
DR PRODOM: PD002052; NCF; 1.
DR SMART: SM00140; NCF; 1.
DR PROSITE: PS00248; NCF_1; 1.
DR PROSITE: PS00270; NCF_2; 1.
DR NON_TER 241 241
SQ SEQUENCE 241 AA; 26876 MW; DEC168E74E01F15 CRC64;

Query Match 97.7%; Score 1247; DB 6; Length 241;
Best Local Similarity 98.3%; Pred. No. 4.9e-115;
Matches 237; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 MSMLFTLTATLTAFLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAATA 61
DB 1 MSMLFTLTATLTAFLIGIOAEHSESNVPAGHTIPQAHMTKLOHSLDTALRRASAPAAATA 60
OY 62 ARVAGOTRNITVDPRLEFKRRRLSPRVLESTOPPREAADTODLDFEVGAAPFNRTHSK 121
DB 61 ARVAGOTRNITVDPRLEFKRRRLSPRVLESTOPPREAADTODLDFEVGAAPFNRTHSK 120
OY 122 RSSHPHFHGFSEVCDVSVMVGDKTATDIDKEVMVLGEVINNSVFOYFEETKCR 181
DB 121 RSSHPHFHGFSEVCDVSVMVGDKTATDIDKEVMVLGEVINNSVFOYFEETKCR 180
OY 182 DPNPVDSCGCGIDSKHNSYCTTHTFVKALTMGKQAAAFRIRIDTACVLSRAVRR 241
DB 181 DPNPVDSCGCGIDSKHNSYCTTHTFVKALTMGKQAAAFRIRIDTACVLSRAVRR 240
OY 242 A 242
DB 241 A 241

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RESULT 7
09N183 PRELIMINARY; PRT: 217 AA.
ID 09N183:
AC 09N183:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Beta nerve growth factor (Fragment).
OS Macaca fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OC NCBI_TaxID=9542;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BL00D;
RA MEDLINE=99270338; PubMed=10340513;
RX Okuno H., Tokuyama W., Li Y.X., Hashimoto T., Miyashita Y.;
RT "Quantitative evaluation of neurotrophin and trk mRNA expression in
RT visual and limbic areas along the occipito-temporo-hippocampal pathway
RT in adult macaque monkeys."
RL J. Comp. Neurol. 408:378-398(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BL00D;
RA Okuno H., Tokuyama W., Li Y.X., Hashimoto T., Miyashita Y.;
RX Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF222682; AAF33790.1;
DR HSSP: P01139; 1BET.
DR InterPro: IPR002072; NCF.
DR Pfam: PF00243; NCF.1.
DR PRINTS: PR00268; NCF.
DR PRODOM: PD002052; NCF.1.
DR SMART: SM00140; NCF.1.
DR PROSITE: PS00248; NCF_1; 1.
DR PROSITE: PS50270; NCF_2; 1.
FT NON_TER 1
FT SEQUENCE 217
SQ SEQUENCE 217 AA; 24240 MM; 36A5A2D1DFCD8D5C CRC64;

Query Match 88.6%; Score 1132; DB 6; Length 217;
Best Local Similarity 98.2%; Pred. No. 9.8e-104;
Matches 213; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 APLIGIOAEPHSESNVPGHTIPQVHTKLOHSIDTLRRARSAPAAIAIARVAGOTRNT 71
DB 1 APLIGIOAEPHSESNVPGHTIPQVHTKLOHSIDTLRRARSAPAAIAIARVAGOTRNT 60
QY 72 TVDPRLEKRRRLSPRVLESTOPPREAADTODLDFEVGGAAPFNRHRSKRSSHPIFHR 131
DB 61 TVDPRLEKRRRLSPRVLESTOPPREAADTODLDFEVGGAAPFNRHRSKRSSHPIFHR 120
QY 132 GEFSSVDSVYVWGDKTTATDIDKGEVNVLCSEVINNSVFKQYFEETKCRDPVDSGCR 191
DB 121 GEFSSVDSVYVWGDKTTATDIDKGEVNVLCSEVINNSVFKQYFEETKCRDPVDSGCR 180
QY 192 GIDSKHNSYCTTATFVATLMDCKQAAMRFIRIDT 228
DB 181 GIDSKHNSYCTTATFVATLMDCKQAAMRFIRIDT 217

RESULT 8
091X84 PRELIMINARY; PRT: 294 AA.
ID 091X84:
AC 091X84:
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Similar to nerve growth factor, beta.
OS NCFB.
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SALIVARY GLAND;
RA Strausberg R.;
RX Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL: BC011123; AAH11123.1;
DR MGI: 97321; N91D.
DR InterPro: IPR002072; NCF.
DR Pfam: PF00243; NCF.1.
DR PRODOM: PD002052; NCF.1.
DR PROSITE: PS00248; NCF_1;
DR PROSITE: PS50270; NCF_2; 1.
SQ SEQUENCE 294 AA; 32326 MM; 9EE7402DAC89229 CRC64;

Query Match 81.3%; Score 1038; DB 11; Length 294;
Best Local Similarity 84.6%; Pred. No. 2.7e-94;
Matches 193; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

QY 2 NSMLFTLITAFILGIOAEPHSESNVPGHTIPQVHTKLOHSIDTLRRARSAPAAIA 61
DB 67 NSMLFTLITAFILGIOAEPTDSNVPEGDSVFEAHHTKLOHSIDTLRRARSAPAAIA 126
QY 62 ARVAGOTRNTVDPRLFKRRRLSPRVLESTOPPREAADTODLDFEVGGAAPFNRHRSK 121
DB 127 ARVAGOTRNTVDPRLFKRRRLSPRVLESTOPPREAADTODLDFEVGGAAPFNRHRSK 186
QY 122 RSSSHPIFHRGFEVSDSVYVWGDKTTATDIDKGEVNVLCSEVINNSVFKQYFEETKCR 181
DB 187 RSSSHPIFHRGFEVSDSVYVWGDKTTATDIDKGEVNVLCSEVINNSVFKQYFEETKCR 246
QY 182 DPNVDSGCRGIDSKHNSYCTTATFVATLMDCKQAAMRFIRIDTA 229
DB 247 ASNPVDSGCRGIDSKHNSYCTTATFVATLMDCKQAAMRFIRIDTA 294

RESULT 9
09DEZ9 PRELIMINARY; PRT: 241 AA.
ID 09DEZ9:
AC 09DEZ9:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Nerve growth factor.
OS Crotales duisus terrificus (South American rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosaurs; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Crotalus.
OC NCBI_TaxID=8732;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=VENOM GLAND;
RA Hayashi M.A.F., Radis-Baptista G., Yamane T., Camargo A.C.M.;
RX "Cloning and sequence of a cDNA coding for a rattlesnake (Crotalus
RX terrificus) nerve growth factor."
RX Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF306533; MAG30924.1;
DR HSSP: P01139; 1BET.
DR InterPro: IPR002072; NCF.
DR Pfam: PF00243; NCF.1.
DR PRODOM: PD002052; NCF.1.
DR SMART: SM00140; NCF.1.
DR PROSITE: PS00248; NCF_1; 1.
DR PROSITE: PS50270; NCF_2; 1.
SQ SEQUENCE 241 AA; 27118 MM; 4A261F42C5D6FF3F CRC64;

Query Match 55.8%; Score 713; DB 13; Length 241;
Best Local Similarity 59.8%; Pred. No. 2.6e-62;
Matches 144; Conservative 29; Mismatches 58; Indels 10; Gaps 4;

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DR ProDom: PD002052; NCF: 1.
 DR SMART: SM00140; NCF: 1.
 DR PROSITE: PS50270; NCF_2: 1.
 FT NON_TER 1
 SQ SEQUENCE 87 AA; 9729 MW; 4539272388FDEE27 CRC64;

Query Match 35.9%; Score 459; DB 4; Length 87;
 Best Local Similarity 94.3%; Pred. No. 8.6e-38;
 Matches 82; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 123 SSSHPFHRGSEFSCSVSWVGDTRTATDIDKGEVNLGEVNIINSVFNQYFEETKCRD 182
 DB 1 SSSHPFHRGSEFSCSVSWVGDTRTATDIDKGEVNLGEVNIINSVFNQYFEETKCRD 60

OY 183 PNPVDSGCGIDSKHNSVCTTHREV 209
 DB 61 PNPVDSGCGIDSKHNSVCTTHREV 87

RESULT 13
 OY 09MU15 PRELIMINARY: PRT: 132 AA.

AC 09MU15: 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Nerve growth factor (Fragment).
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus
 OX NCBI_TaxID=10036;
 RN [1]
 RP Jansen H.T., Lehman M.N., Stevens P.J.:
 RA "Golden Hamster Neurotrophin and Neurotrophin Receptor cDNA."
 RL Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF104239; AAD21010.1; -

FT NON_TER 1
 FT SEQUENCE 132 AA; 14649 MW; 0C36B6283225DA6 CRC64;
 SO SEQUENCE 132 AA; 14649 MW; 0C36B6283225DA6 CRC64;

Query Match 35.2%; Score 449.5; DB 11; Length 132;
 Best Local Similarity 75.4%; Pred. No. 1.3e-36;
 Matches 89; Conservative 10; Mismatches 18; Indels 1; Gaps 1;

OY 2 MSNLFYTLTFLAFLIGIOAEPHSESNYPACHTIPQVHMTKLGHSIDPTALRRASAPAAIA 61
 DB 16 MSNLFYTLTFLAFLIGIOAEPHSESNYPACHTIPQVHMTKLGHSIDPTALRRASAPAAIA 75

OY 62 ARVAGOTRNTVDPRLFKKRLRSPLVLFSTOPPREAADTODDFEVGGAAPFKRTR 119
 DB 76 ARVAGOTRNTVDPRLFKKRLRSPLVLFSTOPPREAADTODDFEVGGAAPFKRTR 132

RESULT 14
 OY 09N182 PRELIMINARY: PRT: 241 AA.

AC 09N182: 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Neurotrophin-3 (Fragment).
 OS Macaca fasciata (Japanese macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9542;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA "TISSUE-BLOOD";
 RL MEDLINE=99270338; PubMed=10340513;
 RA Okuno H., Tokuyama W., Li Y.X., Hashimoto T., Miyashita Y.;

RT "Quantitative evaluation of neurotrophin and trk mRNA expression in
 RT visual and limbic areas along the occipito-temporo-hippocampal pathway
 RT in adult macaque monkeys."
 RT J. Comp. Neurol. 408:378-398(1999).

RM SEQUENCE FROM N.A.
 RC TISSUE-BLOOD.
 RA Hashimoto T., Okuno H., Tokuyama W., Li Y.X., Miyashita Y.:
 RT "Expression of brain-derived neurotrophic factor, neurotrophin-3 and
 RT their receptor messenger RNAs in monkey rhinal cortex."
 RL Neuroscience 0:0-0(2000).

DR EMBL: AF222683; AAF33791.1; -
 DR HSSP: P20783; 1B8K.
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF.
 DR PRINTS: PR00268; NGF.
 DR PRODOM: PD002052; NCF: 1.
 DR SMART: SM00140; NCF: 1.
 DR PROSITE: PS00248; NCF_1; 1.
 DR PROSITE: PS50270; NCF_2; 1.
 FT NON_TER 1
 FT SEQUENCE 241 AA; 27803 MW; AB95E457C7B07113 CRC64;

Query Match 33.4%; Score 426.5; DB 6; Length 241;
 Best Local Similarity 39.1%; Pred. No. 5.1e-34;
 Matches 97; Conservative 35; Mismatches 85; Indels 31; Gaps 6;

OY 5 LFYTLTFLAFLIGIOAEPHSESNYPACHTIPQV-----HWTKLGHSIDPTAL 49
 DB 1 LFYTLTFLAFLIGIOGNMMDRLSDLSLNLKLGADILNKLSKQWVQKENVSTL 60

OY 50 RRA-----RSAPAAIAARVAGOTRNTVDPRLFK-KRLRSPLVLFSTOPPREAADT 101
 DB 61 PKAAPREPERGQAKSEFQPV-----IAMDTELRQGRVRSPLVLSSTPLEPPL 114

OY 102 QDLDFEVGGAAPFKRTRHSRSSHPFHRGSEFSCSVSWVGDTRTATDIDKGEVNL 161
 DB 115 YLMEYVGNPVPVANTRSRRKRYAEHK-SHREGEVSCDSSESLMTWQSSAIDIRGHQTVL 173

OY 152 GEVINNSVFNQYFEETKCRDPPVDSGCGIDSKHNSVCTTHTFVKAATGND-GQQA 220
 DB 174 GEITGNSPVQYFETKCEARPVKNGCRGIDKHMNSCKTSQTVYVALTSENKLVG 233

OY 221 WRFIRIDT 228
 DB 234 WRFIRIDT 241

RESULT 15
 OY 091988 PRELIMINARY: PRT: 286 AA.

AC 091988: 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE Neurotrophin-6 precursor.
 OS Xiphophorus maculatus (Southern platyfish), and
 OS Xiphophorus helleri.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Atherinomorpha;
 OC Cyprinodontiformes; Poeciliidae; Xiphophorus.
 OX NCBI_TaxID=8083, 8084;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=95059452; PubMed=7969471;
 RA Goetz R., Koster R., Winkler C., Raulf F., Lottspeich F., Scharf M.,
 RA Thoenen H.:
 RT "Neurotrophin-6 is a new member of the nerve growth factor family."
 RL Nature 372:266-269(1994).
 RL EMBL: L36942; AAA61923.1; -
 RL EMBL: L36925; AAA61922.1; -

DR EMBL: L66336; AAA61921.1; -.
DR HSP: P01139; 1BET.
DR InterPro: IPR002072; NCF.
DR Pfam: PF00243; NCF_1.
DR PRINTS: PR00268; NCF.
DR ProDom: PD002052; NCF_1.
DR SMART: SM00140; NCF_1.
DR PROSITE: PS00346; NCF_1; 1.
DR PROSITE: PSS0270; NCF_2; 1.
DR Ks signal.
Ks signal.
FT SIGNAL. 1 142
FT CHAIN 143 286
FT CHAIN 286 AA; 3142 AA;
SEQUENCE SEQUENCE 286 AA; 3142 AA; 5607 DBA661972E12D CRC64;

Query Match	33.48;	Score 426;	DB 13;	Length 286;
Best Local Similarity	38.68;	Pred. NO. 7e-34;		
Matches 110; Conservative	31;	Mismatches	84;	Indels 60; Gaps 10;

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OY 9 LTAIFAGTIOAAPHSESVN-----PAGHTIPVH-----WTXKHSIDPALARRA 52
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6 LVLLLTIGVQAVLNMGGGLANPCAAHNSAGQDETAAGGOLSDQDQSYQQRHTTHRTK 65
OY 53 RSAPAA-----IAARVAGOT---RNTVDPRLFKTRRLR--SPRVLSF--TOPPREAA 99
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 66 RTQSAASNNQNTPIVGPSPAGSSPDSSPVDPKLFSSRHRHPRSPRVFESVISHVL 122
OY 100 DDDDDFE--VGGAAPFNTHSKRSSSHPIFHGEFSYSDSYWYGDDTTATDICKGEV 150
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 126 DGGGYTFEVRRL-----KYRKKAISHRMNGEISVCGDSLIVTV--NKTATRDMSGREV 177
OY 159 NPLGEVNNINSFVKQYFEYTKGRDP-----NPVDSGCKGIDSK 196
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 178 TVLSHTVNNKAKKQLEFETTCNSPSTHRSSGIYIGRSGCGKQSGKTSKGTSGCKGIDSK 237
OY 197 HNNSTCTTHTFVKALINDGQAAMRPRIIDTACVCLSRKAVRR 241
Db 238 IYNSICTNDITVSALYFVKQDZAMRIRIINAACVCLSRNMSR 282

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Search completed: December 2, 2002, 15:12:00
Job time : 38.449 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 2, 2002, 15:05:42 ; Search time 16.7386 Seconds
(without alignments) 425.386 Million cell updates/sec

Title: US-10-072-681-1

Sequence: 1 PMSMLFTLITAFLLGIGLAE.....FIRIDTACVCLSRKAVRRA 242

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, AA:*

- 1: /cgn2_6/ptodata/1/laa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/1/laa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/laa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/laa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/laa/PCtus.COMB.pep:*
- 6: /cgn2_6/ptodata/1/laa/Beckfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1277	100.0	242	4	US-09-675-503-1
2	1270	99.5	241	1	US-08-266-080B-4
3	1270	99.5	241	1	US-08-451-947-5
4	1270	99.5	241	2	US-08-424-826A-5
5	1270	99.5	241	2	US-08-595-043A-75
6	1270	99.5	241	3	US-08-970-865-1
7	1270	99.5	241	3	US-08-928-694-5
8	1270	99.5	241	4	US-09-363-573-1
9	1270	99.5	241	4	US-09-447-356-3
10	1270	99.5	241	5	PCR-US91-06950-5
11	1270	99.5	241	5	PCR-US95-05423-4
12	996	78.0	240	3	US-08-910-691-11
13	651	51.0	120	1	US-08-440-049-3
14	651	51.0	120	2	US-08-441-513A-3
15	651	51.0	120	3	US-08-581-662-31
16	651	51.0	120	4	US-08-845-541B-1
17	651	51.0	120	4	US-09-066-065A-1
18	651	51.0	120	4	US-09-447-356-1
19	651	51.0	120	4	US-09-664-295-31
20	651	51.0	120	5	PCR-US95-06918-3
21	648	50.7	120	4	US-08-970-865-2
22	648	50.7	120	4	US-09-363-573-2
23	648	50.7	121	4	US-09-675-503-2
24	648	50.7	127	4	US-09-675-922-4
25	647.5	50.7	167	4	US-09-675-922-8
26	642	50.3	119	3	US-08-753-642-2
27	642	50.3	153	4	US-09-675-922-2

28	642	50.3	163	4	US-09-675-922-6	Sequence 6, Appl1
29	637	49.9	120	4	US-08-845-541B-3	Sequence 3, Appl1
30	637	49.9	120	4	US-09-066-065A-3	Sequence 3, Appl1
31	634	49.6	120	4	US-08-845-541B-4	Sequence 4, Appl1
32	634	49.6	120	4	US-09-066-065A-4	Sequence 4, Appl1
33	629	49.3	120	4	US-08-845-541B-12	Sequence 12, Appl1
34	629	49.3	120	4	US-09-066-065A-12	Sequence 12, Appl1
35	628	49.2	120	4	US-08-845-541B-17	Sequence 17, Appl1
36	628	49.2	120	4	US-08-845-541B-20	Sequence 20, Appl1
37	628	49.2	120	4	US-09-066-065A-17	Sequence 17, Appl1
38	628	49.2	120	4	US-09-066-065A-20	Sequence 20, Appl1
39	626	49.0	120	4	US-08-845-541B-18	Sequence 18, Appl1
40	626	49.0	120	4	US-08-845-541B-21	Sequence 21, Appl1
41	626	49.0	120	4	US-09-066-065A-18	Sequence 18, Appl1
42	626	49.0	120	4	US-09-066-065A-21	Sequence 21, Appl1
43	623	48.8	120	4	US-08-845-541B-13	Sequence 13, Appl1
44	623	48.8	120	4	US-08-845-541B-19	Sequence 19, Appl1
45	623	48.8	120	4	US-09-066-065A-13	Sequence 13, Appl1

ALIGNMENTS

RESULT 1
US-09-675-503-1
Sequence 1, Application US/09675503
Patent No. 6423831
GENERAL INFORMATION:
APPLICANT: Burton, Louis E.
APPLICANT: Schmelzer, Charles H.
APPLICANT: Beck, Joanne T.
TITLE OF INVENTION: ISOLATION OF NEUTROPHILS FROM A
TITLE OF INVENTION: MIXTURE CONTAINING OTHER PROTEINS AND NEUTROPHIL VARIANTS
FILE REFERENCE: GENE 037C2
CURRENT APPLICATION NUMBER: US/09/675,503
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/030838
PRIOR FILING DATE: 1996-11-15
PRIOR APPLICATION NUMBER: 60/047655
PRIOR FILING DATE: 1997-05-29
PRIOR APPLICATION NUMBER: 08/970865
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: 09/363573
PRIOR FILING DATE: 1999-07-29
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 242
TYPE: PRT
ORGANISM: Homo sapien
US-09-675-503-1

Query Match 100.0% Score 1277; DB 4; Length 242;

Best Local Similarity 100.0% Pred. No. 1.7e-143; Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 PMSMLFTLITAFLLGIGLAEHSSSNPAGHTTPOVMTLQSLDTALRRASPAAI 60
1 PMSMLFTLITAFLLGIGLAEHSSSNPAGHTTPOVMTLQSLDTALRRASPAAI 60
61 AARVAGOTRNTVDRLEKRRRLSPVLESTOPREADOTDLEFGCAAPFRTRRS 120
61 AARVAGOTRNTVDRLEKRRRLSPVLESTOPREADOTDLEFGCAAPFRTRRS 120
121 KRSSSHPLFHRGEFVCSVSWVGDRTTATDICKGVNLGVNINNSVFQYFETKC 180
121 KRSSSHPLFHRGEFVCSVSWVGDRTTATDICKGVNLGVNINNSVFQYFETKC 180
181 RDPNVDSCRGIDSKHNSYCTTHTFVKALTDGQAAAPRIRIDTACVCLSRKAVR 240
181 RDPNVDSCRGIDSKHNSYCTTHTFVKALTDGQAAAPRIRIRIDTACVCLSRKAVR 240
181 RDPNVDSCRGIDSKHNSYCTTHTFVKALTDGQAAAPRIRIRIDTACVCLSRKAVR 240

OY 241 RA 242
DB 241 RA 242

RESULT 2

US-08-266-080B-4
Sequence 4, Application US/08266080B
Patent No. 5606031
GENERAL INFORMATION:
APPLICANT: Jack Lille
APPLICANT: Tadahiko Kohno
APPLICANT: Duane Bonam
APPLICANT: Mary S. Rosendahl
TITLE OF INVENTION: Production of Biologically Active
TITLE OF INVENTION: Recombinant Neurotrophic Protein
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 Inch, 360 Kb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/266,080B
FILING DATE: 27-JUNE-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,122
FILING DATE: 09-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/087,912
FILING DATE: 06-JULY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/680,681
FILING DATE: 04-APRIL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/594,126
FILING DATE: 09-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/547,750
FILING DATE: 02-JULY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/505,441
FILING DATE: 06-APRIL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: SYNE200C5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
FEATURE:
NAME/KEY: Inferred amino acid sequence of human NGF
US-08-266-080B-4

Query Match 99.5%; Score 1270; DB 1; Length 241;
Best Local Similarity 100.0%; Pred. No. 1,1e-142;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 MSNLTLLTAFLIGIAQEPHSESNVPAHGHTIPQVHTKLOHSIDTALRRARSAPAAIA 61
DB 1 MSNLTLLTAFLIGIAQEPHSESNVPAHGHTIPQVHTKLOHSIDTALRRARSAPAAIA 60

OY 62 ARVAGOTRNTTVPRLFKKKRLRSPVLFSTQPPREAADTODLFEVGAAPFNRTRSK 121
DB 61 ARVAGOTRNTTVPRLFKKKRLRSPVLFSTQPPREAADTODLFEVGAAPFNRTRSK 120
OY 122 RSSHPLEFRNGEFSVCDSSVWVGDKTTATDITKGEVAVLGEVNIINSVFRQFFETKCR 181
DB 121 RSSHPLEFRNGEFSVCDSSVWVGDKTTATDITKGEVAVLGEVNIINSVFRQFFETKCR 180
OY 182 DPNPVDSCGCGISDKHNSYCTTHTFEVATLMDCKQAAMRIRIDTACVCLSRKAVRR 241
DB 181 DPNPVDSCGCGISDKHNSYCTTHTFEVATLMDCKQAAMRIRIRIDTACVCLSRKAVRR 240
OY 242 A 242
DB 241 A 241

RESULT 3

US-08-451-947-5
Sequence 5, Application US/08451947
Patent No. 5702906
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 Inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: palin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,947
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426419
FILING DATE: 19-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030013
FILING DATE: 22-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 1991
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 666P2C1D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-451-947-5

Query Match 99.5%; Score 1270; DB 1; Length 241;
Best Local Similarity 100.0%; Pred. No. 1,1e-142;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	2	MSHLFTLLTAALIGTIOAEPSSESNVPGHTIIPQVHNHTKLQHSLOALRRASAPAAIA	61
Db	1	MSHLFTLLTAALIGTIOAEPSSESNVPGHTIIPQVHNHTKLQHSLOALRRASAPAAIA	60
QY	62	ARVAGGTNRITVDPLFKRRRLRSRYLVSTQSPREAAADOTDDEFGVGAAPFNTRSK	123
Db	61	ARVAGGTNRITVDPLFKRRRLRSRYLVSTQSPREAAADOTDDEFGVGAAPFNTRSK	120
QY	122	RSSSHIPIFRGEFSCDSVSYWNGDKTTADDIGKEVYVLGSEVNTNNSYKQFFETKCR	184
Db	121	RSSSHIPIFRGEFSCDSVSYWNGDKTTADDIGKEVYVLGSEVNTNNSYKQFFETKCR	180
QY	182	DPNPVDSGCRGIDSKRHMSSTCTTHTFVKALIMDGFOAAMRFIRIDTACVCLSKAVRR	241
Db	181	DPNPVDSGCRGIDSKRHMSSTCTTHTFVKALIMDGFOAAMRFIRIDTACVCLSKAVRR	240
QY	242	A 242	
Db	241	A 241	

```

US-08-424-826A-5
; Sequence 5, Application US/08424826A
; Patent No. 5830858
; GENERAL INFORMATION:
; APPLICANT: Rosenthal, Arnon
; TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,826A
FILING DATE: 19-Apr-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240387
FILING DATE: 10-May-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 25-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0666P1C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/571-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: Amino acid
TOPOLOGY: Linear
US-08-424-826A-5

Query Match          99.5%   Score 1270, DB 2; Length 241;
Best Local Similarity 100.0%   Pred. No. 1,le-142;
Matches 241: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	2	MSMFEFLTAFLIGIOAEPSHESVWPAGCHTIPQVHHTLHLSLDTLARRRASPAALIA	61
Db	1	MSMFEFLTAFLIGIOAEPSHESVWPAGCHTIPQVHHTLHLSLDTLARRRASPAALIA	60
QY	62	ARVAGGTNRITVDPLRFKKRRRLRSPLYLSTQPPREALDQOLDFEGCGAAPPPYTRRSK	121
Db	61	ARVAGGTNRITVDPLRFKKRRRLRSPLYLSTQPPREALDQOLDFEGCGAAPPPYTRRSK	120
QY	122	RSSSHPIFRGCEGSCDSSWYGDKTTAIDDYIGKEVWVLGSEVAINNSVFOYFFETKCR	181
Db	121	RSSSHPIFRGCEGSCDSSWYGDKTTAIDDYIGKEVWVLGSEVAINNSVFOYFFETKCR	180
QY	182	DPNPVNSGCRGIDSKHMSYCTTTHTFVKKALIMDGKQAAARFIRID7ACVCVLSRKAARR	241
Db	181	DPNPVNSGCRGIDSKHMSYCTTTHTFVKKALIMDGKQAAARFIRID7ACVCVLSRKAARR	240
QY	242	A 242	
Db	241	A 241	

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RESULT 5
US-08-595-043A-75
: Sequence 75, Application US/08595043A
: Patent No. 5935824
:
: GENERAL INFORMATION:
:   APPLICANT: SGARLATO, GREGORY D.
:   TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
:   NUMBER OF SEQUENCES: 90
:   CORRESPONDENCE ADDRESS:
:     ADDRESSEE: MEDLEN & CARROLL
:     STREET: 220 MONTGOMERY STREET, SUITE 2200
:     CITY: SAN FRANCISCO
:     STATE: CALIFORNIA
:     COUNTRY: UNITED STATES OF AMERICA
:     ZIP: 94104
:
: COMPUTER READABLE FORM:
:   MEDIUM TYPE: Floppy disk
:   COMPUTER: IBM PC compatible
:   OPERATING SYSTEM: PC-DOS/MS-DOS
:   SOFTWARE: Patent Release #1.0, Version #1.30
:   CURRENT APPLICATION DATA:
:     APPLICATION NUMBER: US/08/595,043A
:     FILING DATE: 31-JAN-1996
:     CLASSIFICATION: 435
:
: ATTORNEY/AGENT INFORMATION:
:   NAME: CARROLL, PETER G.
:   REGISTRATION NUMBER: 32,837
:   REFERENCE/DOCKET NUMBER: SGAR-00371
:
: TELECOMMUNICATION INFORMATION:
:   TELEPHONE: (415) 705-8410
:   TELEFAX: (415) 397-8338
:
: INFORMATION FOR SEQ ID NO: 75:
:   SEQUENCE CHARACTERISTICS:
:     LENGTH: 241 amino acids
:     TYPE: amino acid
:     TOPOLOGY: linear
:   MOLECULE TYPE: protein
:
: US-08-595-043A-75

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QY	242 A 242
QY	122 RSSSHIFPARGFESVCDVSVMVDKNTATDINGKEVMVLGEVNIINSVFNQYPERKCR 183
Db	121 RSSSHIFPARGFESVCDVSVMVDKNTATDINGKEVMVLGEVNIINSVFNQYPERKCR 180
QY	182 DDPVDSGCRGIDSKHNHNSYCCTTHTFVKALIMDGRQAAARFRIIDZACVYLSKAVRR 243
Db	181 DDPVDSGCRGIDSKHNHNSYCCTTHTFVKALIMDGRQAAARFRIIDZACVYLSKAVRR 240
QY	242 A 242
Db	241 A 241

RESULT 8
US-09-363-573-1

```

Sequence 1, Application US/09363573
Patent No. 6184360
GENERAL INFORMATION:
APPLICANT: Louis E. Burton, Charles H. Schmechel
TITLE OF INVENTION: Purification of NGF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Mumpalin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,573
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/970,865
FILING DATE: 14-NO. 6184360-1997
APPLICATION NUMBER: 60/030838
FILING DATE: 11/15/1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047855
FILING DATE: 5/29/1997
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P106382
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

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Query Match	99.5%	Score 1270	DB 4	Length 241
Best Local Similarity	100.0%	Pred. No. 1	je-142	
Matches 241	Conservative	0	Mismatches	0
			Indels	0
			Gaps	0
OY	2	MSMFTLTATATLFIGOAPRHSSESVNPGRTTPOVHMKRLDHSIDTLPRKRSAPAAIA	61	
Db	1	MSMFTLTATATLFIGOAPRHSSESVNPGRTTPOVHMKRLDHSIDTLPRKRSAPAAIA	60	
OY	62	ARVAGGTRATVDPRLFFKRRRLASPRVLESTDPREAADTDLDLPEVGAAPERTIRSK	121	
Db	61	ARVAGGTRATVDPRLFFKRRRLASPRVLESTDPREAADTDLDLPEVGAAPERTIRSK	120	
OY	122	RSSHPILFRGEEFVCDSSVVMVGDKTTATDIDKGEVYVNLGVNINSVFQYEFETKCR	181	

Db 121 RSSSHPIFRGSEFVSODSVWVGDKTTATDINGKEVNLGSENNINSVFQGFPEFKCR 180
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Qy 182 DPNPVSQSGRGIDSKHMSYCTTHTFYKALITDGCQAARFIRIDPACVYLSKAVR 241
 |||||
Db 181 DPNPVSQSGRGIDSKHMSYCTTHTFYKALITDGCQAARFIRIDPACVYLSKAVR 240
 |||||
Qy 242 A 242
 |
Db 241 A 241

RESULT 9
US-09-447-356-3

Sequence 3 Application US/09447356
Patent No. 6395513
GENERAL INFORMATION:
APPLICANT: POSTER, KEITH ALAN
APPLICANT: DUGGAN, MICHAEL JOHN
APPLICANT: SHONE, CLIFFORD CHARLES
TITLE OF INVENTION: CLOSTRIDIAL TOXIN DERIVATIVES ABLE TO MODIFY PERIPHERAL
TITLE OF INVENTION: SENSORY AFFERENT FUNCTIONS
FILE REFERENCE: 023223/0104
CURRENT APPLICATION NUMBER: US/09/447,356
CURRENT FILING DATE: 1999-11-22
PRIOR APPLICATION NUMBER: 08/945,037
PRIOR FILING DATE: 1998-01-12
PRIOR APPLICATION NUMBER: GB 9508204.6
PRIOR FILING DATE: 1995-04-21
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 241
TYPE: PR1
ORGANISM: Murline sp.
US-09-447-356-3

[illegible]

RESULT 10
PCT-112917

Sequence 5, Application PC/TUS9106950
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
APPLICANT: ROSSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd

CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: palin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/06950
FILING DATE: 19910924
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/644882
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
ATTORNEY/AGENT INFORMATION:
NAME: Hensley, Max D.
REGISTRATION NUMBER: 27,043
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/266-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
PCT-US91-06950-5

Query Match 99.5%; Score 1270; DB 5; Length 241;
Best Local Similarity 100.0%; Pred. No. 1,1e-142;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 MSMLFTLTAFILGIAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAIA 61
1 MSMLFTLTAFILGIAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAIA 60
Oy 62 ARVAGOTRNTIVDPRLFKRRRLSPRVLESTOPPREAADTODLDFEVGCAAPFRRTIRSK 121
1 ARVAGOTRNTIVDPRLFKRRRLSPRVLESTOPPREAADTODLDFEVGCAAPFRRTIRSK 120
Db 61 ARVAGOTRNTIVDPRLFKRRRLSPRVLESTOPPREAADTODLDFEVGCAAPFRRTIRSK 120
Oy 122 RSSHPHFHRRGEFSVCDVSVMVGDKTTATDICKREVVLGEVINNSVFEQYFEETKCR 181
121 RSSHPHFHRRGEFSVCDVSVMVGDKTTATDICKREVVLGEVINNSVFEQYFEETKCR 180
Oy 182 DPNPVDSCRGIDSKHNSCTTHTFVKALTDGKQAMRFIRIDTACVLSRKAARR 241
181 DPNPVDSCRGIDSKHNSCTTHTFVKALTDGKQAMRFIRIDTACVLSRKAARR 240
Oy 242 A 242
1 A 241
Db 241 A 241

RESULT 11
PCT-US95-05423-4
Sequence 4, Application PC/TUS9505423
GENERAL INFORMATION:
APPLICANT: Jack Lille
APPLICANT: Tadahiko Kohno
APPLICANT: Duane Bonham
APPLICANT: Mary S. Rosendahl
TITLE OF INVENTION: Production of Biologically Active
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado

COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05423
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/266,090
FILING DATE: 27-JUNE-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,122
FILING DATE: 09-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/087,912
FILING DATE: 06-JULY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/680,681
FILING DATE: 04-APRIL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/594,126
FILING DATE: 09-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/547,750
FILING DATE: 02-JULY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/505,441
FILING DATE: 06-APRIL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: STINE200/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
FEATURE:
NAME/KEY: Inferred amino acid sequence of human NGF
PCT-US95-05423-4

Query Match 99.5%; Score 1270; DB 5; Length 241;
Best Local Similarity 100.0%; Pred. No. 1,1e-142;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 MSMLFTLTAFILGIAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAIA 61
1 MSMLFTLTAFILGIAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAIA 60
Oy 62 ARVAGOTRNTIVDPRLFKRRRLSPRVLESTOPPREAADTODLDFEVGCAAPFRRTIRSK 121
1 ARVAGOTRNTIVDPRLFKRRRLSPRVLESTOPPREAADTODLDFEVGCAAPFRRTIRSK 120
Db 61 ARVAGOTRNTIVDPRLFKRRRLSPRVLESTOPPREAADTODLDFEVGCAAPFRRTIRSK 120
Oy 122 RSSHPHFHRRGEFSVCDVSVMVGDKTTATDICKREVVLGEVINNSVFEQYFEETKCR 181
121 RSSHPHFHRRGEFSVCDVSVMVGDKTTATDICKREVVLGEVINNSVFEQYFEETKCR 180
Oy 182 DPNPVDSCRGIDSKHNSCTTHTFVKALTDGKQAMRFIRIDTACVLSRKAARR 241
181 DPNPVDSCRGIDSKHNSCTTHTFVKALTDGKQAMRFIRIDTACVLSRKAARR 240
Oy 242 A 242
1 A 241
Db 241 A 241

RESULT 12

US-08-910-691-11
; Sequence 11, Application US/08910691
; Patent No. 6015552
; GENERAL INFORMATION:
; APPLICANT: MATNABE, Tatsuya
; APPLICANT: YOSHITOMI, Sumie
; APPLICANT: SASADA, Reiko
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR NEUTROPHILIA
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentia Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,691
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/074,969
; FILING DATE: 19930604
; ATTORNEY/AGENT INFORMATION:
; NAME: NEUNER, George W
; REGISTRATION NUMBER: 26964
; REFERENCE/DOCKET NUMBER: 12345
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-910-691-11

Query Match 78.0%; Score 966; DB 3; Length 240;
Best Local Similarity 79.2%; Pred. No. 3.9e-110;
Matches 190; Conservative 19; Mismatches 29; Indels 2; Gaps 2;

QY 2 MSMLFYTLITAFILGIAQPHSESNVPAAGTIPVHNTKLSLDTALRRASAPAAIA 61
DB 1 MSMLFYTLITAFILGIAQPHSESNVPAAGTIPVHNTKLSLDTALRRASAPAAIA 60
QY 62 ARVAGQTNITVDRLFKRRRLSPVLFSTQPPREADTODLDFEVCGAAPFNTRRSK 121
DB 61 ARVAGQTNITVDRLFKRRRLSPVLFSTQPPREADTODLDFEVCGAAPFNTRRSK 120
QY 122 RSSHPFHRGSESVCDVSVMGDKTTATDICKKEVAVLGEVINNSVROKFFETKCD 181
DB 121 RHAENK-SHROEIVCDSESLMAYDKSSAIDINGHOYVLGEIKTNSPVKQFFETKCK 179
QY 183 DPNVDSGCRGIDSKHNSYCTTHTFVKALTMQ-KQAAMRFIRIDTACVLSRAKAVR 240
DB 180 EAPVKNCGCRGIDSKHNSYCTTHTFVKALTMQ-KQAAMRFIRIDTACVLSRAKAVR 239

RESULT 13
US-08-440-049-3
; Sequence 3, Application US/08440049
; Patent No. 5728803
; GENERAL INFORMATION:
; APPLICANT: Uifer, Roman
; APPLICANT: Presta, Leonard G.

APPLICANT: Winslow, John W.
; TITLE OF INVENTION: PANTROPIC NEUTROTROPIC FACTORS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Pointe San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatlin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,049
; FILING DATE: 12-May-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/253937
; FILING DATE: 03-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P0905C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8674
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-440-049-3

Query Match 51.0%; Score 651; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.3e-69;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 SSHPFHRGSESVCDVSVMGDKTTATDICKKEVAVLGEVINNSVROKFFETKCD 182
DB 1 SSHPFHRGSESVCDVSVMGDKTTATDICKKEVAVLGEVINNSVROKFFETKCD 60
QY 183 DPNVDSGCRGIDSKHNSYCTTHTFVKALTMQ-KQAAMRFIRIDTACVLSRAKAVR 242
DB 61 DPNVDSGCRGIDSKHNSYCTTHTFVKALTMQ-KQAAMRFIRIDTACVLSRAKAVR 120

RESULT 14
US-08-441-513A-3
; Sequence 3, Application US/08441513A
; Patent No. 5981480
; GENERAL INFORMATION:
; APPLICANT: Uifer, Roman
; APPLICANT: Presta, Leonard G.
; APPLICANT: Winslow, John W.
; TITLE OF INVENTION: Pantropic Neutrotrophic Factors
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatlin (Genentech)
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/441,513A
FILING DATE: 15-May-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/253937
FILING DATE: 03-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0905C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/953-3881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-441-513A-3

Query Match 51.0%; Score 651; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.3e-69;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 123 SSSHPFHRCGEFVCDVSVMWGDKTTATDINGKEVWVLGEVNINNSVFQYFEETKCRD 182
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DB 1 SSSHPFHRCGEFVCDVSVMWGDKTTATDINGKEVWVLGEVNINNSVFQYFEETKCRD 60
OY 183 PNPVDSGCRGIDSKHNSYCTTHTFVKALTDGKQAAAFRIRIDTACVLSKRAVRA 242
|||||
DB 61 PNPVDSGCRGIDSKHNSYCTTHTFVKALTDGKQAAAFRIRIDTACVLSKRAVRA 120

RESULT 15
US-08-581-662-31
Sequence 31, Application US/08581662
Patent No. 6121235
GENERAL INFORMATION:
APPLICANT: Gao, Wei-Qiang
TITLE OF INVENTION: Treatment of Balance Impairments
FILE REFERENCE: P0981
CURRENT APPLICATION NUMBER: US/08/581,662
CURRENT FILING DATE: 1995-12-29
NUMBER OF SEQ ID NOS: 36
SEQ ID NO 31
LENGTH: 120
TYPE: PRT
ORGANISM: Homo sapiens
US-08-581-662-31

Query Match 51.0%; Score 651; DB 3; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.3e-69;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 123 SSSHPFHRCGEFVCDVSVMWGDKTTATDINGKEVWVLGEVNINNSVFQYFEETKCRD 182
|||||
DB 1 SSSHPFHRCGEFVCDVSVMWGDKTTATDINGKEVWVLGEVNINNSVFQYFEETKCRD 60
OY 183 PNPVDSGCRGIDSKHNSYCTTHTFVKALTDGKQAAAFRIRIDTACVLSKRAVRA 242
|||||
DB 61 PNPVDSGCRGIDSKHNSYCTTHTFVKALTDGKQAAAFRIRIDTACVLSKRAVRA 120

Search completed: December 2, 2002, 15:09:42
Job time: 17.7386 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 2, 2002, 15:08:47 ; Search time 8.5114 Seconds

(without alignments)
452.778 Million cell updates/sec

Title: US-10-072-681-1

Sequence: 1 PMSMLFYLITFLAFLIGIQNE.....FIRIDACVLSRAVRA 242

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 102317 seqs, 15924203 residues

Total number of hits satisfying chosen parameters: 102317

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : Published Applications -AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEM_PUB pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PTCT_NEM_PUB pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEM_PUB pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US07_NEM_PUB pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEM_PUB pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEM_PUB pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEM_PUB pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1277	100.0	242	12	US-10-072-681-1
2	1270	99.5	241	8	US-08-450-842-5
3	1266	99.1	241	10	US-09-872-263-16
4	648	50.7	121	12	US-10-072-681-2
5	648	50.7	157	10	US-09-798-338-4
6	647.5	50.7	167	10	US-09-798-338-8
7	642	50.3	153	10	US-09-798-338-2
8	642	50.3	163	10	US-09-798-338-6
9	621	48.6	121	9	US-09-813-398-9
10	584	45.7	121	12	US-10-072-681-3
11	481.5	37.7	257	8	US-08-450-842-4
12	452	35.4	142	10	US-08-450-842-52
13	390	30.5	172	10	US-09-848-664-21
14	388.5	30.4	119	10	US-09-745-032-6
15	388.5	30.4	119	10	US-09-742-600-6
16	388.5	30.4	119	10	US-09-872-090-6
17	388.5	30.4	120	10	US-09-745-032-3
18	388.5	30.4	120	10	US-09-742-600-3
19	388.5	30.4	120	10	US-09-872-090-3

20	387.5	30.3	117	10	US-09-745-032-7	Sequence 7, Appl1
21	387.5	30.3	117	10	US-09-742-600-7	Sequence 7, Appl1
22	387.5	30.3	117	10	US-09-872-090-7	Sequence 7, Appl1
23	387.5	30.3	118	10	US-09-745-032-5	Sequence 5, Appl1
24	387.5	30.3	118	10	US-09-742-600-5	Sequence 5, Appl1
25	387.5	30.3	118	10	US-09-872-090-5	Sequence 5, Appl1
26	383.5	30.0	120	10	US-09-745-032-1	Sequence 1, Appl1
27	383.5	30.0	120	10	US-09-742-600-1	Sequence 1, Appl1
28	383.5	30.0	120	10	US-09-872-090-1	Sequence 1, Appl1
29	376.5	29.5	120	9	US-09-813-398-11	Sequence 11, Appl1
30	373.5	29.2	120	12	US-10-072-681-5	Sequence 5, Appl1
31	363	28.4	247	8	US-08-450-842-3	Sequence 3, Appl1
32	337.5	26.4	120	10	US-09-745-032-10	Sequence 10, Appl1
33	337.5	26.4	120	10	US-09-742-600-10	Sequence 10, Appl1
34	337.5	26.4	210	8	US-08-450-842-2	Sequence 2, Appl1
35	333.5	26.1	120	10	US-09-745-032-9	Sequence 9, Appl1
36	333.5	26.1	120	10	US-09-742-600-9	Sequence 9, Appl1
37	329.5	25.8	168	8	US-08-450-842-6	Sequence 6, Appl1
38	327.5	25.6	120	10	US-09-745-032-8	Sequence 8, Appl1
39	327.5	25.6	120	10	US-09-742-600-8	Sequence 8, Appl1
40	323.5	25.3	130	8	US-08-450-842-47	Sequence 47, Appl1
41	311.5	24.4	119	12	US-10-072-681-4	Sequence 4, Appl1
42	310	24.3	132	8	US-08-450-842-51	Sequence 51, Appl1
43	309.5	24.2	120	9	US-09-813-398-10	Sequence 10, Appl1
44	306.5	24.0	130	8	US-08-450-842-23	Sequence 23, Appl1
45	304.5	23.8	130	8	US-08-450-842-22	Sequence 22, Appl1

ALIGNMENTS

RESULT 1
US-10-072-681-1
Sequence 1, Application US/10072681
Patent No. US20020137893A1
GENERAL INFORMATION:
APPLICANT: Burton, Louis E.
APPLICANT: Schmeizer, Charles H.
APPLICANT: Beck, Joanne T.
TITLE OF INVENTION: PURIFICATION OF NGF
FILE REFERENCE: GENDT.031C3
CURRENT APPLICATION NUMBER: US/10/072.681
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/030838
PRIOR FILING DATE: 1996-11-15
PRIOR APPLICATION NUMBER: 60/047855
PRIOR FILING DATE: 1997-05-29
PRIOR APPLICATION NUMBER: 08/970865
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: 09/363573
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: 09/675,503
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 242
TYPE: PRT
ORGANISM: Homo sapien
US-10-072-681-1
Query Match 100.0%; Score 1277; DB 12; Length 242;
Best local similarity 100.0%; Pred. No. 1.8e-127;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PMSMLFYLITFLAFLIGIQNEPSESNNVAGTTTQVNTKLQSLDTALRRASAPAAI 60
DB 1 PMSMLFYLITFLAFLIGIQNEPSESNNVAGTTTQVNTKLQSLDTALRRASAPAAI 60
QY AAIVAGQTNINIVDRLFKKRLRSRVLFTSTPPREAAVDTODLDFEVCGAAPFNTHRS 120
DB 61 AAIVAGQTNINIVDRLFKKRLRSRVLFTSTPPREAAVDTODLDFEVCGAAPFNTHRS 120

OY 121 RKSHPHFHNGEFSVCDVSVWVGDKTTATDIDKKEVNVLGSEVNIINSVFKQYFEETKCR 180
DB 121 RKSHPHFHNGEFSVCDVSVWVGDKTTATDIDKKEVNVLGSEVNIINSVFKQYFEETKCR 180
OY 181 RDPNPDSCGCGIDSKHNSYCTTHTFVKALTMDCQKAAHFRIRIDTACVCLSKAVR 240
DB 181 RDPNPDSCGCGIDSKHNSYCTTHTFVKALTMDCQKAAHFRIRIDTACVCLSKAVR 240
OY 241 RA 242
DB 241 RA 242

RESULT 2

US-08-450-842-5
Sequence 5, Application US/08450842
Patent No. US20020045576A1

GENERAL INFORMATION:

APPLICANT: GENE TECH, INC.
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 Inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,842

FILING DATE:

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426419

FILING DATE: 19-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030013

FILING DATE: 22-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482

FILING DATE: 31-JAN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707

FILING DATE: 1991
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.

REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 666P2C103

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674

TELEFAX: 415/952-9881
TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids

TYPE: amino acid
TOPOLOGY: linear

US-08-450-842-5

Query Match 99.5%; Score 1270; DB 8; Length 241;
Best Local Similarity 100.0%; Pred. No. 9.8e-127;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 MSMLFYTLITAFGLIGIOAEPHSESNYPAGHTIPQVHTKLGHSIDTALRRASAPAAIA 61
DB 1 MSMLFYTLITAFGLIGIOAEPHSESNYPAGHTIPQVHTKLGHSIDTALRRASAPAAIA 60

OY 62 ARVAGOTRNTITVDPRLFKRRRLRSRVLFSQPPREAADTODLDFEYGAAPFNRTNRK 121
DB 61 ARVAGOTRNTITVDPRLFKRRRLRSRVLFSQPPREAADTODLDFEYGAAPFNRTNRK 120
OY 122 RKSHPHFHNGEFSVCDVSVWVGDKTTATDIDKKEVNVLGSEVNIINSVFKQYFEETKCR 181
DB 121 RKSHPHFHNGEFSVCDVSVWVGDKTTATDIDKKEVNVLGSEVNIINSVFKQYFEETKCR 180
OY 182 DPNPDSCGCGIDSKHNSYCTTHTFVKALTMDCQKAAHFRIRIDTACVCLSKAVR 241
DB 181 DPNPDSCGCGIDSKHNSYCTTHTFVKALTMDCQKAAHFRIRIDTACVCLSKAVR 240
OY 242 A 242
DB 241 A 241

RESULT 3

US-09-822-263-16
Sequence 16, Application US/09822263
Patent No. US20020036598A1

GENERAL INFORMATION:

APPLICANT: Prayaga, Sudhirdas
APPLICANT: Verneil, Corine
APPLICANT: Shimketa, Richard A
APPLICANT: Burgess, Catherine
APPLICANT: Spylek, Kimberly
APPLICANT: Tchernev, Velizar T
TITLE OF INVENTION: No. US20020036598A1el Polynucleotides and Polypeptides Encoded
FILE REFERENCE: 15966-572 C1P1
CURRENT APPLICATION NUMBER: US/09/822,263

CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 09/672,665

PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/156,745

PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 60/158,942

PRIOR FILING DATE: 1999-10-06
PRIOR APPLICATION NUMBER: 60/159,248

PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/169,344

PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 60/215,048

PRIOR FILING DATE: 2000-06-29
NUMBER OF SEQ ID NOS: 36

SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16

LENGTH: 241
TYPE: PRT
ORGANISM: Homo sapiens

US-09-822-263-16

Query Match 99.1%; Score 1266; DB 10; Length 241;
Best Local Similarity 99.6%; Pred. No. 2.6e-126;
Matches 240; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 MSMLFYTLITAFGLIGIOAEPHSESNYPAGHTIPQVHTKLGHSIDTALRRASAPAAIA 61
DB 1 MSMLFYTLITAFGLIGIOAEPHSESNYPAGHTIPQVHTKLGHSIDTALRRASAPAAIA 60
OY 62 ARVAGOTRNTITVDPRLFKRRRLRSRVLFSQPPREAADTODLDFEYGAAPFNRTNRK 121
DB 61 ARVAGOTRNTITVDPRLFKRRRLRSRVLFSQPPREAADTODLDFEYGAAPFNRTNRK 120
OY 122 RKSHPHFHNGEFSVCDVSVWVGDKTTATDIDKKEVNVLGSEVNIINSVFKQYFEETKCR 181
DB 121 RKSHPHFHNGEFSVCDVSVWVGDKTTATDIDKKEVNVLGSEVNIINSVFKQYFEETKCR 180
OY 182 DPNPDSCGCGIDSKHNSYCTTHTFVKALTMDCQKAAHFRIRIDTACVCLSKAVR 241
DB 181 DPNPDSCGCGIDSKHNSYCTTHTFVKALTMDCQKAAHFRIRIDTACVCLSKAVR 240
OY 242 A 242

Db 241 A 241

RESULT 4
US-10-072-681-2
Sequence 3 Amplification (US10072681)

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; GENERAL INFORMATION:
; APPLICANT: Burton, Louis E.
; APPLICANT: Schmelzer, Charles H.
; APPLICANT:
;

```

```

1  TITLE OF INVENTION: PURIFICATION OF NGF
2  FILE REFERENCE: GENEHT.037C3
3  CURRENT APPLICATION NUMBER: US/10/072.681
4  CURRENT FILING DATE: 2002-02-08
5  PRIOR APPLICATION NUMBER: 60/030838
6  PRIOR FILING DATE: 1996-11-15
7  PRIOR APPLICATION NUMBER: 60/047855
8  PRIOR FILING DATE: 1997-05-29
9  PRIOR APPLICATION NUMBER: 08/970865
10 PRIOR FILING DATE: 1997-11-14
11 PRIOR APPLICATION NUMBER: 09/363573
12 PRIOR FILING DATE: 1999-07-29
13 PRIOR APPLICATION NUMBER: 09/675,503
14 PRIOR FILING DATE: 2000-09-29
15 NUMBER OF SEQ ID NOS: 6
16 SOFTWARE: Fastseq for Windows Version 4.0
17 SEQ ID NO 1
18 LENGTH: 121
19 TYPE: prt
20 ORGANISM: Homo sapien
21 US-10-072-681-2

```

Query Match	50.78;	Score 648;	DB 12;	Length 121,
Best Local Similarity	99.28;	Pred. NO. 2e-61;		
Matches 119;	Conservative	1;	Mismatches	0; Indels

0Y	123	SSSHPIFHHGEESVCDSDSVWVWGKRTATIDIKKEVYVJGCVINNSVYKQFFETKRD	187
Db	2	SSSHPIFHHGEESVCDSDSVWVWGKRTATIDIKKEVYVJGCVINNSVYKQFFETKRD	61
0Y	183	PNVVSGCGGIDSKNNNSCTTTTPKALITNGKQAAFRIRIDPACVYLSKRAARA	242
Db	62	PNVVSGCGGIDSKNNNSCTTTTPKALITNGKQAAFRIRIDPACVYLSKRAARA	121

RESULT 5
US-09-798-338-4
: Sequence 4, Application US/09798338
: Patent No. US20010020086A1
: General Information

APPLICANT: Hubbell, Jeffrey A.
 APPLICANT: Schense, Jason C.
 APPLICANT: Saklyama, Shelly E.
 TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FLTRIN FOR TISSUE
 TITLE OF INVENTION: EN지니어ING: INCORPORATION OF PROTEINS
 FILE REFERENCE: 87662-66879
 CURRENT APPLICATION NUMBER: US/09/798,338
 CURRENT FILING DATE: 2001-03-02
 PRIOR APPLICATION NUMBER: 09/141,153

```

: OTHER INFORMATION: Description of Artificial Sequence:Artificial
: OTHER INFORMATION: Protein Sequence
US-09-798-338-4

```

Query Match	50.7%;	Score 648;	DB 10;	Length 157;
Best Local Similarity	92.4%;	Pred. No. 2.9e-61;		
Matches 121; Conservative	3;	Mismatches 1;	Indels 6;	Gaps 1;

QY	116	RTSRSR-----SSSHIFRGEVCDSDSVWGDKTTADIDNGKEVMVLGEVNIINS	169
QY	116	RTSRSR-----SSSHIFRGEVCDSDSVWGDKTTADIDNGKEVMVLGEVNIINS	169
Db	26	RLRSRKLEVELESSSHPIFRHGEVSDSDSVWGDKTTADIDNGKEVMVLGEVNIINS	85
QY	170	VFQYFFETKCDPMPVDSGCGIDSKHNSCTTTHYKALTDGQAAFRITDA	225
Db	86	VFQYFFETKCDPMPVDSGCGIDSKHNSCTTTHYKALTDGQAAFRITDA	145
QY	230	CVCYSRKRAVR	240
Db	146	CVCYSRKRAVR	156

RESULT 6
US-09-798-338-8
; Sequence 8, Application US/09798338

1 APPLICANT: Hubbard, Jeffrey A.
 2 APPLICANT: Schense, Jason C.
 3 APPLICANT: Saityama, Shelly E.
 4 TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE
 5 TITLE OF INVENTION: ENGINEERING: INCORPORATION OF PROTEINS
 6 FILE REFERENCE: 8/662-68879
 7 CURRENT APPLICATION NUMBER: US/09/798,338
 8 CURRENT FILING DATE: 2001-03-02
 9 PRIOR APPLICATION NUMBER: 09/141,153
 10 PRIOR FILING DATE: 1998-08-27
 11 NUMBER OF SEQ ID NOS: 9
 12 SOFTWARE: PatentIn Ver. 2.0

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; OTHER INFORMATION: Description of Artificial Sequence:Artificial
; OTHER INFORMATION: Protein Sequence
US-09-798-338-B

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Query Match	50.78;	Score 647.5;	DB 10;	Length 167;
Best Local Similarity	75.68;	Pred. No. 3.6e-61;		
Matches 127; Conservative	6;	Mismatches 10;	Indels 25;	Gaps 3;

```

0y 74 DP-RLKRRRLSSPVLSTOPEPDAADTODLEFGAAPPNTRHSRRSSPHFRG 132
    | | : : : | : : | : | : | : | : | : | : | : | : | : | : |
Db 23 DPRRLYSRSLKLPVELPLIKMP-----VELE-----SSRHIFRG 58

0y 133 EFQVCGSVVMVGDITTDIDKGEVMVLGEVNNINSVFKOYFEETKCRDPVPDSCRG 132
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 59 EFQVCGSVVMVGDITTDIDKGEVMVLGEVNNINSVFKOYFEETKCRDPVPDSCRG 118

0y 193 ISDKHANSICITTHFPVALTMDSQQAAMRPIRIDPACVCYLSRAVR 340
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 119 ISDKHANSICITTHFPVALTMDSQQAAMRPIRIDPACVCYLSRAVR 166

```

RESULT 7
 US-09-798-338-2
 : Sequence 2, Application US/09798338
 : Patent No. US20010020086A1
 : GENERAL INFORMATION:
 :
 : APPLICANT: Rubbells, Jeffrey A.
 : APPLICANT: Schenck, Jason C.
 : APPLICANT: Sakiyama, Shelly E.
 : TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE
 : TITLE OF INVENTION: ENGINEERING: INCORPORATION OF PROTEINS
 : FILE REFERENCE: 8/662-68879
 : CURRENT APPLICATION NUMBER: US/09/798,338
 : CURRENT FILING DATE: 2001-03-02

PRIOR APPLICATION NUMBER: 09/141.153
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 153
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Artificial
US-09-798-338-2

Query Match 50.3%; Score 642; DB 10; Length 153;
Best Local Similarity 100.0%; Pred. No. 1,2e-60;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 123 SSSHPIFRHRGEFSVCDVSVMVGDKTATDIDIKGEVNLGEVNNINSVFQYFEETKCD 182
DB 35 SSSHPIFRHRGEFSVCDVSVMVGDKTATDIDIKGEVNLGEVNNINSVFQYFEETKCD 94
OY 183 PNPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAAAFRIRIDTACVLSRAVR 240
DB 95 PNPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAAAFRIRIDTACVLSRAVR 152

RESULT 8

US-09-798-338-6
Sequence 6, Application US/09798338
Patent No. US20010020086A1
GENERAL INFORMATION:
APPLICANT: Hubbell, Jeffrey A.
APPLICANT: Schenae, Jason C.
APPLICANT: Sakiyama, Shelly E.
TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE
FILE REFERENCE: 87662-68879
CURRENT APPLICATION NUMBER: US/09/798.338
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 09/141.153
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 163
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Artificial
US-09-798-338-6

Query Match 50.3%; Score 642; DB 10; Length 163;
Best Local Similarity 100.0%; Pred. No. 1,3e-60;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 123 SSSHPIFRHRGEFSVCDVSVMVGDKTATDIDIKGEVNLGEVNNINSVFQYFEETKCD 182
DB 45 SSSHPIFRHRGEFSVCDVSVMVGDKTATDIDIKGEVNLGEVNNINSVFQYFEETKCD 104
OY 183 PNPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAAAFRIRIDTACVLSRAVR 240
DB 105 PNPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAAAFRIRIDTACVLSRAVR 162

RESULT 9

US-09-813-398-9
Sequence 9, Application US/09813398
Patent No. US20020169292A1
GENERAL INFORMATION:
APPLICANT: Bruce D. Weintraub
APPLICANT: Mariusz W. Szklinski
APPLICANT: University of Maryland

TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
FILE REFERENCE: USFMD.003C1
CURRENT APPLICATION NUMBER: US/09/813.398
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: PCT/US99/05908
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: PCT/US98/19772
PRIOR FILING DATE: 1998-09-22
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 121
TYPE: PRT
ORGANISM: HOMO SAPIEN
US-09-813-398-9

Query Match 48.6%; Score 621; DB 9; Length 121;
Best Local Similarity 95.8%; Pred. No. 1,4e-58;
Matches 115; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 123 SSSHPIFRHRGEFSVCDVSVMVGDKTATDIDIKGEVNLGEVNNINSVFQYFEETKCD 182
DB 2 SSSHPIFRHRGEFSVCDVSVMVGDKTATDIDIKGEVNLGEVNNINSVFQYFEETKCD 61
OY 183 PNPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAAAFRIRIDTACVLSRAVR 242
DB 62 PNPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAAAFRIRIDTACVLSRAVR 121

RESULT 10

US-10-072-681-3
Sequence 3, Application US/10072681
Patent No. US20020137893A1
GENERAL INFORMATION:
APPLICANT: Burton, Louis E.
APPLICANT: Schmeizer, Charles H.
APPLICANT: Beck, Joanne T.
TITLE OF INVENTION: PURIFICATION OF NGR
FILE REFERENCE: GENENT.037C3
CURRENT APPLICATION NUMBER: US/10/072.681
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/030838
PRIOR FILING DATE: 1996-11-15
PRIOR APPLICATION NUMBER: 60/047855
PRIOR FILING DATE: 1997-05-29
PRIOR APPLICATION NUMBER: 08/970865
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: 09/363573
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: 09/675.503
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 121
TYPE: PRT
ORGANISM: mouse
US-10-072-681-3

Query Match 45.7%; Score 584; DB 12; Length 121;
Best Local Similarity 89.9%; Pred. No. 1,2e-54;
Matches 107; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 123 SSSHPIFRHRGEFSVCDVSVMVGDKTATDIDIKGEVNLGEVNNINSVFQYFEETKCD 182
DB 2 SSSHPIFRHRGEFSVCDVSVMVGDKTATDIDIKGEVNLGEVNNINSVFQYFEETKCD 61
OY 183 PNPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAAAFRIRIDTACVLSRAVR 241
DB 62 PNPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAAAFRIRIDTACVLSRAVR 120

RESULT 11

US-09-848-664-21
: Sequence 21, Application US/09848664
: Patent No. US20020146414A1
: GENERAL INFORMATION:
: APPLICANT: Sakiyama-Elbert, Shelly E.
: APPLICANT: Hubbard, Jeffrey A.
: TITLE OF INVENTION: Controlled Release of No. US20020146414A1-Heparin Binding Growth
: TITLE OF INVENTION: Factors from Heparin Containing Matrices
: FILE REFERENCE: ETH 108
: CURRENT APPLICATION NUMBER: US/09/848,664
: PRIOR FILING DATE: 2001-05-03
: PRIOR APPLICATION NUMBER: 09/298,084
: NUMBER OF SEQ ID NOS: 31
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 21
: LENGTH: 72
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-848-664-21

Query Match 30.4%; Score 390; DB 10; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.8e-34;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 123 SSSHPFHRGEFSCVDSVYWGDKTTATDIKGEVNLGEVINNSVFKQYFFETKCRD 182
DB 1 SSSHPFHRGEFSCVDSVYWGDKTTATDIKGEVNLGEVINNSVFKQYFFETKCRD 60
QY 183 PNPVDSGCRGID 194
DB 61 PNPVDSGCRGID 72

RESULT 14
US-09-745-032-6
: Sequence 6, Application US/09745032
: Patent No. US20010027179A1
: GENERAL INFORMATION:
: APPLICANT: Boone, Thomas C.
: APPLICANT: Cheung, Ellen N.
: APPLICANT: Herhenson, Susan I.
: APPLICANT: Young, John D.
: TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS
: FILE REFERENCE: A-411A US Revised073100
: CURRENT APPLICATION NUMBER: US/09/745,032
: PRIOR FILING DATE: 2000-12-19
: PRIOR APPLICATION NUMBER: 09/214,214
: PRIOR FILING DATE: 1998-12-23
: PRIOR APPLICATION NUMBER: US 08/684,353
: PRIOR FILING DATE: 1996-07-19
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 6
: LENGTH: 119
: TYPE: PRT
: ORGANISM: Human
US-09-745-032-6

Query Match 30.4%; Score 388.5; DB 10; Length 119;
Best Local Similarity 61.6%; Pred. No. 5.2e-34;
Matches 69; Conservative 18; Mismatches 24; Indels 1; Gaps 1;
QY 130 HRGEFSCVDSVYWGDKTTATDIKGEVNLGEVINNSVFKQYFFETKCRDPNPVDSG 189
DB 7 HRGEFSCVDSVYWGDKTTATDIKGEVNLGEVINNSVFKQYFFETKCRDPNPVDSG 66
QY 190 CRGIDSKHNSYCTTHTFVKALTM-D-CROAMRFIRIDTACVLSRKA VR 240
DB 67 CRGIDSKHNSYCTTHTFVKALTM-D-CROAMRFIRIDTACVLSRKA VR 118

RESULT 15

US-09-742-600-6
: Sequence 6, Application US/09742600
: Patent No. US20020010135A1
: GENERAL INFORMATION:
: APPLICANT: Boone, Thomas C.
: APPLICANT: Cheung, Ellen N.
: APPLICANT: Herhenson, Susan I.
: APPLICANT: Young, John D.
: TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS
: FILE REFERENCE: A-411A US Revised073100
: CURRENT APPLICATION NUMBER: US/09/742,600
: PRIOR FILING DATE: 2000-12-19
: PRIOR APPLICATION NUMBER: 09/214,214
: PRIOR FILING DATE: 1998-12-23
: PRIOR APPLICATION NUMBER: US 08/684,353
: PRIOR FILING DATE: 1996-07-19
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 6
: LENGTH: 119
: TYPE: PRT
: ORGANISM: Human
US-09-742-600-6

Query Match 30.4%; Score 388.5; DB 10; Length 119;
Best Local Similarity 61.6%; Pred. No. 5.2e-34;
Matches 69; Conservative 18; Mismatches 24; Indels 1; Gaps 1;
QY 130 HRGEFSCVDSVYWGDKTTATDIKGEVNLGEVINNSVFKQYFFETKCRDPNPVDSG 189
DB 7 HRGEFSCVDSVYWGDKTTATDIKGEVNLGEVINNSVFKQYFFETKCRDPNPVDSG 66
QY 190 CRGIDSKHNSYCTTHTFVKALTM-D-CROAMRFIRIDTACVLSRKA VR 240
DB 67 CRGIDSKHNSYCTTHTFVKALTM-D-CROAMRFIRIDTACVLSRKA VR 118

Search completed: December 2, 2002, 15:14:33
Job time : 9.51114 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002. Compugen Ltd.

OK protein - protein search, using sw model

Run on: December 2, 2002, 15:05:37 ; Search time 24.1149 Seconds

(without alignments)
668.605 Million cell updates/sec

Title: US-10-072-681-2

Perfect score: 658

Sequence: 1 PSSSHPIFRGERSVCDSVS.....FTRIDACVLSKRAVRA 121

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Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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16: /SID52/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SID52/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SID52/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	648	98.5	120 20	AA81117
2	648	98.5	120 21	AA829141
3	648	98.5	120 22	AA664994
4	648	98.5	120 22	AA835944
5	648	98.5	124 13	AA821851
6	648	98.5	241 12	AA813063
7	648	98.5	241 12	AA811474
8	648	98.5	241 12	AA813858
9	648	98.5	241 12	AA813886
10	648	98.5	241 16	AA877419

11	648	98.5	241 16	AA866688	Human nerve growth
12	648	98.5	241 18	AA826237	Human preproNGF.
13	648	98.5	241 19	AA848886	Human prepro-nerve
14	648	98.5	241 20	AA807303	Human nerve growth
15	648	98.5	241 22	AA867865	Amino acid sequenc
16	648	98.5	241 22	AA866939	Human NGF. Homo s
17	648	98.5	241 23	AA818904	Human beta nerve g
18	648	98.5	241 23	AA804994	Human beta nerve g
19	648	98.5	245 5	AA840038	Sequence encoded b
20	648	98.5	307 14	AA85241	Human pre-pro nerv
21	648	98.5	307 19	AA869725	Human beta-nerve g
22	648	97.9	307 14	AA837799	Human NGF. Homo s
23	640	97.3	120 17	AA890511	Paratropic neurotro
24	639	97.1	118 10	AA891034	Human nerve growth
25	639	97.1	119 5	AA840040	Sequence encoded b
26	639	97.1	119 12	AA813064	Human NCF HINDIII-
27	639	97.1	119 16	AA877420	Nerve growth facto
28	639	97.1	119 21	AA803347	Human beta-nerve g
29	639	97.1	129 14	AA837359	Recombinant beta-N
30	639	97.1	129 18	AA824145	Factor XIIIa subst
31	639	97.1	152 23	AA850302	Amino acid sequenc
32	639	97.1	153 22	AA867676	Human growth hormo
33	639	97.1	154 13	AA822751	Nerve growth facto
34	639	97.1	155 23	AA850303	Nerve growth facto
35	639	97.1	157 21	AA801586	Nerve growth facto
36	639	97.1	157 22	AA867677	Nerve growth facto
37	639	97.1	157 23	AA857725	Synthetic nerve gr
38	639	97.1	162 23	AA850300	Factor XIIIa subst
39	639	97.1	163 23	AA867678	Amino acid sequenc
40	639	97.1	166 22	AA850301	Nerve growth facto
41	639	97.1	167 22	AA867679	Amino acid sequenc
42	639	97.1	222 21	AA890884	Human proNGF prote
43	639	97.1	261 10	AA891299	Human nerve growth
44	639	97.1	262 7	AA861033	Human beta-nerve g
45	634	96.4	120 20	AA81119	Nerve growth facto

ALIGNMENTS

RESULT 1
AA81117 standard: protein: 120 AA.
ID: AA81117;
AC: AA81117;
DT: 01-MAR-1999 (first entry)
XX: Nerve growth factor wild type.
DE: Nerve growth factor: tkc; neuron; neural disease; animal feed;
KW: neurotrophin assay; nerve cell culture media; neurotrophic factor; NT-3;
KM: tkc; tkc.
XX: Homo sapiens.
OS: Homo sapiens.
PN: WO9849308-A1.
XX: PD 05-NOV-1998.
XX: PF 23-APR-1998; 98WO-US08242.
XX: PR 29-APR-1997; 97US-0841045.
XX: PR 25-APR-1997; 97US-0845541.
XX: PA (GETH) GENENTECH INC.
XX: PI Presta LG, Ufer R, Winslow JW;
XX: WPI: 1999-009429/01.
XX: New variants of nerve growth factor able to bind tkc - contain
PT specified mutations and have multiple neurotrophic activities in a

PT single molecule, used for treating, e.g. peripheral neuropathy

XX Example 1: Page 32-33; 53pp; English.

CC Nerve growth factor was used to produce new variants of nerve growth
CC factor (NGF) with substitutions at amino acid positions: G23 and H84, and
CC one or both of V18 and V10, so that it acquires the ability to bind trkB.
CC The variants can be used to promote development, maintenance and
CC regeneration of neurons in vivo or in vitro, so can be used to treat a
CC wide range of neural diseases, e.g. Alzheimer's, Parkinson's,
CC Huntington's and Meniere's diseases; stroke; amyotrophic lateral
CC sclerosis; epilepsy; Down's syndrome; nerve deafness; Bell's palsy, or
CC specifically, peripheral neuropathy. They are also used as cognitive
CC enhancers and can also be used for diagnosis; in animal feeds; as
CC standards for neurotrophin assays; as additives for nerve cell culture
CC media, and for generation of specific antibodies. By introducing trkB
CC binding/signaling inducing activity, the variants acquire the ability to bind trkB
CC and/or b and therefore provide several activities in a single molecule,
CC with more predictable pharmacokinetic and other properties than a mixture
CC of agents each with a single activity, and better pan-neurotrophic
CC activity than known compounds.

SO Sequence 120 AA;

Query Match 98.5%; Score 648; DB 20; Length 120;

Best Local Similarity 99.2%; Pred. No. 2,3e-69;

Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSSHPFHRGFEFVCDVSVMVGDKTTATDIDKKEVNLGEVINNSVFRQYFEETKCD 61

DB 1 SSSHPFHRGFEFVCDVSVMVGDKTTATDIDKKEVNLGEVINNSVFRQYFEETKCD 60

OY 62 PNPVDSGCGIDSKHNSCTTHTFVKALTMDSKQAMRFIRIDTACVCLSRKAVRRA 121

DB 61 PNPVDSGCGIDSKHNSCTTHTFVKALTMDSKQAMRFIRIDTACVCLSRKAVRRA 120

RESULT 2

AAB29141 ID AAB29141 standard; Protein: 120 AA.

XX AAB29141;

XX 02-FEB-2001 (first entry)

XX N-terminal of neurotrophic growth factor.

XX Neurotrophin; trkB; ototoxicity-related balance impairment;

XX Meniere's syndrome; myringitis; otitis media;

XX acute vestibular neuronitis; herpes zoster oticus; labyrinthitis;

XX middle; labyrinthine tumour; petrositis; otosclerosis; bacteria.

XX Homo sapiens.

XX US6121235-A.

XX 19-SEP-2000.

XX 29-DEC-1995; 95US-0581662.

XX 29-DEC-1995; 95US-0581662.

XX (GETH) GENENTECH INC.

XX Gao W;

XX WPI: 2000-618200/59.

PT Treating ototoxicity-induced neuronal-related balance impairment and
PT promoting vestibular ganglion neuron survival prior to, upon or after
PT exposure to an ototoxin, comprises administering a trkB or trkB agonist

XX Disclosure: Column 57-58; 40pp; English.

CC The present invention relates to treating ototoxicity-induced
CC neuronal-related balance impairment in a mammal by administering a
CC trkB or trkB agonist, particularly neurotrophin-4/5 (NT-4/5).
CC Ototoxicity-related balance impairment includes Meniere's syndrome,
CC myringitis, otitis media, acute vestibular neuronitis, herpes zoster
CC oticus, labyrinthitis, middle or labyrinthine tumour, petrositis and
CC otosclerosis. NT-4/5 may also be used to treat diseases
CC induced by gram positive, gram negative and acid-fast bacteria. The
CC present sequence is a protein used in the invention.

SO Sequence 120 AA;

Query Match 98.5%; Score 648; DB 21; Length 120;

Best Local Similarity 99.2%; Pred. No. 2,3e-69;

Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSSHPFHRGFEFVCDVSVMVGDKTTATDIDKKEVNLGEVINNSVFRQYFEETKCD 61

DB 1 SSSHPFHRGFEFVCDVSVMVGDKTTATDIDKKEVNLGEVINNSVFRQYFEETKCD 60

OY 62 PNPVDSGCGIDSKHNSCTTHTFVKALTMDSKQAMRFIRIDTACVCLSRKAVRRA 121

DB 61 PNPVDSGCGIDSKHNSCTTHTFVKALTMDSKQAMRFIRIDTACVCLSRKAVRRA 120

RESULT 3

AAG64994 ID AAG64994 standard; protein: 120 AA.

XX AAG64994;

XX 25-SEP-2001 (first entry)

XX Nerve growth factor variant related protein SEQ ID NO: 1.

XX Nerve growth factor; NCF; trkB-binding activity; trkB; neuropathy;

XX neuronal disorder; neurotrophin; variant; mutant; mutein; Bell's palsy;

XX amyotrophic lateral sclerosis; paralysis; neurodegenerative disease;

XX Parkinson's disease; Alzheimer's disease; multiple sclerosis.

XX unidentified.

XX US2001012625-A1.

XX 09-AUG-2001.

XX 24-APR-1998; 98US-0066065.

XX 25-APR-1997; 97US-0044918.

XX (PREST) PRESTA L G.

XX (URFE) URFER R.

XX (WINS) WINSLOW J W.

XX Presta LG, Urfer R, Winslow JW;

XX WPI: 2001-464388/50.

XX Disclosure: Page 19; 34pp; English.

PT Nerve growth factor variants which have trkB-binding activity and
PT trkB-signal inducing activity, useful for treating a neural disorder in
PT a mammal such as peripheral neuropathy (e.g. diabetic peripheral
PT neuropathy) -
XX The present invention provides a number of nerve growth factor (NGF)
XX variants with trkB-binding activity and trkB-signal inducing activity.
XX They may also be capable of binding to trkB and trkB. The variants are
XX useful in the treatment of neuronal disorders, including peripheral
XX neuropathy and motor-neurone disorders, such as amyotrophic lateral

CC sclerostis, Bell's palsy, and various conditions involving spinal muscular
 CC atrophy, or paralysis. They are also useful for treating other human
 CC neurodegenerative disorders, such as Alzheimer's disease, Parkinson's
 CC disease, epilepsy, multiple sclerosis, Huntington's disease, Down's
 CC Syndrome, nerve deafness, Meniere's disease and other conditions
 CC characterized by necrosis or loss of neurones, whether central,
 CC peripheral, or motor neurones.

XX Sequence 120 AA:

Query Match 98.5% Score 648: DB 22: Length 120:
 Best Local Similarity 99.2% Pred. No. 2.3e-69;
 Matches 119: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

0Y 2 SSSHPFHRGFEFSCDSVSWVGDKTATDINKGEVWVLGEVWLNNSVFRQYFEETKCRD 61
 Db 1 SSSHPFHRGFEFSCDSVSWVGDKTATDINKGEVWVLGEVWLNNSVFRQYFEETKCRD 60
 0Y 62 PNPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAMRIRIDTACVLSRKAVRRA 121
 Db 61 PNPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAMRIRIDTACVLSRKAVRRA 120

RESULT 4
 AAB35944
 ID AAB35944 standard: protein: 120 AA.

XX AAB35944:

XX 26-FEB-2001 (first entry)

XX NGF-beta amino acid sequence.

XX Heparin binding: vascular graft; matrix; cell adhesion; growth factor;
 XX wound healing; dermal wound; wound healing; NGF-beta.

XX Unidentified.

XX WO200064481-A1.

XX 02-NOV-2000.

XX 22-APR-1999: 99MO-IB00800.

XX 22-APR-1999: 99MO-IB00800.

XX (ETH2-) ETH ZURICH & UNITV ZURICH.

XX Sakiyama SE, Hubbell JA:

XX WPI: 2001-024627/03.

XX Matrix for controlled release of growth factor for wound healing, has
 XX substrate that attaches heparin binding peptide, protein growth factor
 XX that bind heparin with low affinity, and heparin or heparin-like
 XX polymer.

XX Example 5: Page 21: 48pp: English.

XX This invention relates to a matrix comprising a substrate capable of
 CC providing attachment of a heparin binding peptide (HBP), a peptide
 CC comprising a binding domain which binds heparin with high affinity,
 CC heparin or heparin-like polymer, and a protein growth factor or peptide
 CC fragment which has a domain that binds heparin with low affinity.
 CC Included in the invention is a vascular graft comprising the matrix,
 CC which is capable of supporting cell adhesion. The matrix is used for
 CC delivering low heparin binding affinity growth factor proteins or
 CC peptides in a controlled manner suitable for wound healing. The matrix
 CC can be used in an article for treating dermal wounds, and in an
 CC implantable sterilized composition capable of supporting cell adhesion.
 CC The present sequence represents a growth factor protein. The protein is
 CC used in an example illustrating that non-heparin binding growth factors
 CC can be released in a controlled manner from heparin-based drug delivery

CC systems based on their low affinity for heparin.

XX Sequence 120 AA:

Query Match 98.5% Score 648: DB 22: Length 120:
 Best Local Similarity 99.2% Pred. No. 2.3e-69;
 Matches 119: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

0Y 2 SSSHPFHRGFEFSCDSVSWVGDKTATDINKGEVWVLGEVWLNNSVFRQYFEETKCRD 61
 Db 1 SSSHPFHRGFEFSCDSVSWVGDKTATDINKGEVWVLGEVWLNNSVFRQYFEETKCRD 60
 0Y 62 PNPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAMRIRIDTACVLSRKAVRRA 121
 Db 61 PNPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAMRIRIDTACVLSRKAVRRA 120

RESULT 5
 AAR21851
 ID AAR21851 standard: protein: 124 AA.

XX AAR21851:

XX 10-JUN-1992 (first entry)

XX Chimeric neurotrophic factor R1.

XX Human BDNF: brain derived neurotrophic factor; NGF;

XX neurotrophic growth factor; Alzheimer's disease; ageing; peripheral;

XX peripheral neuropathies; Parkinson's disease; Huntington's chorea;

XX amyotrophic lateral sclerosis; nervous system disorders.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..4 /note= "human BDNF preprosequence"

XX Peptide 5..124 /note= "full mature human NGF"

XX WO9202620-A.

XX 20-FEB-1992.

XX 07-AUG-1991: 91MO-US05610.

XX 08-AUG-1990: 90US-0564929.

XX (REGG-) REGENERON PHARM INC.

XX Shooter EM, Suter U, Ip N, Squinto SP, Furch ME, Lindsay RM;

XX Yancopoulos GD:

XX WPI: 1992-080074/10.

XX New chimeric neurotrophic factors - useful in treating nervous

XX conditions caused by trauma, surgery, ischemia, infection,

XX metabolic diseases, nutritional deficiency, etc.

XX Claim 36: Fig 5; 114pp: English.

XX The sequence is that of a chimeric neurotrophic factor (NF) R1 which
 CC comprises the preprosequence of human brain derived neurotrophic
 CC factor (hbdnf) and the full mature sequence of human neurotrophic
 CC growth factor (hngf). It may provide the activity of 2 NFs in a
 CC single mol. or may serve as a superagonist of an endogenous NF
 CC thereby enabling an increased biological response at lower doses.
 CC It may also be useful in targeting an active cpd. to cells
 CC responsive to NF. The design of chimeric Nfs, such as R1, which
 CC retain specific biological activity but which are directed to a
 CC subset of factor-responsive cells may enable treatment of neurological
 CC disorders but avoid the complications of more widespread activity
 CC of parent moles. It may be used in the treatment to eliminate

CC diseased cells, e.g. virus infected cells or tumours of nervous system
 CC orlin. It may also be used to treat patients whose nervous system has
 CC been damaged by trauma, surgery, ischemia, infection (e.g. polio or
 CC AIDS), metabolic disease, nutritional deficiency, malignancy or toxic
 CC agents. Also to treat e.g. Alzheimer's disease, ageing, peripheral
 CC neuropathies, Parkinson's disease, Huntington's chorea or amyotrophic
 CC lateral sclerosis. The NF or antibodies to it can also be used in the
 CC diagnosis and study of nervous system disorders. See also
 CC AAR31857-R21874 and AAQ2080-022131.

XX Sequence 124 AA:

Query Match

Best Local Similarity 98.5%; Score 648; DB 13; Length 241;

Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSSHPFHRGFEFVSVDVSWVGDKTATDIDKKEVNLGEVNNINSVFROFETKCRD 61
 DB 5 SSSHPFHRGFEFVSVDVSWVGDKTATDIDKKEVNLGEVNNINSVFROFETKCRD 64
 OY 62 PNPVDSGCGIDSKHNSYCTTHTFFKALTMDSKQAAMFIRIDTACVLSRKAARRA 121
 DB 65 PNPVDSGCGIDSKHNSYCTTHTFFKALTMDSKQAAMFIRIDTACVLSRKAARRA 124

RESULT 6

AAR3063
 ID AAR3063 standard: Protein: 241 AA.

XX AAR3063:

XX 30-SEP-1991 (first entry)

XX Human NGF SmaI-ApaI fragment prod.

XX Expression vector: human nerve growth factor; yeast;

XX Senile dementia.

XX Homo sapiens.

XX JF03139285-A.

XX 13-JUN-1991.

XX 20-DEC-1989: 89JP-0328199.

XX 27-JUL-1989: 89JP-0192581.

XX (TAKE) TAKEDA CHEMICAL IND KK.

XX WPI: 1991-218449/30.

XX N-PSDB: AAQ12638.

XX New yeast expression vector - used in prodn. of human nerve growth

XX factor from corresp. yeast.

XX Disclosure: Fig 1(1-2); 14pp; Japanese.

XX Human NGF is useful as a reagent for study of the nervous system, and

XX for treatment of senile dementia. The DNA encoding this fragment was

XX derived from the human gene or is synthesised chemically.

XX See also AAQ12639.

XX Sequence 241 AA:

Query Match

Best Local Similarity 98.5%; Score 648; DB 13; Length 241;

Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSSHPFHRGFEFVSVDVSWVGDKTATDIDKKEVNLGEVNNINSVFROFETKCRD 61
 DB 122 SSSHPFHRGFEFVSVDVSWVGDKTATDIDKKEVNLGEVNNINSVFROFETKCRD 181

OY 62 PNPVDSGCGIDSKHNSYCTTHTFFKALTMDSKQAAMFIRIDTACVLSRKAARRA 121
 DB 182 PNPVDSGCGIDSKHNSYCTTHTFFKALTMDSKQAAMFIRIDTACVLSRKAARRA 241

RESULT 7

AAR1474
 ID AAR1474 standard: Protein: 241 AA.

XX AAR1474:

XX 26-APR-1991 (first entry)

XX Human nerve growth factor.

XX NGF; senile dementia.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..18 /label- signal sequence

FT Protein 19..241 /label- pro-NGF

FT Protein 122..241 /label- mature NGF

FT Disulfide-bond 135..202

FT Disulfide-bond 180..230

FT Disulfide-bond 190..232

XX EP414151-A.

XX 27-FEB-1991.

XX 17-AUG-1990: 90EP-0115815.

XX 21-AUG-1989: 89JP-0212980.

XX 20-DEC-1989: 89JP-0328198.

XX 13-APR-1980: 90JP-0096252.

XX 07-JUN-1990: 90JP-0147392.

XX (TAKE) TAKEDA CHEMICALS IND KK.

XX Kakinuma A, Nakahama K, Yoshimura K, Kaisho Y, Iwano M;

XX WPI: 1991-059398/09.

XX N-PSDB: AAQ10620.

XX Human nerve growth factor containing cysteine residues - used as

XX reagent and therapeutic drug for senile dementia.

XX Claim 1: Fig 1: 33pp; English.

XX The sequence was deduced from a clone isolated from a lambda EMBL3

XX genomic library prepd. from human leukocyte DNA, using a probe

XX synthesised based on the sequence of the known human NGF gene [A.

XX Ulrich et al., Nature 303: 821 (1983)]. The clone, betaLN2113,

XX isolated from the library was cleaved with SmaI and ApaI to remove

XX a 1kb fragment contg. the gene which was then inserted into plasmid

XX pUC19 using SpeI and XbaI (Biochemical). The gene was sequenced from

XX this plasmid using Sequenase (Biochemical). The sequence of the

XX protein coding region was found to be in complete agreement with

XX that of Ulrich et al. The sequence was used to produce

XX recombinant h-NGF for use in the prodn. of drugs for e.g. senile

XX dementia.

XX Sequence 241 AA:

Query Match

Best Local Similarity 98.5%; Score 648; DB 12; Length 241;

Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSSHPFHRGFEFVSVDVSWVGDKTATDIDKKEVNLGEVNNINSVFROFETKCRD 61

```

Db      122 SSSHPIFRGFEVSVDVSVWVGDKTTATDICKGEVWVLDGVNINNSVFRQYFFETKCD 181
OY      62 PNPVDSGCRGIDSKHNSYCTTHTFPVKALTMGKQAAAFRIIDTACVLSRAKAVRA 121
Db      182 PNPVDSGCRGIDSKHNSYCTTHTFPVKALTMGKQAAAFRIIDTACVLSRAKAVRA 241

```

RESULT 8

```

AAR13858
ID      AAR13858 standard; Protein: 241 AA.
XX
AC      AAR13858;
XX
DT      21-NOV-1991 (first entry)
XX
DE      Human nerve growth factor.
XX
KM      hNGF.
XX
OS      Homo sapiens.
XX
PM      JP03175976-A.
XX
PD      31-JUL-1991.
XX
PF      12-DEC-1989; 89JP-0320483.
XX
PR      30-SEP-1989; 89JP-0253796.
XX
PR      15-DEC-1988; 88JP-0314860.
XX
PR      12-DEC-1989; 89JP-0320483.
XX
PA      (TAKE ) TAKEDA CHEMICAL IND KK.
XX
DR      WPI: 1991-269694/37.
XX
DR      N-PSDB; AAQ13397.
XX
PT      Secretory prepn. of animal protein - by culturing
XX
PT      Schizosaccharomyces pombe which retains DNA at 3'-terminal of
XX
PT      promoter region.
XX
PS      Disclousure: Fig 3; 12pp; Japanese.
XX
CC      The amino acid sequence is encoded that of human nerve growth factor
XX
CC      (NGF). It may be expressed in Schizosaccharomyces pombe using the
XX
CC      glyceraldehyde-3-phosphate dehydrogenase (GPD) gene promoter.
XX
SQ      Sequence 241 AA;

```

Query Match

```

Best Local Similarity 98.5%; Score 648; DB 12; Length 241;
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      2 SSSHPIFRGFEVSVDVSVWVGDKTTATDICKGEVWVLDGVNINNSVFRQYFFETKCD 61
Db      122 SSSHPIFRGFEVSVDVSVWVGDKTTATDICKGEVWVLDGVNINNSVFRQYFFETKCD 181
OY      62 PNPVDSGCRGIDSKHNSYCTTHTFPVKALTMGKQAAAFRIIDTACVLSRAKAVRA 121
Db      182 PNPVDSGCRGIDSKHNSYCTTHTFPVKALTMGKQAAAFRIIDTACVLSRAKAVRA 241

```

RESULT 9

```

AAR13886
ID      AAR13886 standard; Protein: 241 AA.
XX
AC      AAR13886;
XX
DT      04-DEC-1991 (first entry)
XX
DE      NGF with pro-region and signal sequence.
XX
KM      Nerve growth factor; cerebral nerve system; senile dementia;
XX
OS

```

vector: expression.

```

Key      Location/Qualifiers
Region   1..18
Region   /label= sig-sequence
Region   19..28
Region   /label= pro-region
Protein  29..241
          /label= NGF

```

JP03183485-A.

09-AUG-1991.

26-JUL-1990; 90JP-0196270.

26-JUL-1990; 90JP-0196270.

27-JUL-1989; 89JP-0192581.

30-SEP-1989; 89JP-0253796.

(TAKE) TAKEDA CHEMICAL IND KK.

WPI: 1991-277586/38.

N-PSDB; AAQ13592.

Human nerve growth factor for treating senile dementia - obtd. by

culturing yeast transformed by yeast expression vector contg. NGF

encoding DNA.

Disclousure: Fig 1+3; 11pp; Japanese.

A human NGF gene (obtd. from PNGF107G) or its chemically synthesised

DNA were used; opt. cleaved by restriction enzymes. In the human NGF,

arginine and alanine may added to the C-terminal. A fragment of

pngf107G was ligated into pGUD906-1 contg. a GPD promoter to obtain

pgcn428. DNA comprising nucleotides 1-99 of this sequence and a

partial sequence of pgcn428 and pGUD906-1 were ligated to obtain

pgcn301.

S. cerevisiae NA74-3A(Pho-)/pgcn301 (FERM-P2532) contains the

expression vector and is useful for the prodn. of human NGF.

CC The NGF is used as a reagent to study the cerebral nerve system

and to treat senile dementia.

Sequence 241 AA;

Query Match 98.5%; Score 648; DB 12; Length 241;

Best Local Similarity 99.2%; Pred. No. 5.9e-69; Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

OY      2 SSSHPIFRGFEVSVDVSVWVGDKTTATDICKGEVWVLDGVNINNSVFRQYFFETKCD 61
Db      122 SSSHPIFRGFEVSVDVSVWVGDKTTATDICKGEVWVLDGVNINNSVFRQYFFETKCD 181
OY      62 PNPVDSGCRGIDSKHNSYCTTHTFPVKALTMGKQAAAFRIIDTACVLSRAKAVRA 121
Db      182 PNPVDSGCRGIDSKHNSYCTTHTFPVKALTMGKQAAAFRIIDTACVLSRAKAVRA 241

```

RESULT 10

```

AAR77419
ID      AAR77419 standard; Protein: 241 AA.
XX
AC      AAR77419;
XX
DT      10-FEB-1996 (first entry)
XX
DE      Human nerve growth factor.
XX
KM      Nerve growth factor; neurotrophic factor; therapeutic;
XX
KM      protein refolding; NGF.
XX
OS      Homo sapiens.
XX

```

```

FH Key Location/Qualifiers
FT Protein 122..241
FT /note="mature protein"
FT Region 1..121
FT /note="pre-region"
XX MO9530686-A1.
XX 16-NOV-1995.
XX 02-MAY-1995; 95MO-US05423.
XX 27-JUN-1994; 94US-0266080.
XX 09-MAY-1994; 94US-0240122.
XX (SYNT ) SYNTEX-SYNERGEN NEUROSCIENCE JOINT VENTU.
XX Bonam D, Kohno T, Lille J, Rosendahl MS;
XX MPI: 1995-404080/51.
XX N-PSDB; AAT05437.
XX Process for bacterial expression of recombinant neurotrophic factor
XX - useful for promoting the survival and maintaining phenotypic
XX differentiation of nerve and glial cells.
XX
XX Disclosure: Page 33-34; 57pp: English.
XX
XX The nerve growth factor (NGF) gene is expressed in Escherichia
XX coli cells. The recombinant protein is solubilized and
XX sulfonated and allowed to refold in the presence of PEG and urea.
XX Biologically active NGF, used for promoting the survival of and
XX maintaining the phenotypic differentiation of nerve and glial cells,
XX is isolated and purified. This method breaks incorrectly formed
XX disulphide bonds and allows refolding of the factor into the correct
XX tertiary structure required for maximum yield of full active protein.
XX
XX Sequence 241 AA:
XX
XX Query Match 98.5%; Score 648; DB 16; Length 241;
XX Best Local Similarity 99.2%; Pred. No. 5.9e-69;
XX Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 2 SSSHPIFHGRGEFSVCDVSVMVGDKTATDIDIKGEVNLGEVININSVFROYFEETKCRD 61
XX |||||||
XX Db 122 SSSHPIFHGRGEFSVCDVSVMVGDKTATDIDIKGEVNLGEVININSVFROYFEETKCRD 181
XX |||||||
XX Oy 62 PNPVDSGCRGIDSKHNSCTTHTFVKALTMDSGQAAMRFIRIDTACVLSKAVRRA 121
XX |||||||
XX Db 182 PNPVDSGCRGIDSKHNSCTTHTFVKALTMDSGQAAMRFIRIDTACVLSKAVRRA 241
XX |||||||
XX
XX RESULT 11
XX AAR66688
XX ID AAR66688 standard; Protein: 241 AA.
XX
XX AC AAR66688;
XX
XX DT 23-AUG-1995 (first entry)
XX
XX DE Human nerve growth factor.
XX
XX DE Human nerve growth factor.
XX
XX KW Human nerve growth factor; hNGF; polyclonal antibody;
XX immunogen; enzyme immunoassay.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Peptide 1..18
XX FT /label="sig-peptide"
XX FT Peptide 19..121
XX FT /label="pro-peptide"
XX FT Misc-difference 8

```

```

FT /note="corresponding codon TCG"
FT Misc-difference 59
FT /note="corresponding codon TAT"
FT Misc-difference 173
FT /note="corresponding codon TAG"
FT Disulfide-bond 136..201
FT Disulfide-bond 179..229
FT Disulfide-bond 189..231
XX JP06317587-A.
XX 15-NOV-1994.
XX 14-FEB-1991; 91JP-0021181.
XX 31-AUG-1990; 90JP-0231317.
XX (TAKE ) TAKEDA CHEM IND LTD.
XX MPI: 1995-033116/05.
XX N-PSDB; AAQ79871.
XX Polyclonal antibody against human nerve growth factor (NGF) -
XX useful to detect human NGF, for diagnosis of disease
XX
XX Example 1; Pages 31-33; 35pp: Japanese.
XX
XX AAQ79871 encodes AAR66688 human nerve growth factor (hNGF), the
XX protein was used as an immunogen to generate a polyclonal
XX antibody against hNGF. The polyclonal antibody can be used
XX to detect and determine hNGF pref. by enzyme immunoassay.
XX
XX Sequence 241 AA:
XX
XX Query Match 98.5%; Score 648; DB 16; Length 241;
XX Best Local Similarity 99.2%; Pred. No. 5.9e-69;
XX Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 2 SSSHPIFHGRGEFSVCDVSVMVGDKTATDIDIKGEVNLGEVININSVFROYFEETKCRD 61
XX |||||||
XX Db 122 SSSHPIFHGRGEFSVCDVSVMVGDKTATDIDIKGEVNLGEVININSVFROYFEETKCRD 181
XX |||||||
XX Oy 62 PNPVDSGCRGIDSKHNSCTTHTFVKALTMDSGQAAMRFIRIDTACVLSKAVRRA 121
XX |||||||
XX Db 182 PNPVDSGCRGIDSKHNSCTTHTFVKALTMDSGQAAMRFIRIDTACVLSKAVRRA 241
XX |||||||
XX
XX RESULT 12
XX AAW26237
XX ID AAW26237 standard; Protein: 241 AA.
XX
XX AC AAW26237;
XX
XX DT 16-MAR-1998 (first entry)
XX
XX DE Human preproNGF.
XX
XX DE Fusion protein; hydrophilic spacer; recombinant; expression system;
XX carboxypeptidase; preproNGF.
XX
XX OS Homo sapiens.
XX
XX MO9728272-A1.
XX 07-AUG-1997.
XX 31-JAN-1997; 97MO-US01470.
XX 31-JAN-1996; 96US-03595043.
XX (TECH-) TECHNOLOGENE INC.
XX Sgarlato GD;

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XX WPI: 1997-402624/37.
 DR N-PSDB: AAT80162.
 XX
 PT Recombinant protein expression system for fusion protein production
 PT - useful for high quantity production of authentic recombinant
 PT proteins
 XX
 PS Example 6; Page 140-141; 194pp; English.
 XX
 CC A novel recombinant vector has been developed which comprises a
 CC nucleotide sequence encoding a fusion protein. The fusion protein
 CC comprises three domains joined together in order, from N-terminus to
 CC C-terminus, of a first domain comprising a protein of interest, a second
 CC domain comprising a hydrophilic spacer and an affinity domain, each
 CC domain comprising amino acid residues. The present sequence represents
 CC human preproNGF, used in example 6 of the present invention. The
 CC recombinant vector is used for the production of authentic recombinant
 CC proteins of interest. The method of the invention is useful for the
 CC expression of fusion proteins capable of isolation by affinity
 CC chromatography in pro- or eukaryotic cells. This method allows
 CC for the efficient cleavage and generation of authentic proteins of
 CC interest that do not contain extraneous (i.e. non-naturally occurring)
 CC amino acids.
 CC
 XX Sequence 241 AA:
 S0
 Query Match 98.5%; Score 648; DB 18; Length 241;
 Best Local Similarity 99.2%; Pred. No. 5.9e-69;
 Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 2 SSSHPFRHGEFSVCSVSWVGDKTTATDINGKREYVNLGEVYNNVSFRQFFETKCD 61
 Db 122 SSSHPFRHGEFSVCSVSWVGDKTTATDINGKREYVNLGEVYNNVSFRQFFETKCD 181
 Oy 62 PNPVDSGCGIDSKHNSYCTTHTFEVKALTMQKQAAHFRIDTACVLSRAVRA 121
 Db 182 PNPVDSGCGIDSKHNSYCTTHTFEVKALTMQKQAAHFRIDTACVLSRAVRA 241
 RESULT 13
 AAM48886
 ID AAM48886 standard; Protein: 241 AA.
 AC AAM48886;
 XX
 D7 12-OCT-1998 (first entry)
 XX
 DE Human prepro-nerve growth factor beta chain.
 XX
 KM Neurotrophin: nerve growth factor; NGF: human; purification;
 KW hydrophobic interaction chromatography.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Protein 1..121
 FT /label= Prepro-region
 FT Protein 122..241
 FT /label= Mat_protein
 FT Modified-site 167
 FT /note= "N-glycosylated"
 FT Region 179..189
 FT /note= "conserved Cys-containing region involved in
 FT Cys knot motif"
 FT Region 229..231
 FT /note= "conserved Cys-containing region involved in
 FT Cys knot motif"
 XX
 PN MO9821234-A2.
 XX
 PD 22-MAY-1998.

PF 14-NOV-1997; 97WO-US21068.
 XX
 PR 29-MAY-1997; 97US-0047855.
 PR 15-NOV-1996; 96US-0030838.
 XX
 PA (GERTH) GENENTECH INC.
 XX
 PI Beck JT, Burton LE, Schmelzer CH;
 XX
 DR WPI: 1998-32233/28.
 XX
 PT Isolation of neurotrophin(s) from, e.g. mis-folded or glycosylated
 PT variant(s) - using hydrophobic interaction chromatography,
 PT optionally in combination with high performance cation exchange
 PT chromatography
 XX
 PS Disclosure; Fig 4; 59pp; English.
 XX
 CC This polypeptide comprises the human nerve growth factor (NGF)
 CC beta chain precursor. Methods are provided for large-scale
 CC purification of neurotrophins, including mature NGF, suitable for
 CC clinical use. A claimed method comprises: (1) separating the
 CC neurotrophin from the other proteins using a hydrophobic
 CC interaction chromatography resin (HICR); and optionally (2)
 CC separating the neurotrophin from a chemical variant by high
 CC performance cation exchange chromatography (HPEC). The processes
 CC can also be used for purification of e.g. mouse NGF (see AAM48887),
 CC brain-derived neurotrophic factor (see AAM48888), neurotrophin-4/5
 CC (see AAM48890) and neurotrophin-3 (see AAM48889). The processes allow
 CC separation of neurotrophins from various undesirable misprocessed,
 CC misfolded, size, glycosylated or charge forms. They allow selective
 CC separation from their variants and other molecules, and from other
 CC polypeptides with high pi. The processes are applicable to
 CC starting materials from various sources, including fermentation
 CC broths or lysed bacterial or mammalian cells.
 XX
 S0 Sequence 241 AA:
 Query Match 98.5%; Score 648; DB 19; Length 241;
 Best Local Similarity 99.2%; Pred. No. 5.9e-69;
 Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 2 SSSHPFRHGEFSVCSVSWVGDKTTATDINGKREYVNLGEVYNNVSFRQFFETKCD 61
 Db 122 SSSHPFRHGEFSVCSVSWVGDKTTATDINGKREYVNLGEVYNNVSFRQFFETKCD 181
 Oy 62 PNPVDSGCGIDSKHNSYCTTHTFEVKALTMQKQAAHFRIDTACVLSRAVRA 121
 Db 182 PNPVDSGCGIDSKHNSYCTTHTFEVKALTMQKQAAHFRIDTACVLSRAVRA 241
 RESULT 14
 AAT07303
 ID AAT07303 standard; Protein: 241 AA.
 AC AAT07303;
 XX
 D7 06-JUL-1999 (first entry)
 XX
 DE Human nerve growth factor beta protein.
 XX
 KM Cerebrospinal; axon; growth; mamma; spinal cord injury; lesion; NGF2;
 KW expression vector; neurotrophin; nerve growth factor 2; neurotrophin 3;
 NT3; voluntary motor function.
 XX
 OS Homo sapiens.
 XX
 PN MO9900148-A2.
 XX
 PD 07-JAN-1999.
 XX
 PF 30-JUN-1998; 98WO-US13778.
 XX

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OM protein - protein search, using sw model

Run on: December 2, 2002, 15:05:43 : Search time 9.64596 Seconds
(without alignments)
1205.921 Million cell updates/sec

Title: US-10-072-681-2

Perfect score: 658

Sequence: 1 PSSSHPIFRGGEFVCDVS.....FIRIDACVLSRKAVRA 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database :

1: PIR-73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	648	98.5	286	1 NGHUBM	nerve growth facto
2	640	97.3	229	2 I46614	nerve growth facto
3	628	95.4	125	2 A26312	nerve growth facto
4	599	91.0	243	2 I56570	beta-nerve growth
5	587	89.2	307	1 NGMSMG	nerve growth facto
6	581	88.3	243	2 A26311	nerve growth facto
7	580	88.1	241	2 J10097	nerve growth facto
8	569	86.5	303	1 NGMRBA	nerve growth facto
9	563	85.6	235	2 S14481	nerve growth facto
10	488	74.2	243	2 S15193	nerve growth facto
11	481	73.1	117	2 S28161	nerve growth facto
12	449.5	68.3	116	1 NGNXXI	nerve growth facto
13	445.5	67.7	116	2 A58566	nerve growth facto
14	445.5	67.7	246	2 A59218	nerve growth facto
15	388	59.0	194	2 I51709	nerve growth facto
16	380.5	57.8	257	2 C40304	neurotrophin-3 pre
17	380.5	57.8	257	2 I50400	neurotrophin-3 pre
18	380.5	57.8	258	2 S09155	neurotrophin-3 pre
19	380.5	57.8	282	2 A35781	hippocampus-derive
20	348	52.9	286	2 S50855	neurotrophin-6 - s
21	324.5	49.3	247	2 A40304	brain-derived neur
22	324.5	49.3	249	2 S12555	brain-derived neur
23	324.5	49.3	249	2 B40304	brain-derived neur
24	324.5	49.3	252	2 A30361	brain-derived neur
25	320.5	48.7	114	2 I84765	brain-derived neur
26	318.5	48.4	248	2 JC6183	brain-derived neur
27	313.5	47.6	114	2 I50606	brain-derived neur
28	310.5	47.2	269	2 I51708	brain-derived neur
29	308.5	46.9	236	2 JH0400	neurotrophin-4 pre

30	307.5	46.7	210	2 A42687	neurotrophin-4 pre
31	305.5	46.4	209	2 B42687	neurotrophin-4 pre
32	304.5	46.3	114	2 I51599	brain-derived neur
33	76.5	11.6	835	2 C97332	probable alpha-ara
34	74.5	11.3	365	2 T08577	hypothetical prote
35	73	11.1	229	2 C69806	hypothetical prote
36	71.5	10.9	499	2 S53637	protein kinase clk
37	69.5	10.6	481	2 T27655	hypothetical prote
38	68.5	10.4	1254	2 E82064	conserved hypothet
39	68.5	10.4	4544	1 S02392	alpha-2-macroglobu
40	68.5	10.4	4545	1 S25111	alpha-2-macroglobu
41	68	10.3	518	2 B48088	beta-transducin re
42	67.5	10.3	351	2 T48029	hypothetical prote
43	67.5	10.3	554	2 A86211	hypothetical prote
44	67.5	10.3	1155	2 T40522	hypothetical prote
45	67.5	10.3	4543	1 A53102	alpha-2-macroglobu

ALIGNMENTS

RESULT 1

NGHUBM nerve growth factor beta chain precursor - human (fragment)

C:Species: Homo sapiens (man)
C>Date: 19-Feb-1984
C:Accession: A01399; S10253
R:Ulrich, A.; Gray, A.; Berman, C.; Dull, T.J.

A>Title: Human beta-nerve growth factor gene sequence highly homologous to that of mo

A:Reference number: A93305; MUID:83244969; PMID:6688123

A:Accession: A01399

A:Molecule type: DNA

A:Residues: 1-286 <DB>
R:Bozsan, G.; Pizutti, A.; Ruggeri, E.I.; Falini, A.; Silani, V.; Sidoli, A.; Scarla

Nucleic Acids Res. 18, 4020, 1990

A>Title: CDNA sequence of human beta-NGF.

A:Reference number: S10253; MUID:90326556; PMID:2374737

A:Accession: S10253

A:Molecule type: mRNA

A:Status: translation not shown

A:Residues: 46-286 <DB>

A:Cross-references: EXBL:X52599; NID:929476; PID:CA56832.1; PID:929477

C:Comment: Nerve growth factor is found in submaxillary gland in large quantities and

nic sensory ganglia in vivo and in vitro and to increase cellular neurotubule levels

C:Genetics:

A:Gene: GDB:NGF8

A:Cross-references: GDB:120233; OMIM:162030

A:Map position: 1p13.1-1p13.1

A:Introns: 41/3

C:Complex: nerve growth factor is composed of two alpha chains, two beta chains, and

C:Keywords: glycoprotein; growth factor; submandibular gland

F:1-166/Domain: signal sequence and propeptide (fragment) status predicted <SIG>

F:167-286/Product: nerve growth factor beta chain status predicted <MA>

F:26,114,159,211/Binding site: carbohydrate (Aan) (covalent) status predicted

F:181-246,224-274,234-276/Disulfide bonds: status predicted

Query Match 98.5% Score 648; DB 1; Length 286;

Best Local Similarity 99.2% Pred. No. 1.9e-61;

Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 167 SSSHPPIFRGGEFVCDVSVMVGDITATDIXGKEVNLGEVINNSVFOFEETKCD 61

DB 227 PNVDSGCGIDSKHNSCTTTRTFVAKLTMDCKQAAMRIRIDACVLSRKAVRA 121

DB 227 PNVDSGCGIDSKHNSCTTTRTFVAKLTMDCKQAAMRIRIDACVLSRKAVRA 286

RESULT 2 I46614

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nerve growth factor B - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
C:Accession: I46614
R:Landolt-Mansals, Y.; Mellink, C.; Verle, M.; Gellin, J.
Cytogenet. Cell Genet. 67, 120-123, 1994
A:Title: A new marker (NGF) on pig chromosome 4, isolated by using consensus sequence
A:Reference number: I46614; MUID:94313891; PMID:8039422
A:Accession: I46614
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-229 <L4H>
A:Cross-references: GB:L31698; NID:g476732; PIDN:AAA11301.1; PID:g533771
C:Genetics:
A:Gene: NGFB
C:Superfamily: nerve growth factor beta chain

Query Match          97.3%: Score 640; DB 2; Length 229;
Best Local Similarity 97.5%: Pred. No. 1,le-00;
Matches 117; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 SSSHPFIRGGEFSVCDSSVWVGDKTTATDIDKRGKVVVLGEVNNNSVFHFYFETKCRD 61
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 110 SSSHPFIRGGEFSVCDSSVWVGDKTTATDIDKRGKVVVLGEVNNNSVFHFYFETKCRD 169
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

OY 62 PNPVDSGCRGIDSKHMNSYCTTHTFVKALTMDOGQAAMRFIRIDTACVLSKRAVRA 121
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 170 PNPVDSGCRGIDSKHMNSYCTTHTFVKALTMDOGQAAMRFIRIDTACVLSKRAVRA 229
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
A26312
nerve growth factor beta chain precursor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 16-Jul-1999
C:Accession: A26312
R:Meier, R.; Becker-Andre, M.; Goeltz, R.; Heumann, R.; Shaw, A.; Thoenen, H.
EMBO J. 5, 1489-1493, 1986
A:Title: Molecular cloning of bovine and chick nerve growth factor (NGF): delineation of
A:Reference number: A26312; MUID:86300647; PMID:2427334
A:Accession: A26312
A:Molecule type: mRNA
A:Residues: 1-125 <ME>
A:Cross-references: GB:M26809; NID:g163419; PIDN:AAA30666.1; PID:g163420
C:Comment: Nerve growth factor stimulates neurite outgrowth from sympathetic and embryonic
C:Superfamily: nerve growth factor beta chain
C:Keywords: growth factor; homodimer; seminal vesicle
F:6-135/Product: nerve growth factor #status predicted <MAT>
F:20-85;63-113;73-113/Disulfide bonds: #status predicted

Query Match          95.4%: Score 628; DB 2; Length 125;
Best Local Similarity 94.2%: Pred. No. 1e-59;
Matches 113; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 2 SSSHPFIRGGEFSVCDSSVWVGDKTTATDIDKRGKVVVLGEVNNNSVFHFYFETKCRD 61
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 SSSHPFIRGGEFSVCDSSVWVGDKTTATDIDKRGKVVVLGEVNNNSVFHFYFETKCRD 65
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

OY 62 PNPVDSGCRGIDSKHMNSYCTTHTFVKALTMDOGQAAMRFIRIDTACVLSKRAVRA 121
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 PNPVDSGCRGIDSKHMNSYCTTHTFVKALTMDOGQAAMRFIRIDTACVLSKRAVRA 125
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
I36570
beta-nerve growth factor - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C:Accession: I36570
R:Whittemore, S. R.; Friedman, P. L.; Larhammar, D. G.; Persson, H.; Gonzalez-Carvajal, M.;
J. Neurosci. Res. 20, 403-410, 1988
A:Title: Rat beta-nerve growth factor sequence and site of synthesis in the adult hippocampus
A:Reference number: I36570; MUID:89037223; PMID:3184206

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A:Accession: I56570
 A:Status: preliminary: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-245 <RES>
 A:Cross-references: GB:M6589; NID:g205691; PIDN:AAA41697.1; PID:g205692
 C:Superfamily: nerve growth factor beta chain
 Query Match 91.0%; Score 599; DB 2; Length 245:
 Best Local Similarity 91.6%; Pred. No. 2, 7e-56;
 Matches 109; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 Oy 2 SSSHHFHHGGEFVSDSVSWVWGDKTTATIDIKGEVVLGEVINSVPROYFETKCRD 61
 Db 126 SSTHPFHHGGEFVSDSVSWVWGDKTTATIDIKGEVVLGEVINSVPROYFETKCRD 185
 Oy 62 PNEVSGCGRGIDSKHNSICTTHTFYKALTMGKQAMNRFITIDTACVLSKNAAR 120
 Db 186 PNEVSGCGRGIDSKHNSICTTHTFYKALTMGKQAMNRFITIDTACVLSKNAAR 244
 RESULT 5
 NGMSKG
 nerve growth factor beta chain precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Nov-1980 (sequence revision 19-Feb-1984, *ext-change 21-Jul-2000
 C:Accession: A93301; A93305; A90366; 149689; 152881; A01400; 149690
 R:Scott, J.; Selby, M.; Uden, A.; Qutroga, M.; Bell, G.I.; Rutter, W.J.
 Nature 302, 538-540, 1983
 A>Title: Isolation and nucleotide sequence of a cDNA encoding the precursor of mouse
 A:Reference number: A93301; MUID:83167518; PMID:6336309
 A:Accession: A93301
 A:Molecule type: mRNA
 A:Residues: 1-307 <SCO>
 A:Cross-references: GB:V00836; NID:g53364; PIDN:CAA24221.1; PID:g53365
 R:Ullrich, A.; Gray, A.; Berman, C.; Dull, T.J.
 Nature 303, 821-825, 1983
 A>Title: Human beta-nerve growth factor gene sequence highly homologous to that of mo
 A:Reference number: A93305; MUID:83244969; PMID:6688123
 A:Accession: A93305
 A:Molecule type: mRNA
 A:Residues: 1-307 <DUL>
 A:Cross-references: GB:K01759; NID:g200051; PIDN:AAA39820.1; PID:g387495
 A:Note: these authors believe that Met-67 is probably the amino-terminal residue and
 R:Biochemistry 12, 100-115, 1973
 A>Title: Amino acid sequences of mouse 2,5S nerve growth factor. II. Isolation and ch
 A:Reference number: A90366; MUID:73075048; PMID:4565923
 A:Accession: A90366
 A:Molecule type: protein
 A:Residues: 188-216, 'N', 218-305 <ANG>
 R:Selby, M.J.; Edwards, R.; Sharp, F.; Rutter, W.J.
 Mol. Cell. Biol. 7, 3057-3064, 1987
 A>Title: Mouse nerve growth factor gene: Structure and expression.
 A:Reference number: 149689; MUID:88038855; PMID:3670305
 A:Accession: 149689
 A:Status: preliminary: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-307 <RES>
 A:Cross-references: GB:M17298; NID:g193493; PIDN:AAA37687.1; PID:g467311
 R:Ullrich, A.; Gray, A.; Berman, C.H.; Coussens, L.; Dull, T.J.
 Cold Spring Harb. Symp. Quant. Biol. 49, 435-442, 1983
 A>Title: Sequence homology of human and mouse beta-NGF subunit genes.
 A:Reference number: 152891; MUID:84206565; PMID:63277169
 A:Accession: 152891
 A:Status: preliminary: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-307 <RES>
 A:Cross-references: GB:M14805; NID:g200053; PIDN:AAA39821.1; PID:g200054
 C:Comment: The active molecule is a dimer of identical chains associated by noncovalent
 C:Comment: Nerve growth factor is found in submaxillary gland in large quantities and
 C:Comment: in sensory ganglia in vivo and in vitro and to increase cellular neurotubule levels
 C:Genetics:
 A:Gene: NGFB

A:Introns: 21/2: 62/3
C:Superfamily: nerve growth factor beta chain
C:Keywords: glycoprotein; growth factor; homodimer
F:1-167/Domain: signal sequence and propeptide #status predicted <SIG>
F:188-305/Product: nerve growth factor beta chain #status experimental <MAT>
F:135-180/Binding site: carboxylate (Asn) (covalent) #status predicted
F:202-267,245-295,255-297/Disulfide bonds: #status experimental
F:232/Binding site: carboxylate (Asn) (covalent) #status absent

Query Match 89.2% Score 587; DB 1; Length 307;
Best Local Similarity 90.8%; Pred. No. 6.7e-55;
Matches 108; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 2 SSSHPFIRHGEFSVCDVSVMVGDKTTATDINGKENVVLGEVINNSVFRQFEETCRD 61
DB 188 STHPVFMHGEFSVCDVSVMVGDKTTATDINGKENVVLGEVINNSVFRQFEETCRD 247
P:188-305/Product: nerve growth factor beta chain #status experimental <MAT>
F:135-180/Binding site: carboxylate (Asn) (covalent) #status predicted
F:202-267,245-295,255-297/Disulfide bonds: #status experimental
F:232/Binding site: carboxylate (Asn) (covalent) #status absent

OY 62 PNPVDSGCRGIDSKHNSCTTHTFVKALTMGKQAMRFRIIDTACVLSRKAVR 120
DB 248 SNPVDSGCRGIDSKHNSCTTHTFVKALTMGKQAMRFRIIDTACVLSRKATR 306

RESULT 6
A:65311
C:Species: Gallus gallus (chicken)
C:Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 21-Jul-2000
C:Accession: A26311; A24857; S00127; S12532
R:Bedard, T.; Larnham, D.; Persson, H.
EMBO J. 5, 1483-1487, 1986
A:Title: Structure and expression of the chicken beta nerve growth factor gene.
A:Reference number: A26311; MUID:86300646; PMID:3017695
A:Accession: A26311
A:Molecule type: mRNA
A:Residues: 1-243 <EB>
A:Cross-references: GB:000010; GB:N00010; GB:X04067; MUID:9222840; PIND:BA00008.1; PID:9
R:Becker, R.; Becker-Andre, M.; Goetz, R.; Heumann, R.; Smay, A.; Thoenen, H.
EMBO J. 5, 1489-1493, 1986
A:Title: Molecular cloning of the avian beta-nerve growth factor gene: transcription in
A:Reference number: A24857; MUID:86300647; PMID:3720959
A:Accession: A24857
A:Molecule type: DNA
A:Residues: 118-243 <MO>
A:Cross-references: GB:000010; GB:N00010; GB:X04067; MUID:9222840; PIND:BA00008.1; PID:9
R:Becker, R.; Becker-Andre, M.; Goetz, R.; Heumann, R.; Smay, A.; Thoenen, H.
EMBO J. 5, 1489-1493, 1986
A:Title: Molecular cloning of the avian beta-nerve growth factor gene: delineation of
A:Reference number: A26312; MUID:86300647; PMID:2427334
A:Accession: S00127
A:Status: preliminary: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 121-243 <ME>
A:Cross-references: GB:M26810; MUID:9212446; PIND:AAA8984.1; PID:9212447
R:Danesh, C.F.; Halldoback, F.; Edendal, T.; Persson, H.
EMBO J. 9, 1477-1483, 1990
A:Title: Structure-function studies of nerve growth factor: functional importance of his
A:Reference number: S12532; MUID:90228346; PMID:2328722
A:Accession: S12532
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 126-243 <IBA>
C:Superfamily: nerve growth factor beta chain
C:Keywords: growth factor
F:1-135/Domain: signal sequence #status predicted <SIG>
F:126-243/Product: nerve growth factor beta chain #status predicted <MAT>

Query Match 88.3% Score 581; DB 2; Length 243;
Best Local Similarity 88.0%; Pred. No. 2.2e-54;
Matches 103; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

OY 3 SSSHPFIRHGEFSVCDVSVMVGDKTTATDINGKENVVLGEVINNSVFRQFEETCRD 62
DB 126 TAPVLRHGEFSVCDVSVMVGDKTTATDINGKENVVLGEVINNSVFRQFEETCRD 185

OY 63 NPVDSGCRGIDSKHNSCTTHTFVKALTMGKQAMRFRIIDTACVLSRKAVR 119
DB 186 RPSVDSGCRGIDSKHNSCTTHTFVKALTMGKQAMRFRIIDTACVLSRKAGR 242
P:186-305/Product: nerve growth factor beta chain #status experimental <MAT>
F:135-180/Binding site: carboxylate (Asn) (covalent) #status predicted
F:202-267,245-295,255-297/Disulfide bonds: #status experimental
F:232/Binding site: carboxylate (Asn) (covalent) #status absent

Query Match 86.5% Score 569; DB 1; Length 303;
Best Local Similarity 87.4%; Pred. No. 5.4e-53;
Matches 104; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

OY 2 SSSHPFIRHGEFSVCDVSVMVGDKTTATDINGKENVVLGEVINNSVFRQFEETCRD 61
DB 184 STHPVFMHGEFSVCDVSVMVGDKTTATDINGKENVVLGEVINNSVFRQFEETCRD 243
P:184-305/Product: nerve growth factor beta chain #status experimental <MAT>
F:135-180/Binding site: carboxylate (Asn) (covalent) #status predicted
F:202-267,245-295,255-297/Disulfide bonds: #status experimental
F:232/Binding site: carboxylate (Asn) (covalent) #status absent

RESULT 7
A:10097
C:Species: Cavia porcellus (guinea pig)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 15-Mar-1996
C:Accession: J10097
R:Schwartz, M.A.; Fisher, D.; Bradshaw, R.A.; Isackson, P.J.
J. Neurochem. 52, 1203-1209, 1989
A:Title: Isolation and sequence of a cDNA clone of beta-nerve growth factor from the
A:Reference number: J10097; MUID:89177243; PMID:2926397
A:Accession: J10097
A:Molecule type: mRNA
A:Residues: 1-241 <SCH>
A:Note: the authors translated the codon GCU for residue 214 as Asp
C:Genetics:
A:Gene: Beta-NGF
C:Superfamily: nerve growth factor beta chain
C:Keywords: glycoprotein; growth factor; hormone
F:1-121/Domain: propeptide #status predicted <PRO>
F:122-241/Product: nerve growth factor beta chain #status predicted <MAT>
F:146-154/Region: receptor binding #status predicted
F:69,114/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 88.1% Score 580; DB 2; Length 241;
Best Local Similarity 87.4%; Pred. No. 2.8e-54;
Matches 104; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

OY 2 SSSHPFIRHGEFSVCDVSVMVGDKTTATDINGKENVVLGEVINNSVFRQFEETCRD 61
DB 122 STHPVFMHGEFSVCDVSVMVGDKTTATDINGKENVVLGEVINNSVFRQFEETCRD 181
P:122-241/Product: nerve growth factor beta chain #status predicted <MAT>
F:135-180/Binding site: carboxylate (Asn) (covalent) #status predicted
F:202-267,245-295,255-297/Disulfide bonds: #status experimental
F:232/Binding site: carboxylate (Asn) (covalent) #status absent

OY 62 PNPVDSGCRGIDSKHNSCTTHTFVKALTMGKQAMRFRIIDTACVLSRKAVR 120
DB 182 PNPVDSGCRGIDSKHNSCTTHTFVKALTMGKQAMRFRIIDTACVLSRKAVR 240

RESULT 8
A:NGRBA
C:Species: Mastomys natalensis
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 18-Jun-1999
C:Accession: J10343
R:Fahnestock, M.; Bell, R.A.
Gene 69, 257-264, 1988
A:Title: Molecular cloning of a cDNA encoding the nerve growth factor precursor from
A:Reference number: J10343; MUID:89172070; PMID:3234767
A:Accession: J10343
A:Molecule type: mRNA
A:Residues: 1-303 <FAH>
A:Cross-references: GB:M22748; MUID:9202514; PIND:AAA0599.1; PID:9202515
A:Note: it is uncertain whether Met-1 or Met-63 is the initiator
C:Superfamily: nerve growth factor beta chain
C:Keywords: glycoprotein; growth factor; homodimer; submaxillary gland
F:184-301/Product: nerve growth factor beta chain #status predicted <MAT>
F:131,176,228/Binding site: carboxylate (Asn) (covalent) #status predicted
F:198-263,241-291,251-293/Disulfide bonds: #status predicted

Query Match 86.5% Score 569; DB 1; Length 303;
Best Local Similarity 87.4%; Pred. No. 5.4e-53;
Matches 104; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

OY 2 SSSHPFIRHGEFSVCDVSVMVGDKTTATDINGKENVVLGEVINNSVFRQFEETCRD 61
DB 184 STHPVFMHGEFSVCDVSVMVGDKTTATDINGKENVVLGEVINNSVFRQFEETCRD 243
P:184-305/Product: nerve growth factor beta chain #status experimental <MAT>
F:135-180/Binding site: carboxylate (Asn) (covalent) #status predicted
F:202-267,245-295,255-297/Disulfide bonds: #status experimental
F:232/Binding site: carboxylate (Asn) (covalent) #status absent

OY 62 PNPVDSGCRGIDSKHNSCTTHTFVKALTMGKQAMRFRIIDTACVLSRKAVR 120
DB 182 PNPVDSGCRGIDSKHNSCTTHTFVKALTMGKQAMRFRIIDTACVLSRKAVR 240

A:Accession: A58566
 A:Molecule type: protein
 A:Residues: 1-116 <ODA>
 A:Experimental source: venom
 C:Comment: Nerve growth factor is necessary for the development of embryonic sympathetic
 C:Complex: homodimer
 C:Superfamily: nerve growth factor beta chain
 C:Keywords: growth factor; homodimer; venom
 F:14-78,56-106,66-108/Disulfide bonds: status predicted

Query Match 67.7%; Score 445.5; DB 2; Length 116;
 Best Local Similarity 69.6%; Pred. No. 2,7e-40;
 Matches 78; Conservative 16; Mismatches 17; Indels 1; Gaps 1;

OY 5 HPFRGEFVSVDVSVWGDKTATDIDKGEVNLGEVINNSVROFEFTKCRDPNP 64
 DB 3 HPVHNLGSHVSCDVSANV-TKTATDIDKNTVTVMENVDKVKYKQFFETCKRNP 61
 OY 65 VDSGCRGIDSKHNSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRK 116
 DB 62 EPGCGRGIDSSHMSYCTETDTFIKALTMGNOASMRIRIETACVITRK 113

RESULT 14

A:Accession: A59218
 A:Molecule type: mRNA
 A:Residues: 1-246 <SEL>
 R:Inoue, S.; Oda, T.; Koyama, J.; Ikeda, K.; Hayashi, K.
 FEBS Lett. 279, 38-40, 1991
 A:Title: Amino acid sequences of nerve growth factors derived from cobra venoms.
 A:Reference number: S13927; MUID:9118755; PMID:1995338
 A:Accession: S13965
 A:Molecule type: protein
 A:Residues: 131-246 <INO>
 A:Experimental source: venom
 C:Comment: Nerve growth factor is necessary for the development of embryonic sympathetic
 C:Complex: homodimer
 C:Superfamily: nerve growth factor beta chain
 C:Keywords: growth factor; homodimer; venom
 F:1-23/Domain: signal sequence; status predicted <SIG>
 F:131-246/Product: nerve growth factor beta chain; status experimental <MAT>
 F:144-208,186-236,196-238/Disulfide bonds: status predicted

Query Match 67.7%; Score 445.5; DB 2; Length 246;
 Best Local Similarity 69.6%; Pred. No. 6.3e-40;
 Matches 78; Conservative 16; Mismatches 17; Indels 1; Gaps 1;

OY 5 HPFRGEFVSVDVSVWGDKTATDIDKGEVNLGEVINNSVROFEFTKCRDPNP 64
 DB 133 HPVHNLGSHVSCDVSANV-TKTATDIDKNTVTVMENVDKVKYKQFFETCKRNP 191
 OY 65 VDSGCRGIDSKHNSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRK 116
 DB 192 EPGCGRGIDSSHMSYCTETDTFIKALTMGNOASMRIRIETACVITRK 243

RESULT 15

A:Accession: A51709
 A:Molecule type: protein
 A:Residues: 1-116 <ODA>
 A:Experimental source: venom
 C:Comment: Nerve growth factor is necessary for the development of embryonic sympathetic
 C:Complex: homodimer
 C:Superfamily: nerve growth factor beta chain
 C:Keywords: growth factor; homodimer; venom
 F:1-23/Domain: signal sequence; status predicted <SIG>
 F:131-246/Product: nerve growth factor beta chain; status experimental <MAT>
 F:144-208,186-236,196-238/Disulfide bonds: status predicted

A:Title: Brain-derived neurotrophic factor is more highly conserved in structure and
 A:Reference number: 151708; MUID:92333301; PMID:1629719
 A:Accession: 151709
 A:Status: preliminary; translated from GR/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-194 <GOT>
 A:Cross-references: EMBL:X59941; NID:965277; PIDN:CAA42566.1; PID:965278
 C:Genetics:
 A:Gene: NGF
 C:Superfamily: nerve growth factor beta chain
 C:Keywords: glycoprotein; growth factor
 F:1-14/Domain: signal sequence; status predicted <SIG>
 F:15-79/Domain: signal sequence; status predicted <PRO>
 F:80-194/Product: nerve growth factor beta chain; status predicted <MAT>
 F:90-155,133-183,143-185/Disulfide bonds: status predicted
 F:99/Binding site: carbohydrate (Asn) (covalent); status predicted

Query Match 59.0%; Score 388; DB 2; Length 194;
 Best Local Similarity 66.1%; Pred. No. 6.5e-34;
 Matches 72; Conservative 11; Mismatches 26; Indels 0; Gaps 0;

OY 9 HRGEFVSVDVSVWGDKTATDIDKGEVNLGEVINNSVROFEFTKCRDPNPVDSG 68
 DB 83 HRGVSVCSVSVMGKTKATDIDSGKEVTLPTVINNNVKKYFETCTHSPGSGSR 142
 OY 69 CRGIDSKHNSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRK 117
 DB 143 CLGIDARHNSHCTNSHFEVRLTISSENOVAMRLIRIVACVLSRK 191

Search completed: December 2, 2002, 15:13:58
 Job time: 10.646 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 2, 2002, 15:05:43 ; Search time 4.96483 Seconds
(without alignments)
1010.837 Million cell updates/sec

Title: US-10-072-681-2

Perfect score: 1 PSSMPTFRHGRFSVCDYS.....FIRIDTACVCLSRKAVRA 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	648	98.5	241 1	NGF_HUMAN
2	640	97.3	229 1	NGF_PIG
3	618	93.9	231 1	NGF_BOVIN
4	599	91.0	241 1	NGF_RAT
5	587	89.2	241 1	NGF_MOUSE
6	581	88.3	243 1	NGF_CHICK
7	580	88.1	241 1	NGF_CAVPO
8	569	86.5	241 1	NGF_PANNA
9	563	85.6	231 1	NGF_XENLA
10	488	74.2	243 1	NGF_BUNMU
11	481	73.1	117 1	NGF_DABRR
12	446.5	67.9	116 1	NGF_MAJAT
13	442.5	67.2	116 1	NGF_MAJAT
14	388	59.0	134 1	NGF_XIPMA
15	380.5	57.8	257 1	NGF_CHICK
16	380.5	57.8	257 1	NT3_HUMAN
17	380.5	57.8	258 1	NT3_MOUSE
18	380.5	57.8	258 1	NT3_XENLA
19	379.5	57.7	260 1	NT3_RAT
20	376.5	57.2	257 1	NT3_FELCA
21	370.5	56.3	223 1	NT3_BRARE
22	365.5	55.5	140 1	NT_CYPCA
23	345.5	49.5	255 1	BDNF_CAVPO
24	345.5	49.3	247 1	BDNF_HUMAN
25	345.5	49.3	247 1	BDNF_PROLO
26	345.5	49.3	247 1	BDNF_URSAR
27	345.5	49.3	247 1	BDNF_URSML
28	345.5	49.3	249 1	BDNF_MOUSE
29	345.5	49.3	249 1	BDNF_RAT
30	340.5	48.7	232 1	BDNF_PIG
31	340.5	48.7	114 1	BDNF_MACMU
32	340.5	48.7	247 1	BDNF_FELCA
33	319.5	48.6	270 1	BDNF_CYPCA

34	318.5	48.4	248 1	BDNF_BOVIN	095106 bos taurus
35	317.5	48.3	246 1	BDNF_CHICK	P25429 gallus gall
36	310.5	47.2	269 1	BDNF_XIPMA	002193 xiphophorus
37	308.5	46.9	236 1	NT4_XENLA	P24727 xenopus lae
38	307.5	46.7	210 1	NT5_HUMAN	P34130 homo sapien
39	305.5	46.4	209 1	NT5_RAT	P34131 rattus norv
40	304.5	46.3	114 1	BDNF_XENLA	P25432 xenopus lae
41	215	33.7	257 1	NT6B_HUMAN	P34133 homo sapien
42	214	33.5	186 1	NT6A_HUMAN	P34134 homo sapien
43	212	32.2	257 1	NGF_HUMAN	P25428 viper lae
44	190	28.9	42 1	NGF_VIPLE	P25430 raja claval
45	129	19.6	43 1	BDNF_RAVCL	

RESULT 1	ALIGNMENTS
NGF_HUMAN	
ID NGF_HUMAN	STANDARD: PRT: 241 AA.
AC P01138:	
DT 21-JUL-1986 (Rel. 01, Created)	
DT 01-JAN-1990 (Rel. 13, Last sequence update)	
DT 16-OCT-2001 (Rel. 40, Last annotation update)	
DE Beta-nerve growth factor precursor (Beta-NGF).	
GN NGFB.	
OS Homo sapiens (Human).	
OC Eukaryote; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	
OX NCBI_Taxid:9606;	
NP [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE-83244969; PubMed-6688123;	
RA Ullrich A., Gray A., Berman C., Dull T.J.:	
RT "Human beta-nerve growth factor gene sequence highly homologous to	
RT that of mouse."	
RL Nature 303:821-825(1983).	
RN [2]	
RP SEQUENCE FROM N.A.	
RX MEDLINE-84205655; PubMed-6327169;	
RA Ullrich A., Gray A., Berman C., Coussens L., Dull T.J.:	
RT "Sequence homology of human and mouse beta-NGF subunit genes."	
RL Cold Spring Harb. Symp. Quant. Biol. 48:435-442(1983).	
RN [3]	
RP SEQUENCE FROM N.A.	
RX MEDLINE-90326556; PubMed-2374737;	
RA Borzani G., Pizzuti A., Ruggeri E.I., Fallini A., Sallani V.,	
RT "CDNA sequence of human beta-NGF."	
RL Nucleic Acids Res. 18:4020-4020(1990).	
RN [4]	
RP SEQUENCE OF 178-219 FROM N.A.	
RX MEDLINE-9122573; PubMed-2025430;	
RA Hallboeck F., Ibanez C.F., Persson H.:	
RT "Evolutionary studies of the nerve growth factor family reveal a	
RT novel member abundantly expressed in xenopus ovary."	
RL Neuron 6:845-858(1991).	
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND	
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT	
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND	
CC EMBRYONIC SENSORY NEURONS.	
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.	
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.	
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CC EMBL: V01511; CAA24755.1; -
DR EMBL: M21062; AA59931.1; -
DR EMBL: X52589; CAA16832.1; -
DR PIR: A01399; NCUBM.
DR PIR: S10253; S10253.
DR HSSP: P01139; 1BET.
DR HSSP: P01139; 1BET.
DR GeneW: HGNC:7808; NGFB.
DR MIM: 162030; -
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF_1.
DR PRINTS: PR00268; NGF.
DR PRODOM: PD002052; NGF_1.
DR SMART: SM00140; NGF_1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS0270; NGF_2; 1.
DR Growth factor: Signal.
KW SIGNAL.
FT PROPEP 1 18
FT CHAIN 122 241
FT DISULFID 136 201
FT DISULFID 179 229
FT DISULFID 189 231
FT CARBOHYD 69 69
FT CARBOHYD 114 114
SO SEQUENCE 241 AA; 26987 MW; CF1D84DC6B736B0F CRC64;

```

Query Match 98.5%: Score 648; DB 1; Length 241;

Best Local Similarity 99.2%: Pred. No. 4,4e-62; Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 2 SSSHPFHRGFEVSCDSVWVGDKTTATDIDKRENVVLCGEVNIINSVFRQYFEETKCD 61
DB 122 SSSHPFHRGFEVSCDSVWVGDKTTATDIDKRENVVLCGEVNIINSVFRQYFEETKCD 181
OY 62 PNPVDSGCGIDSKHNSYCTTHTFYKALTMDSKQAMRIRIDTACVCLSKKAVRA 121
DB 182 PNPVDSGCGIDSKHNSYCTTHTFYKALTMDSKQAMRIRIDTACVCLSKKAVRA 241

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RESULT 2

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NGF_PIG STANDARD: PRT: 229 AA.
AC 029074;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Beta-nerve growth factor precursor (Beta-NGF) (Fragment).
GN NGFB.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
NCBI_TaxID=9823;
RX NCBI_TaxID=9823;
RP SEQUENCE FROM N.A.
RC STRAIN=Large white; TISSUE=Blood;
RC MEDLINE=94313891; PubMed=8039422;
RA Lablbld-Mansala Y.; Mellink C.; Terle M.; Gellin J.;
RA "A new marker (NGFB) on pig chromosome 4, isolated by using a
RT consensus sequence conserved among species."
RT Cytogenet. Cell Genet. 67:120-125(1994).
RL FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
EMBRYONIC SENSORY NEURONS.
CC SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC -----
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CC EMBL: L31898; AAA21301.1; -
DR HSSP: P01139; 1BET.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF_1.
DR PRODOM: PD002052; NGF_1.
DR SMART: SM00140; NGF_1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS0270; NGF_2; 1.
DR Growth factor: Signal.
KW NON_TER
FT SIGNAL 1 1
FT PROPEP 7 109
FT CHAIN 110 229
FT DISULFID 124 189
FT DISULFID 167 217
FT DISULFID 177 219
FT CARBOHYD 57 57
FT CARBOHYD 102 102
FT CARBOHYD 154 154
SO SEQUENCE 229 AA; 25275 MW; FE8890771CBA3189 CRC64;

```

Query Match 97.3%: Score 640; DB 1; Length 229;

Best Local Similarity 97.3%: Pred. No. 3e-61; Matches 117; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

OY 2 SSSHPFHRGFEVSCDSVWVGDKTTATDIDKRENVVLCGEVNIINSVFRQYFEETKCD 61
DB 110 SSSHPFHRGFEVSCDSVWVGDKTTATDIDKRENVVLCGEVNIINSVFRQYFEETKCD 169
OY 62 PNPVDSGCGIDSKHNSYCTTHTFYKALTMDSKQAMRIRIDTACVCLSKKAVRA 121
DB 170 PNPVDSGCGIDSKHNSYCTTHTFYKALTMDSKQAMRIRIDTACVCLSKKAVRA 229

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RESULT 3

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NGF_BOVIN STANDARD: PRT: 231 AA.
AC P13600; O18969.
DT 01-JAN-1980 (Rel. 13, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Beta-nerve growth factor precursor (beta-NGF) (Fragment).
GN NGFB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovine; Bos.
NCBI_TaxID=9913;
RX NCBI_TaxID=9913;
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RC MEDLINE=97430845; PubMed=9284944;
RA Elidugue C.; Laurent P.; Hayes H.; Rodellar C.; Levezuel H.;
RA Zaragoza P.;
RA "Assignment of the beta-nerve growth factor (NGFB) to bovine
RT chromosome 3 band q23 by in situ hybridization."
RT Cytogenet. Cell Genet. 77:306-307(1997).
RL EMBL J. 51489-1493(1986).
RP SEQUENCE OF 107-231 FROM N.A.
RX MEDLINE=86300647; PubMed=2427334;
RA Meiler R.; Becker-Andre M.; Goltz R.; Heumann R.; Shaw A.; Thoenen H.;
RA "Molecular cloning of bovine and chick nerve growth factor (NGF):
RT delineation of conserved and unconserved domains and their
RT relationship to the biological activity and antigenicity of NGF."
RL EMBL J. 51489-1493(1986).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
EMBRYONIC SENSORY NEURONS.
CC SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.

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CC      -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: Y09566; CAA70759.1; -
CC      DR EMBL: M25809; AAA30666.1; -
CC      DR PIR: A26312; A26312.
CC      DR HSSP: P01139; 1BET.
CC      DR InterPro: IPR002072; NGF.
CC      DR Pfam: PF00243; NGF; 1.
CC      DR ProDom: PD002052; NGF; 1.
CC      DR SMART: SM00140; NGF; 1.
CC      DR PROSITE: PS00248; NGF_1; 1.
CC      DR PROSITE: PS50270; NGF_2; 1.
CC      KM Growth factor; Signal.
CC      FT SIGNAL 1
CC      FT PROPEP 9
CC      FT CHAIN 111
CC      FT DISULFID 126
CC      FT DISULFID 169
CC      FT DISULFID 179
CC      FT CARBOHYD 156
CC      FT CONFLICT 118
CC      FT CONFLICT 161
CC      FT CONFLICT 230
CC      SQ SEQUENCE 231 AA; 25437 MW; 01605099291A418C CRC64;

Query Match          93.9%; Score 618; DB 1; Length 231;
Best Local Similarity 96.5%; Pred. No. 6, 8e-59;
Matches 111; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY      2 SSSHHFIRGERSVCDVSVMGDKTTATDITDKGEVYVLCGVNINNSVFRQYFFETKCRD 61
DB      112 SSSHHVLRHGFSEVCDVSVMGDKTTATDITDKGEVYVLCGVNINNSVFRQYFFETKCRD 171
OY      62 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDCOKAAMRFIRIDTACVCLSRK 116
DB      172 PNPVDSGCRGIDAKHNSYCTTHTFVKALTMDCOKAAMRFIRIDTACVCLSRK 226

RESULT 4
NGF_RAT
ID NGF_RAT STANDARD: PRT; 241 AA.
AC P25427;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Beta-nerve growth factor precursor (Beta-NGF).
GN NGFB.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=89037223; PubMed=1184206;
RA Whittemore S.R., Friedman P.L., Lathamar D.G., Persson H.,
RT Gonzalez-Carvajal M., Molets V.R.;
RT "Rat beta-nerve growth factor sequence and site of synthesis in the
RT adult hippocampus.";
RL J. Neurosci. Res. 20:403-410(1988).
RN 12
RP SEQUENCE OF 178-219 FROM N.A.
RX STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=9122573; PubMed=2025430;
RA Hallboeck F., Ibanez C.F., Persson H.;

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RT      *Evolutionary studies of the nerve growth factor family reveal a
RT      novel member abundantly expressed in Xenopus ovary.*;
RT      Neuron 6:845-858(1991).
CC      -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC      MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC      STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC      EMBRYONIC SENSORY NEURONS.
CC      -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
CC      -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC      -----
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: M3589; AAA1697.1; ALT_INIT.
CC      DR HSSP: P01139; 1BET.
CC      DR InterPro: IPR002072; NGF.
CC      DR Pfam: PF00243; NGF; 1.
CC      DR PRINTS: PRO0268; NGF.
CC      DR ProDom: PD002052; NGF; 1.
CC      DR SMART: SM00140; NGF; 1.
CC      DR PROSITE: PS00248; NGF_1; 1.
CC      DR PROSITE: PS50270; NGF_2; 1.
CC      KM Growth factor; Signal.
CC      FT SIGNAL 1
CC      FT PROPEP 19
CC      FT CHAIN 122
CC      FT DISULFID 136
CC      FT DISULFID 179
CC      FT DISULFID 189
CC      FT CARBOHYD 69
CC      FT CARBOHYD 114
CC      FT CARBOHYD 166
CC      SQ SEQUENCE 241 AA; 27009 MW; 665F4237156323D CRC64;

Query Match          91.0%; Score 599; DB 1; Length 241;
Best Local Similarity 91.6%; Pred. No. 7, 6e-57;
Matches 109; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY      2 SSSHHFIRGERSVCDVSVMGDKTTATDITDKGEVYVLCGVNINNSVFRQYFFETKCRD 61
DB      122 SSSHHVLRHGFSEVCDVSVMGDKTTATDITDKGEVYVLCGVNINNSVFRQYFFETKCRD 181
OY      62 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDCOKAAMRFIRIDTACVCLSRK 120
DB      182 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDCOKAAMRFIRIDTACVCLSRK 240

RESULT 5
NGF_MOUSE
ID NGF_MOUSE STANDARD: PRT; 241 AA.
AC P01139; Q63864;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Beta-nerve growth factor precursor (Beta-NGF).
GN NGFB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=83167518; PubMed=6336309;
RA Scott J., Selby M.J., Urdas M.S., Ouliroga M., Bell G.I., Ruter M.J.;
RT "Isolation and nucleotide sequence of a cDNA encoding the precursor
RT of mouse nerve growth factor.";
RL Nature 302:538-540(1983).
RN 12

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RP SEQUENCE FROM N.A.
 RX MEDLINE-83244969; PubMed-6688123;
 RA Ullrich A., Gray A., Berman C., Dull T.J.;
 RT "Human beta-nerve growth factor gene sequence highly homologous to
 RL that of mouse.";
 RN Nature 303:821-825(1983).
 RP SEQUENCE FROM N.A.
 RX MEDLINE-84206565; PubMed-63377169;
 RA Ullrich A., Gray A., Berman C., Coussens L., Dull T.J.;
 RT "Sequence homology of human and mouse beta-MGF subunit genes.";
 RL Cold Spring Harb. Symp. Quant. Biol. 48:435-442(1983).
 RP SEQUENCE FROM N.A.
 RX MEDLINE-88038855; PubMed-3670305;
 RA Selby M.J., Edwards R., Sharp F., Rutter W.J.;
 RT "Mouse nerve growth factor gene: structure and expression.";
 RL Mol. Cell. Biol. 7:3057-3064(1987).
 RP SEQUENCE FROM N.A.
 RX MEDLINE-93264918; PubMed-1284621;
 RA Yamamoto T., Yamakuni T., Okabe N., Amano T.;
 RT "Production and secretion of nerve growth factor by clonal striated
 RL muscle cell line, 88-1.";
 RN Neurochem. Int. 21:251-258(1992).
 RP SEQUENCE OF 127-239.
 RX MEDLINE-73075048; PubMed-4566923;
 RA Angeletti R.H., Hermodson M.A., Bradshaw R.A.;
 RT Amino acid sequences of mouse 2.5S nerve growth factor. II.
 RL Isolation and characterization of the thermolabile and peptic peptides
 and the complete covalent structure.";
 RN Biochemistry 12:1100-115(1973).
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE-93065986; PubMed-1956407;
 RA McDonald N.O., Lapatto R., Murray-Rust J., Gunning J., Wlodawer A.,
 RL Blundell T.L.;
 RT "New protein fold revealed by a 2.3-A resolution crystal structure of
 RL nerve growth factor.";
 RN Nature 354:411-414(1991).
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE-94260545; PubMed-8201620;
 RA Holland D.R., Coussens L.S., Meng W., Matthews B.W.;
 RT "Nerve growth factor in different crystal forms displays structural
 RL flexibility and reveals a zinc binding sites.";
 RN J. Mol. Biol. 239:385-400(1994).
 RP X-RAY CRYSTALLOGRAPHY (3.15 ANGSTROMS) OF 7S COMPLEX.
 RX STRAIN-Swiss Webster; TISSUE-Submaxillary gland;
 RL MEDLINE-98035451; PubMed-9351801;
 RA Bax B., Blundell T.L., Murray-Rust J., McDonald N.O.;
 RT "Structure of mouse 7S NGF: a complex of nerve growth factor with
 RL four binding proteins.";
 RN Structure 5:1175-1285(1997).
 RP MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 CC EMBRYONIC SENSORY NEURONS.
 CC -1- SUBUNIT. HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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 CC -----
 CC EMBL; M35075; AAA39818.1; ALT_INIT.

DR EMBL; V00836; CAA24221.1; ALT_INIT.
 DR EMBL; K01759; AAA39820.1; ALT_INIT.
 DR EMBL; M14805; AAA39821.1; ALT_INIT.
 DR EMBL; M17298; AAA37687.1; ALT_INIT.
 DR EMBL; M17296; AAA37687.1; JOINED.
 DR EMBL; M17297; AAA37687.1; JOINED.
 DR EMBL; S62089; CAB32081.2; ALT_SEQ.
 DR PIR; A01400; NGNSMG.
 DR PDB; 1BET; 31-MAY-94.
 DR PDB; 1BFG; 08-MAR-96.
 DR PDB; 1SGF; 27-MAY-98.
 DR MGD; MGI:97321; Ngf.
 DR InterPro; IPR02072; NGF.
 DR Pfam; PF00243; NGF; 1.
 DR PRINTS; PR0268; NGF.
 DR ProDom; PD02052; NGF; 1.
 DR SMART; SM00140; NGF; 1.
 DR PROSITE; PS00248; NGF_1; 1.
 DR PROSITE; PS0270; NGF_2; 1.
 KW Growth factor; Signal; 3D-structure.
 FT SIGNAL 1 18
 FT PROPEP 19 121
 FT CHAIN 122 241 BETA-NERVE GROWTH FACTOR.
 FT DISULFID 136 201
 FT DISULFID 179 229
 FT DISULFID 189 231
 FT CARBOHYD 69 69
 FT CARBOHYD 114 114 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CONFLICT 233 241 LSKRATRG -> CSACRLOEFA (IN REF. 5).
 SQ SEQUENCE 241 AA; 27076 MW; 164465EDC55081 CRC64;
 Query Match 89.2%; Score 587; DB 1; Length 241;
 Best Local Similarity 90.8%; Pred. No. 1,56-55;
 Matches 108; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
 Oy 2 SSSHPFHRGESEFVCSVWVGDKTTATDINGKENVLAGEVINNSVFRQYFEETCRD 61
 Db 122 SSTRHPFHRGESEFVCSVWVGDKTTATDINGKENVLAGEVINNSVFRQYFEETCR 181
 Oy 62 PNPVDSGCRGIDSKHNSYCTTHTFYVALTMDGQAARIRIDTCVCLSKKAVR 120
 Db 182 SNPVESGCRGIDSKHNSYCTTHTFYVALTMDGQAARIRIDTCVCLSKKATR 240
 RESULT 6
 NGF_CHICK STANDARD; PRT; 243 AA.
 ID NGF_CHICK
 AC P05200;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Beta-nerve growth factor precursor (Beta-NGF).
 GN NGFB.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-86300646; PubMed-3017695;
 RA Ebendahl T., Larhammar D., Persson H.;
 RT "Structure and expression of the chicken beta nerve growth factor
 RL gene.";
 RN EMBL J. 5:1483-1487(1986).
 RP SEQUENCE OF 118-243 FROM N.A.
 RX MEDLINE-86248129; PubMed-3720959;
 RA Wion D., Perret C., Frechin N., Keller A., Behar G., Brachet P.,
 RA Auffrey C.;
 RT "Molecular cloning of the avian beta-nerve growth factor gene:
 RT transcription in brain";
 RL FEBS Lett. 203:82-86(1986).

```

RN [3]
RN SEQUENCE OF 121-243 FROM N.A.
RX MEDLINE-86300647; PubMed-2427334;
RX Meier R., Becker-Andre M., Gotz R., Heumann R., Shaw A., Thoenen H.;
RT "Molecular cloning of bovine and chick nerve growth factor (NGF):
RT delineation of conserved and unconserved domains and their
RT relationship to the biological activity and antigenicity of NGF.";
RL EMBL J. 5:1489-1493(1986).
RN [4]
RN SEQUENCE OF 181-222 FROM N.A.
RX MEDLINE-91222573; PubMed-2025430;
RX Hallboeek F., Ibanez C.F., Persson H.;
RT "Evolutionary studies of the nerve growth factor family reveal a
RT novel member abundantly expressed in Xenopus ovary.";
RL Neuron 6:845-858(1991).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS.
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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CC -----
DR EMBL: X04003; CAA27633.1; ALT_INIT.
DR EMBL: X04067; CAA27703.1; -.
DR EMBL: M26810; AAA48984.1; -.
DR PIR: A24857; A24857.
DR PIR: A26311; A26311.
DR HSP: P01139; 1BER.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF.
DR PRINTS: PR00268; NGF.
DR PRODOM: PD002052; NGF. 1.
DR SMART: SM00140; NGF. 1.
DR PROSITE: PS00248; NGF. 1.
DR PROSITE: PS50270; NGF_2; 1.
KW Growth factor; Signal.
FT SIGNAL 1 22
FT PROPEP 23 125
FT CHAIN 126 243
FT DISULFID 139 204
FT DISULFID 182 232
FT DISULFID 192 234
SQ SEQUENCE 243 AA; 27138 MM; 74C306CB2079DA07 CRC64;

Query Match 88.38; Score 581; DB 1; Length 243;
Best Local Similarity 88.08; Pred. No. 6.4e-55;
Matches 103; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

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GN NGF.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathii; Caviidae; Cavia.
OX NCBI_TaxID:10141;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE-89177243; PubMed-2926397;
RX Schwartz M.A., Fisher D., Bradshaw R.A., Isackson P.J.;
RT "Isolation and sequence of a cDNA clone of beta-nerve growth factor
RT from the guinea pig prostate gland.";
RL J. Neurochem. 52:1203-1209(1989).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS.
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC PIR: J10097; J10097.
DR HSP: P01139; 1BER.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF. 1.
DR PRINTS: PR00268; NGF. 1.
DR PRODOM: PD002052; NGF. 1.
DR SMART: SM00140; NGF. 1.
DR PROSITE: PS00248; NGF. 1.
DR PROSITE: PS50270; NGF_2; 1.
KW Growth factor; Signal.
FT SIGNAL 1 18
FT PROPEP 19 121
FT CHAIN 122 241
FT DISULFID 136 201
FT DISULFID 179 229
FT DISULFID 189 231
FT CARBOHYD 69 69
FT CARBOHYD 114 114
SQ SEQUENCE 241 AA; 26821 MM; 2F4E26B197804BF4 CRC64;

Query Match 88.18; Score 580; DB 1; Length 241;
Best Local Similarity 87.48; Pred. No. 8.1e-55;
Matches 104; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

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RESULT 7
NGF_CAVPO STANDARD: PRT; 241 AA.
ID NGF_CAVPO
AC P19093;
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Beta-nerve growth factor precursor (Beta-NGF).

Db 3 SSHPIHNGEFSVCDVSVMWGDKTATADIKGEVWVLGEVINNNVSFYRQYFEETKCRDP 62
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 126 TAPVYHNGEFSVCDVSVMWGDKTATADIKGEVWVLGEVINNNVSFYRQYFEETKCRDP 185
OY 63 PNPVDSGCRGIDSKHNSYCTTHTFVKALTWGQKQAMRFRIDTACVCLSKRAVR 119
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 186 RPYSSGCRGIDSKHNSYCTTHTFVKALTWGQKQAMRFRIDTACVCLSKRAVR 242

RESULT 8
NGF_PPRANA STANDARD: PRT; 241 AA.
ID NGF_PPRANA
AC P20675;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Beta-nerve growth factor precursor (Beta-NGF).
GN NGF.
OS Praomys natalensis (African soft-furred rat) (Mastomys natalensis).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
OX Mastomys.
OX NCBI_TaxID:10112;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE-89172070; PubMed-3234767;
RX Fahnestock M., Bell R.A.;
RT "Molecular cloning of a cDNA encoding the nerve growth factor
RT precursor from Mastomys natalensis.";
Gene 69:257-264(1988).

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CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS.
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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CC -----
CC EMBL: M22748; AAA40599.1; ALT_INIT.
CC DR PIR: J70343; NGRTBA.
CC DR HSSP: P01139; 1BRTG.
CC DR InterPro: IPR002072; NGF.
CC DR Pfam: PF00243; NGF_1.
CC DR PRINTS: PR00268; NGF.
CC DR PRODOM: PD002052; NGF_1.
CC DR SMART: SM00140; NGF_1.
CC DR PROSITE: PS00248; NGF_1; 1.
CC DR PROSITE: PS50270; NGF_2; 1.
CC KW Growth factor; Signal.
CC FT SIGNAL 1 18 POTENTIAL.
CC FT PROPEP 19 121 BETA-NERVE GROWTH FACTOR.
CC FT CHAIN 132 241 BY SIMILARITY.
CC FT DISULFID 136 201 BY SIMILARITY.
CC FT DISULFID 179 229 BY SIMILARITY.
CC FT DISULFID 189 231 BY SIMILARITY.
CC FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SO SEQUENCE 241 AA; 27035 MW; 88FB8207A1F8B2E7 CRC64;

Query Match 86.5%; Score 569; DB 1; Length 241;
Best Local Similarity 87.4%; Pred. No. 1.2e-53;
Matches 104; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

OY 2 SSSHPFRGEFSVCDSSVWVGDKTTATDINGKEVNLGCVNINNSVFOYFEETKCRD 61
DB 122 SSTRPVQMGESVCDSSVWVGDKTTATDINGKEVNLGCVNINNSVFOYFEETKCR 101
OY 62 PNPVDSGRCIDSKHNSYCTTHTFFVKALTMGDKQAMRFRIIDTACVCLSKAVRR 120
DB 182 RNPVSSGCRGIDSKHNSYCTTHTFFVKALTMGDKQAMRFRIIDTACVCLSKAVRR 240

RESULT 9
NGF_XENLA STANDARD: PRT; 231 AA.
ID NGF_XENLA P31617;
AC 01-MAY-1991 (Rel. 18, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Nerve growth factor precursor (NGF).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8155;
RN 11;
RP SEQUENCE FROM N.A.
RA Cardiero F., Campioni M., Cardinelli B., Pierandrea-Maidi P.;
RT "Structure and expression of the nerve growth factor gene in Xenopus
RT oocytes and embryos."
RL Mol. Reprod. Dev. 29:313-322(1991).
RM 121
RC SEQUENCE OF 170-211 FROM N.A.
TISSUE=Liver;

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RX MEDLINE-91222573; PubMed-2025430;
RA Hallboeck F., Ibanez C.F., Persson H.;
RT "Evolutionary studies of the nerve growth factor family reveal a
RT novel member abundantly expressed in Xenopus ovary."
RL Neuron 6:845-858(1991).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS.
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC -----
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CC -----
CC EMBL: X55716; CAA39249.1; ALT_INIT.
CC DR PIR: S14481; S14481.
CC DR HSSP: P01139; 1BET.
CC DR InterPro: IPR002072; NGF.
CC DR Pfam: PF00243; NGF_1.
CC DR PRINTS: PR00268; NGF.
CC DR PRODOM: PD002052; NGF_1.
CC DR SMART: SM00140; NGF_1.
CC DR PROSITE: PS00248; NGF_1; 1.
CC DR PROSITE: PS50270; NGF_2; 1.
CC KW Growth factor; Signal.
CC FT SIGNAL 1 18 POTENTIAL.
CC FT PROPEP 19 114 NERVE GROWTH FACTOR.
CC FT CHAIN 115 231 BY SIMILARITY.
CC FT DISULFID 118 201 BY SIMILARITY.
CC FT DISULFID 171 221 BY SIMILARITY.
CC FT DISULFID 181 223 BY SIMILARITY.
CC FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 107 107 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SO SEQUENCE 231 AA; 26416 MW; 72A04E7D00B858C5 CRC64;

Query Match 85.6%; Score 563; DB 1; Length 231;
Best Local Similarity 88.4%; Pred. No. 5.1e-53;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

OY 5 HPIFRGEFSVCDSSVWVGDKTTATDINGKEVNLGCVNINNSVFOYFEETKCRDNP 64
DB 117 HPIVLRGEFSVCDSSVWVGDKTTATDINGKEVNLGCVNINNSVFOYFEETKCRDNP 176
OY 65 VDSGCRGIDSKHNSYCTTHTFFVKALTMGDKQAMRFRIIDTACVCLSKR 116
DB 177 VSSGCRGIDSKHNSYCTTHTFFVKALTMGDKQAMRFRIIDTACVCLSKR 228

RESULT 10
NGF_BUNMU STANDARD: PRT; 243 AA.
ID NGF_BUNMU P34128;
AC 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Nerve growth factor precursor (NGF).
OS Bungarus multicinctus (Many-banded krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Serpentes; Colubroidea;
OC Elapidae; Bungarinae; Bungarus.
OX NCBI_TaxID=8616;
RN 11;
RP SEQUENCE FROM N.A.
RA Tissue=Venom gland;
RC MEDLINE-93192074; PubMed-7916740;
RA Danse J.M., Garnier J.M.;

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RT      "Molecular cloning of a cDNA encoding a nerve growth factor precursor
RL      from the krait, Bungarus multicinctus."
CC      8:77-86(1993).
CC      -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC      MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC      STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC      EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
CC      NEURONS IN THE BRAIN.
CC      -1- SUBUNIT: HOMODIMER.
CC      -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC      -----
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CC      entities requires a license agreement (See http://www.1sb-rib.ch/announce/
CC      or send an email to license@1sb.ch).
CC      -----
DR      EMBL: S56213; AAB25729.1; -
DR      HSSP: P01139; 1BET.
DR      InterPro: IPR002072; NGF.
DR      Pfam: PF00243; NGF; 1.
DR      PRINTS: PR00268; NGF.
DR      ProDom: PD002052; NGF; 1.
DR      SMART: SM00140; NGF; 1.
DR      PROSITE: PS00248; NGF_1; 1.
DR      PROSITE: PS50270; NGF_2; 1.
KM      Growth factor, Signal.
FT      SIGNAL 1 18
FT      PROPEP 19 125
FT      CHAIN 126 243
FT      DISULFID 139 204
FT      DISULFID 182 232
FT      DISULFID 192 234
SQ      SEQUENCE 243 AA; 27514 MW; E33F6B142179A08 CRC64;

Query Match 74.2%; Score 488; DB 1; Length 243;
Best Local Similarity 73.0%; Pred. No. 5.5e-45;
Matches 84; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

OY      2 SSSPIRFRGEFSVCDVSVWVGDKTATDIDKREVMVLGEVINNSVPROYFETKCRDNP 61
DB      125 NENPVPNNGEHSVCDVSVWVANKTKATIDIGNVTYVAVDNLNENYKQFFETKCRN 184
OY      62 PNPVDSGCRGIDSKHNSYCTTHTTFVKALYMDGKQAMRFRIIDPACVCLSRK 116
DB      185 PNPVDSGCRGIDSKHNSYCTTHTTFVKALYMDGKQAMRFRIIDPACVCLSRK 239

RESULT 11
NGF_DABRR
ID      NGF_DABRR STANDARD: PRT; 117 AA.
AC      P30894;
DT      01-JUL-1993 (Rel. 26, Created)
DT      01-JUL-1993 (Rel. 26, Last sequence update)
DT      01-NOV-1997 (Rel. 35, Last annotation update)
DE      Nerve growth factor (NGF).
OS      Dabolia russelli russelli (Russell's viper) (Vipera russelli russelli).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Lepidosteauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC      Viperidae; Viperinae; Dabolia.
OX      NCBI_TaxID=31159;
RN      [1]
RP      SEQUENCE.
RC      TISSUE-Venom;
RA      MEDLINE-93120151; PubMed-1477101;
RA      Koyama J.-I., Inoue S., Ikeda K., Hayashi K.;
RT      "Purification and amino acid sequence of a nerve growth factor from
RL      the venom of Vipera russelli russelli."
RL      Biochim. Biophys. Acta 1160:287-292(1992).
CC      -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC      MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT

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CC      STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC      EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
CC      NEURONS IN THE BRAIN.
CC      -1- SUBUNIT: HOMODIMER.
CC      -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC      PIR: S28161; S28161.
DR      HSSP: P01139; 1BET.
DR      InterPro: IPR002072; NGF.
DR      Pfam: PF00243; NGF; 1.
DR      PRINTS: PR00268; NGF.
DR      ProDom: PD002052; NGF; 1.
DR      SMART: SM00140; NGF; 1.
DR      PROSITE: PS00248; NGF_1; 1.
DR      PROSITE: PS50270; NGF_2; 1.
KM      Glycoprotein; Growth factor.
FT      DISULFID 12 77
FT      DISULFID 55 105
FT      DISULFID 65 107
FT      CARBOHYD 21 21
SQ      SEQUENCE 117 AA; 13283 MW; A64559C5FEC11P66 CRC64;

Query Match 73.1%; Score 481; DB 1; Length 117;
Best Local Similarity 73.2%; Pred. No. 1.4e-44;
Matches 82; Conservative 20; Mismatches 10; Indels 0; Gaps 0;

OY      5 HPIFRGEFSVCDVSVWVGDKTATDIDKREVMVLGEVINNSVPROYFETKCRDNP 64
DB      1 HPIFRGEFSVCDVSVWVANKTKATIDIGNVTYVAVDNLNENYKQFFETKCRN 60
OY      65 VDSGCRGIDSKHNSYCTTHTTFVKALYMDGKQAMRFRIIDPACVCLSRK 116
DB      61 VPSGCRGIDAKHNSYCTTHTTFVKALYMDGKQAMRFRIIDPACVCLSRK 112

RESULT 12
NGF_NAJNA
ID      NGF_NAJNA STANDARD: PRT; 116 AA.
AC      P01140;
DT      21-JUL-1986 (Rel. 01, Created)
DT      01-MAY-1991 (Rel. 18, Last sequence update)
DT      01-JUL-1993 (Rel. 26, Last annotation update)
DE      Nerve growth factor (NGF).
OS      Naja naja (Indian cobra).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Lepidosteauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC      Elapidae; Elapinae; Naja.
OX      NCBI_TaxID=35670;
RN      [1]
RP      SEQUENCE.
RC      TISSUE-Venom;
RA      MEDLINE-91138755; PubMed-1995338;
RA      Inoue S., Oda T., Koyama J., Ikeda K., Hayashi K.;
RT      "Amino acid sequences of nerve growth factors derived from cobra
RL      venoms."
RL      FEBS Lett. 279:38-40(1991).
RN      [2]
RP      PRELIMINARY SEQUENCE.
RC      TISSUE-Venom;
RA      MEDLINE-76114772; PubMed-1247508;
RA      Hogue-Angelle R.A., Frazier W.A., Jacobs J.W., Mall H.D.,
RA      Bradshaw R.A.;
RT      "Purification, characterization, and partial amino acid sequence of
RT      nerve growth factor from cobra venom."
RL      Biochemistry 15:26-34(1976).
CC      -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC      MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC      STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC      EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
CC      NEURONS IN THE BRAIN.
CC      -1- SUBUNIT: HOMODIMER.
CC      -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC      PIR: A01401; NGNXXI.
DR      PIR: S13927; S13927.

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DR HSSP: P01139; 1BET.
DR InterPro: IPR002400; GF_cyskn0t.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF_1.
DR PRINTS: PR00438; GFCYSKN0T.
DR PRINTS: PR00258; NGF.
DR PRODOM: PD002052; NGF_1.
DR SMART: SM00140; NGF_1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS50270; NGF_2; 1.
DR PROSITE: PS50270; NGF_2; 1.
KM Growth factor.
FT DISULFID 14 78 BY SIMILARITY.
FT DISULFID 56 106 BY SIMILARITY.
FT DISULFID 66 108 BY SIMILARITY.
SO SEQUENCE 116 AA; 13022 MW; DAB346B1093E37E06 CRC64;

Query Match 67.9%; Score 446.5; DB 1; Length 116;
Best Local Similarity 69.6%; Pred. No. 6.6e-41;
Matches 78; Conservative 16; Mismatches 17; Indels 1; Gaps 1;

OY 5 HPFHGEFSCDVSVMWGDKTTATDICKGEVNLCEVININSVFOYFEETKCRDNP 64
DB 3 HPVNLCEHSVCDSVSAMV-TKTATADIKGNTVTMEVNLNDKVKYKEFFETKCRKNP 61
OY 65 VDSGCRGIDSKHNSYCTTHTFVKALTMDSKQAMRFIRIDTACVCLSRK 116
DB 62 EPSCRCGIDSHHNSYCTETDFIRKALTMEGNQASMRIRIDTACVCLTRK 113

RESULT 13
NGF_NAJAT
ID NGF_NAJAT STANDARD; PRT; 116 AA.
AC P21377;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Nerve growth factor (NGF).
OS Naja atra (Chinese cobra), and
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosteura; Squamata; Sclerozoosae; Serpentes; Colubridae;
OC Elapidae; Elapinae; Naja.
OX NCBI_Taxid=8656, 8649;
RN 11;
RP SEQUENCE.
RC SPECIES-N.a.atra; TISSUE-Venom;
RX MEDLINE-90147847; Pubmed-2619756;
RA Oda T., Ohta M., Inoue S., Ikeda K., Furukawa S., Hayashi K.;
RT *Amino acid sequence of nerve growth factor purified from the venom
RT of the Formosan cobra Naja atra.
RL Biochem. Int. 19:909-917(1989).
RN 12;
RP SEQUENCE.
RC SPECIES-N.a.kaouthia; TISSUE-Venom;
RX MEDLINE-91138755; Pubmed-1995338;
RA Inoue S., Oda T., Koyama J., Ikeda K., Hayashi K.;
RT *Amino acid sequences of nerve growth factors derived from cobra
RT venoms.
RL FEBS Lett. 279:38-40(1991).
RN 13;
RP SEQUENCE.
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
CC NEURONS IN THE BRAIN.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
DR HSSP: P01139; 1BET.
DR InterPro: IPR002400; GF_cyskn0t.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF_1.
DR PRINTS: PR00438; GFCYSKN0T.
DR PRINTS: PR00258; NGF.

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DR PRODOM: PD002052; NGF_1.
DR SMART: SM00140; NGF_1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS50270; NGF_2; 1.
DR PROSITE: PS50270; NGF_2; 1.
KM Growth factor.
FT DISULFID 14 78 BY SIMILARITY.
FT DISULFID 56 106 BY SIMILARITY.
FT DISULFID 66 108 BY SIMILARITY.
SO SEQUENCE 116 AA; 13064 MW; DAB35421093F3806 CRC64;

Query Match 67.2%; Score 442.5; DB 1; Length 116;
Best Local Similarity 68.8%; Pred. No. 1.8e-40;
Matches 77; Conservative 17; Mismatches 17; Indels 1; Gaps 1;

OY 5 HPFHGEFSCDVSVMWGDKTTATDICKGEVNLCEVININSVFOYFEETKCRDNP 64
DB 3 HPVNLCEHSVCDSVSAMV-TKTATADIKGNTVTMEVNLNDKVKYKEFFETKCRKNP 61
OY 65 VDSGCRGIDSKHNSYCTTHTFVKALTMDSKQAMRFIRIDTACVCLSRK 116
DB 62 EPSCRCGIDSHHNSYCTETDFIRKALTMEGNQASMRIRIRIDTACVCLTRK 113

RESULT 14
NGF_XIPMA
ID NGF_XIPMA STANDARD; PRT; 194 AA.
AC P34129;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Nerve growth factor precursor (NGF).
OS Xiphophorus maculatus (Southern platyfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphia; Acanthopterygii; Percomorphi; Atherinomorphi;
OC Cyprinodontiformes; Poeciliidae; Xiphophorus.
OX NCBI_Taxid=8083;
RN 11;
RP SEQUENCE FROM N.A.
RX MEDLINE-9233301; Pubmed-1629719;
RA Gotz R., Raulf F., Schmitt M.;
RT *Brain-derived neurotrophic factor is more highly conserved in
RT structure and function than nerve growth factor during vertebrate
RT evolution.
RL J. Neurochem. 59:432-442(1992).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
CC NEURONS IN THE BRAIN.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL: X59941; CAA42566.1; -.
DR HSSP: P01139; 1BET.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF_1.
DR PRINTS: PR00258; NGF.
DR PRODOM: PD002052; NGF_1.
DR SMART: SM00140; NGF_1.
DR PROSITE: PS00248; NGF_1; FALSE_NEG.
DR PROSITE: PS50270; NGF_2; 1.
KM Growth factor; Signal.
FT SIGNAL 1 30 POTENTIAL.
FT PROPEP 31 79

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OM protein - protein search, using SW model

Run on: December 2, 2002, 15:05:42 : Search time 18.7245 Seconds

(without alignments)
1331.501 Million cells updates/sec

Title: US-10-072-681-2

Perfect score: 658

Sequence: 1 PSSHPHFHRCFSCVSDSVS.....FIRIDPACVCLSRKAVRA 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp-phage:*
10: sp_plant:*
11: sp-protent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	648	98.5	241	4 Q9P208	Q9P208 homo sapien
2	648	98.5	241	4 Q9UKT8	Q9UKT8 homo sapien
3	648	98.5	241	6 Q9N2T1	Q9N2T1 pan troglod
4	648	98.5	241	6 Q9N2T0	Q9N2T0 gorilla gor
5	648	98.5	241	6 Q9N2E9	Q9N2E9 pongo pygma
6	640	97.3	241	4 Q9P6P0	Q9P6P0 homo sapien
7	578	87.8	217	6 Q9N183	Q9N183 macaca fusc
8	529	80.4	294	11 Q91XB4	Q91XB4 mus musculu
9	499	75.8	241	13 Q9OWJ8	Q9OWJ8 bothrops ja
10	492	74.8	241	13 Q9PDE9	Q9PDE9 crocatalus du
11	459	69.8	87	6 Q9TTC3	Q9TTC3 cervus elap
12	458	69.6	87	4 Q9P2Z4	Q9P2Z4 homo sapien
13	348	52.9	286	13 Q91988	Q91988 xiphophorus
14	338.5	51.4	241	6 Q9N182	Q9N182 macaca fusc
15	324.5	49.3	153	11 Q9CYL3	Q9CYL3 mus musculu
16	324.5	49.3	247	6 Q97759	Q97759 allurus ful

17	324.5	49.3	249	11 Q9VHK4	Q9VHK4 mus musculu
18	318.5	48.4	246	13 Q8OG76	Q8OG76 japeura sp
19	317.5	48.3	177	13 Q918L2	Q918L2 poephila sp
20	314.5	47.8	270	13 Q9YH42	Q9YH42 brachydantio
21	312.5	47.5	246	13 Q8OG75	Q8OG75 phrynocephalo
22	304.5	46.3	246	13 Q8OG74	Q8OG74 cyclophlops
23	304.5	45.1	247	13 Q8OG77	Q8OG77 tyototritlo
24	291.5	44.3	101	6 Q9PRT2	Q9PRT2 macaca fusc
25	283	43.0	324	13 Q9XK95	Q9XK95 lampetra fl
26	271.5	41.3	186	12 Q9J5D9	Q9J5D9 fowlpox vlr
27	224	34.0	42	6 Q02802	Q02802 trichosaurus
28	223	33.9	85	6 Q02790	Q02790 macropus fu
29	217	33.0	85	6 Q13114	Q13114 isodon mac
30	217	33.0	85	6 Q13122	Q13122 tarapaea ro
31	217	33.0	85	6 Q02795	Q02795 ornithorhyn
32	217	33.0	85	6 Q02798	Q02798 petarus br
33	217	33.0	85	6 Q13104	Q13104 cercartetus
34	217	33.0	85	6 Q02792	Q02792 notoryctes
35	217	33.0	85	6 Q13105	Q13105 dasyuroides
36	217	33.0	85	6 Q02801	Q02801 lachylosus
37	216	32.8	85	6 Q02803	Q02803 trichosurus
38	211	32.1	42	6 Q02794	Q02794 ornithorhyn
39	209	31.8	42	6 Q02800	Q02800 tachylosus
40	166	25.2	42	13 Q13118	Q13118 protoplectus
41	156	23.7	185	11 Q99NV9	Q99NV9 pedetes cap
42	156	23.7	186	6 Q9BEF0	Q9BEF0 chetophrac
43	155	23.6	184	6 Q9BEF5	Q9BEF5 cupala mmo
44	155	23.6	185	6 Q9BEF6	Q9BEF6 talpa alai
45	155	23.6	185	6 Q9BEF5	Q9BEF5 condylura c

ALIGNMENTS

RESULT 1

ID Q9P208 PRELIMINARY; PRT: 241 AA.

AC Q9P208: Q9P208: (TREMREL. 15, Created)

DT 01-OCT-2000 (TREMREL. 15, Last sequence update)

DT 01-OCT-2000 (TREMREL. 19, Last annotation update)

DE 01-DEC-2001 (TREMREL. 19, Last annotation update)

DE Beta-nerve growth factor (Fragment).

OS Beta-NGF.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_TaxID=9606;

XP [1]

RA SEQUENCE FROM N.A.

RA Kitano T., Kobayakawa H., Saitou N.;

RT Silver Project.

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

RL EMBL: AB037517; BAA90437.1; --

DR HSSP: P01139; 1BET.

DR InterPro: IPR002072; NGF.

DR Pfam: PF00243; NGF; 1.

DR PRINTS: PR00268; NGF.

DR PRODOM: PD002052; NGF; 1.

DR SMART: SM00140; NGF; 1.

DR PROSITE: PS00248; NGF-1; 1.

DR PROSITE: PS00270; NGF-2; 1.

FT NON_TER 241

SQ SEQUENCE 241 AA; 26998 MW; D5531ED82596C14 CRC64;

Query Match 98.5% Score 648; DB 4; Length 241;

Best Local Similarity 99.2% Pred. No. 2.4e-65;

Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSSHPHFHRCFSCVSDSVNMGDKTATDIDKGEVNLGEVNIINSVYFQFEETRCRD 61
DB 122 SSSHPHFHRCFSCVSDSVNMGDKTATDIDKGEVNLGEVNIINSVYFQFEETRCRD 101
QY 62 PNPDSCRGIDSKHNNVSCCTTHTFVKALITDGRQAAHFRIRIDTACVCLSRKAVRA 121

DB 182 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMGKQAAAFRIRIDTACVLSRKAARRA 241

RESULT 2

ID 090KL8 PRELIMINARY: PRT: 241 AA.

AC 090KL8: 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE Nerve growth factor B.

GN NGF.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE:99256269; PubMed=10322959;

RA Tong Y., Wang H., Chen M.;

RT "Cloning and sequencing of the gene for premature beta nerve growth

factor."

RL Chung Kuo Ying Tung Sheng Li Hsueh Tsa Chih 13:316-318(1997).

RM [2]

RP SEQUENCE FROM N.A.

RA Tong Y., Wang H.;

RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF10960; AAD55975.1;

DR HSP: P01139; 18ET.

DR InterPro: IPR002072; NGF.

DR Pfam: PF00243; NGF.1.

DR PRINTS: PR00268; NGF.

DR PRODOM: PD002052; NGF.1.

DR SMART: SM00140; NGF.1.

DR PROSITE: PS00248; NGF.1; 1.

DR PROSITE: PS50270; NGF.2; 1.

SO SEQUENCE 241 AA; 26959 MW; 619DFC65E3B0671 CRC64;

Query Match

Best Local Similarity 98.5%; Score 648; DB 4; Length 241;

Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2

SSHPFIRHGEFSCDSVSWVGDKTTATDIDKRENVVLGEVINNSVFRQYFEETKCRD 61

DB 122 SSSHPFIRHGEFSCDSVSWVGDKTTATDIDKRENVVLGEVINNSVFRQYFEETKCRD 181

OY 62

PNPVDSCGCRGIDSKHNSYCTTHTFVKALTMGKQAAAFRIRIDTACVLSRKAARRA 121

DB 182 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMGKQAAAFRIRIDTACVLSRKAARRA 241

RESULT 3

O9N2F1

ID 09N2F1 PRELIMINARY: PRT: 241 AA.

AC 09N2F1: 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE Beta-nerve growth factor (Fragment).

GN NGF.

OS Pan troglodytes (Chimpanzee).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.

OX NCBI_TaxID=9599;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CHIMP-220;

RA Kikano T., Kobayakawa H., Saitou N.;

RT "Silver Project."

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AB037518; BA90438.1;

DR HSP: P01139; 18ET.

DR InterPro: IPR002072; NGF.

DR Pfam: PF00243; NGF.1.

DR PRINTS: PR00268; NGF.

DR PRODOM: PD002052; NGF.1.

DR SMART: SM00140; NGF.1.

DR PROSITE: PS00248; NGF.1; 1.

DR PROSITE: PS50270; NGF.2; 1.

FT NON_TER 241

SO SEQUENCE 241 AA; 26868 MW; B39FAA8912C00A0B CRC64;

Query Match

Best Local Similarity 98.5%; Score 648; DB 6; Length 241;

Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2

SSHPFIRHGEFSCDSVSWVGDKTTATDIDKRENVVLGEVINNSVFRQYFEETKCRD 61

DB 122 SSSHPFIRHGEFSCDSVSWVGDKTTATDIDKRENVVLGEVINNSVFRQYFEETKCRD 181

OY 62

PNPVDSCGCRGIDSKHNSYCTTHTFVKALTMGKQAAAFRIRIDTACVLSRKAARRA 121

DB 182 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMGKQAAAFRIRIDTACVLSRKAARRA 241

RESULT 4

O9N2FO

ID 09N2FO PRELIMINARY: PRT: 241 AA.

AC 09N2FO: 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE Beta-nerve growth factor (Fragment).

GN NGF.

OS Gorilla gorilla (gorilla).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Gorilla.

OX NCBI_TaxID=9593;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=GORILLA-UI;

RA Kikano T., Kobayakawa H., Saitou N.;

RT "Silver Project."

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AB037519; BA90439.1;

DR HSP: P01139; 18ET.

DR InterPro: IPR002072; NGF.

DR Pfam: PF00243; NGF.1.

DR PRINTS: PR00268; NGF.

DR PRODOM: PD002052; NGF.1.

DR SMART: SM00140; NGF.1.

DR PROSITE: PS00248; NGF.1; 1.

DR PROSITE: PS50270; NGF.2; 1.

FT NON_TER 241

SO SEQUENCE 241 AA; 26915 MW; 6F54D163C384B834 CRC64;

Query Match

Best Local Similarity 98.5%; Score 648; DB 6; Length 241;

Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2

SSHPFIRHGEFSCDSVSWVGDKTTATDIDKRENVVLGEVINNSVFRQYFEETKCRD 61

DB 122 SSSHPFIRHGEFSCDSVSWVGDKTTATDIDKRENVVLGEVINNSVFRQYFEETKCRD 181

OY 62

PNPVDSCGCRGIDSKHNSYCTTHTFVKALTMGKQAAAFRIRIDTACVLSRKAARRA 121

DB 182 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMGKQAAAFRIRIDTACVLSRKAARRA 241

RESULT 5

O9N2E9

ID 09N2E9 PRELIMINARY: PRT: 241 AA.

AC 09N2E9: 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

```
DE 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE Beta-nerve growth factor (Fragment).
CN BETA-NGF.
OC Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ORAN-UI;
RA Kitano T., Kobayakawa H., Saitou N.;
RT Silver Project.
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB037520; BAA90440.1; -.
DR HSSP: P01139; 1BET.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF_1.
DR PRINTS: PR00268; NGF.
DR PRODOM: PD002052; NGF_1.
DR SMART: SM00140; NGF_1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS50270; NGF_2; 1.
FT NON_TER 241
FT SEQUENCE 241 AA; 26876 MW; DFC168E7E4E01F15 CRC64;
SO QUERY MATCH
Query Match 98.5%; Score 648; DB 6; Length 241;
Best Local Similarity 99.2%; Pred. NO. 2,4e-65;
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 2 SSSHPFHRGFEFVSVCDSVSWVGDKTATADIKGEVNVGLGVNINSVFRQYFFETKCRD 61
DB 122 SSSHPFHRGFEFVSVCDSVSWVGDKTATADIKGEVNVGLGVNINSVFRQYFFETKCRD 181
OY 62 PNPVDSGCRGIDSKHNSYCTTHTFYKALTMDCGKAAAFRIRIDTACVCVLSRAAVRA 121
DB 182 PNPVDSGCRGIDSKHNSYCTTHTFYKALTMDCGKAAAFRIRIDTACVCVLSRAAVRA 241

RESULT 6
OY 096P60 PRELIMINARY; PRT; 241 AA.
AC 096P60;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, last annotation update)
DE Nerve growth factor beta.
GN NGF8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Zhang B., Zhou Y., Peng X., Yuan J., Qiang B.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF411526; AAL05874.1; -.
DR InterPro: IPR02072; NGF.
DR Pfam: PF00243; NGF_1.
DR PRODOM: PD002052; NGF_1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS50270; NGF_2; 1.
FT NON_TER 241
FT SEQUENCE 241 AA; 26866 MW; 745216485C21E558 CRC64;
SO QUERY MATCH
Query Match 97.3%; Score 640; DB 4; Length 241;
Best Local Similarity 97.5%; Pred. NO. 2e-64;
Matches 117; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
OY 2 SSSHPFHRGFEFVSVCDSVSWVGDKTATADIKGEVNVGLGVNINSVFRQYFFETKCRD 61
DB 122 SSSHPFHRGFEFVSVCDSVSWVGDKTATADIKGEVNVGLGVNINSVFRQYFFETKCRD 181
OY 62 PNPVDSGCRGIDSKHNSYCTTHTFYKALTMDCGKAAAFRIRIDTACVCVLSRAAVRA 121
DB 172 PNPVDSGCRGIDSKHNSYCTTHTFYKALTMDCGKAAAFRIRIDTACVCVLSRAAVRA 241

DB 182 PNPVDSGCRGIDSKHNSYCTTHTFYKALTMDCGKAAAFRIRIDTACVCVLSRAAVRA 241

RESULT 7
OY 09N183 PRELIMINARY; PRT; 217 AA.
AC 09N183;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE Beta nerve growth factor (fragment).
OS Macaca fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9542;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RA MEDLINE-99270338; PubMed-10340513;
RA Okuno H., Tokuyama W., Li Y.X., Hashimoto T., Miyashita Y.;
RT "Quantitative evaluation of neurotrophin and trk mRNA expression in
RT visual and limbic areas along the occipito-temporo-hippocampal pathway
RT in adult macaque monkeys."
RL J. Comp. Neurol. 408:378-398(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RA Okuno H., Tokuyama W., Li Y.X., Hashimoto T., Miyashita Y.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF222682; AAF33790.1; -.
DR HSSP: P01139; 1BET.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF_1.
DR PRINTS: PR00268; NGF_1.
DR PRODOM: PD002052; NGF_1.
DR SMART: SM00140; NGF_1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS50270; NGF_2; 1.
FT NON_TER 217
FT SEQUENCE 217 AA; 24240 MW; 36A5A2D1D9D8D5C CRC64;
SO QUERY MATCH
Query Match 87.8%; Score 578; DB 6; Length 217;
Best Local Similarity 99.1%; Pred. NO. 1.8e-57;
Matches 105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 2 SSSHPFHRGFEFVSVCDSVSWVGDKTATADIKGEVNVGLGVNINSVFRQYFFETKCRD 61
DB 112 SSSHPFHRGFEFVSVCDSVSWVGDKTATADIKGEVNVGLGVNINSVFRQYFFETKCRD 171
OY 62 PNPVDSGCRGIDSKHNSYCTTHTFYKALTMDCGKAAAFRIRIDT 107
DB 172 PNPVDSGCRGIDSKHNSYCTTHTFYKALTMDCGKAAAFRIRIDT 217

RESULT 8
OY 091XB4 PRELIMINARY; PRT; 294 AA.
AC 091XB4;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE Similar to nerve growth factor, beta.
GN NGF8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SALIVARY GLAND;
RA Strausberg R.;
```

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC011123; AAI1123.1; -
DR MGD: MGI:97321; Ngef.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF_1.
DR ProDom: PD002052; NGF_1.
DR PROSITE: PS00248; NGF_1; UNKNOWN_1.
DR PROSITE: PS50270; NGF_2; 1.
DR SEQUENCE 294 AA; 33326 MW; 9EE7402DAC899229 CRC64;

Query Match 80.4%; Score 529; DB 11; Length 294;
Best Local Similarity 90.7%; Pred. No. 9, 3e-52;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 2 SSSHHFRRGERSVCDSSVWVGKTTATDICKREYVAGLVNINSVRFYEFKCRD 61
DB 188 STHVFFHRRGERSVCDSSVWVGKTTATDICKREYVAGLVNINSVRFYEFKCRD 247
OY 62 PNPVDSGRCGIDSKHNSYCTTHTFVKALITMDGKQAMRFIRIDTA 108
DB 248 SNPVDSGRCGIDSKHNSYCTTHTFVKALITMDGKQAMRFIRIDTA 294

RESULT 9
O90W38 PRELIMINARY; PRT: 241 AA.
AC O90W38;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Putative neurotrophic growth factor.
GN NGF.
OS Bothrops jararacussu (Jararacussu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperae; Crotalinae; Bothrops.
OX NCBI_TaxID=8726;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=VENOM GLAND;
RA Keshima S., Pereira J.O., Astolfi Filho S., Soares A.M.,
RA Cintra A.C.O., Giglio J.R., Franca S.C.;
RT "Molecular cloning and cDNA sequence of a nerve growth factor
RT precursor from Bothrops jararacussu venomous gland."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF007318; AAG12169.1; -
DR InterPro: IPR002072; NGF.
DR Pfam: PF002052; NGF_1.
DR ProDom: PD002052; NGF_1; UNKNOWN_1.
DR PROSITE: PS00248; NGF_1; NGF_2; 1.
DR PROSITE: PS50270; NGF_2; 1.
DR SEQUENCE 241 AA; 27161 MW; AC57F72A4A6531A8F CRC64;

Query Match 75.8%; Score 499; DB 13; Length 241;
Best Local Similarity 75.9%; Pred. No. 1, 8e-48;
Matches 85; Conservative 19; Mismatches 8; Indels 0; Gaps 0;

OY 5 HPIFRHGRSVCDSSVWVGKTTATDICKREYVAGLVNINSVRFYEFKCRD 64
DB 125 HPIFRHGRSVCDSSVWVGKTTATDICKREYVAGLVNINSVRFYEFKCRD 184
OY 65 VDSGRCGIDSKHNSYCTTHTFVKALITMDGKQAMRFIRIDTA 116
DB 185 VPCGRCGIDSKHNSYCTTHTFVKALITMDGKQAMRFIRIDTA 236

RESULT 10
O9DE29 PRELIMINARY; PRT: 241 AA.
AC O9DE29;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE Nerve growth factor.
OS Crocodylus durissus terrificus (South American rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperae; Crotalinae; Crocodylus.
OX NCBI_TaxID=8732;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=VENOM GLAND;
RA Hayashi M.A.F., Radis-Baptista G., Yamane T., Camargo A.C.M.;
RT "Cloning and sequence of a cDNA coding for a rattlesnake (Crocodylus
RT durissus terrificus) nerve growth factor."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF306533; AAC30924.1; -
DR HSP: P01139; IBER.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF_1.
DR ProDom: PD002052; NGF_1.
DR PRINTS: PR00268; NGF.
DR SMART: SM00140; NGF_1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS50270; NGF_2; 1.
DR SEQUENCE 241 AA; 27118 MW; 4A261F42C5D6F3F CRC64;

Query Match 74.8%; Score 492; DB 13; Length 241;
Best Local Similarity 75.0%; Pred. No. 1, 1e-47;
Matches 84; Conservative 19; Mismatches 9; Indels 0; Gaps 0;

OY 5 HPIFRHGRSVCDSSVWVGKTTATDICKREYVAGLVNINSVRFYEFKCRD 64
DB 125 HPIFRHGRSVCDSSVWVGKTTATDICKREYVAGLVNINSVRFYEFKCRD 184
OY 65 VDSGRCGIDSKHNSYCTTHTFVKALITMDGKQAMRFIRIDTA 116
DB 185 VPCGRCGIDSKHNSYCTTHTFVKALITMDGKQAMRFIRIDTA 236

RESULT 11
O9TTC3 PRELIMINARY; PRT: 87 AA.
AC O9TTC3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Beta nerve growth factor (fragment).
GN NGF.
OS Cervus elaphus scoticus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=109627;
RN [1]
RP SEQUENCE FROM N.A.
RC ROBERTSON T.M., Stanton J.L., Clark D.E., Sheard P.W., Harris A.J.,
RA Suttie J.M.;
RT "NGF expression in Antler."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF145043; AAF1735.1; -
DR HSP: P01139; IBER.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF_1.
DR PRINTS: PR00268; NGF.
DR ProDom: PD002052; NGF_1.
DR SMART: SM00140; NGF_1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS50270; NGF_2; 1.
DR NON_TER 1
FT 1
FT 87
FT 87
SO SEQUENCE 87 AA; 9876 MW; 17E0E6A9AFA7A0A4 CRC64;

Query Match 69.8%; Score 459; DB 6; Length 87;
Best Local Similarity 95.4%; Pred. No. 1, 9e-44;
Matches 83; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

FT NON_TER 1 1
 FT NON_TER 241 241
 SO SEQUENCE 241 AA: 27803 MW: AB95E457C7B07113 CRC64:

Query Match

51.44: Score 338.5: DB 6: Length 241:

Best Local Similarity 59.08: Pred. No. 2.8e-30: Mismatches 22: Indels 1: Gaps 1:

Oy 68 GCGIDSKHNSCYTTHTEFYKALTMDC-KOANRFRIRDTACVCLSKRAVR 119
 Db 101 GCGIDSKHNSCYTTHTEFYKALTMDC-KOANRFRIRDTACVCLSKRAVR 153
 Search completed: December 2, 2002, 15:12:01
 Job time: 19.7245 secs

Oy 9 HRGEFVCDSDSVWVGDTATDIDKKEVNLGEVNNINSVFRQYFEETKCRDPNPDVG 68
 Db 142 HRGEFVCDSDSLMTYDKRSSAIDIRGHQVTLCEIKGNSPVQYFEETKCRKAPVKNG 201

Oy 69 GCGIDSKHNSCYTTHTEFYKALTMDC-KOANRFRIRDT 107
 Db 202 GCGIDSKHNSCYTTHTEFYKALTMDC-KOANRFRIRDT 241

RESULT 15

Oy 09CYL3 PRELIMINARY: PRT: 153 AA.

AC 09CYL3:

DT 01-JUN-2001 (TEMBLrel. 17, Created)

DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)

DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)

DE Brain derived neurotrophic factor.

GN BDNF.

OS Mus musculus (Mouse).

OC Eukaryota; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxId=10090;

RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=EMBRYO;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shimagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Iizawa Y., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Frieschmann W., Gaesteland T., Giasi C., King B., Kochiya H.,

RA Kuehl P., Lewis S., Matsuo Y., Nakaido I., Pesole G., Quackenbush J.,

RA Schirml L.M., Staubli F., Suzuki R., Tomita K., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Bronstein M.J., Buit C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyo-oka K., Wang K.H., Welter C., Whitaker C., Wilmink L.,

RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001);

DR EMBL: AK017559; BAB30805.1; -

DR HSSP: P23560; 1B8M.

DR MGD: MGI:88145; Bdnf.

DR InterPro: IPR002072; NGF.

DR Pfam: PF00243; NGF; 1.

DR PRINTS: PR00268; NGF.

DR PRODOM: PD002052; NGF; 1.

DR SMART: SM00140; NGF; 1.

DR PROSITE: PS00248; NGF; 1.

DR PROSITE: PS50270; NGF; 2; 1.

SO SEQUENCE 153 AA: 17519 MW: CA8EB8944CE5B37 CRC64:

Query Match 49.38: Score 324.5: DB 11: Length 153:

Best Local Similarity 54.98: Pred. No. 6.3e-29:

Matches 62: Conservative 14: Mismatches 34: Indels 3: Gaps 2:

Oy 10 RGEFVCDSDSVWVGDTATDIDKKEVNLGEVNNINSVFRQYFEETKCRDPNPDVG 67

Db 41 RGEFVCDSDSLMTYDKRSSAIDIRGHQVTLCEIKGNSPVQYFEETKCRKAPVKNG 100

GenCore version 5.1.3
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OM protein - protein search, using SW model

Run on: December 2, 2002, 15:05:42 : Search time 8.36928 Seconds
(Without alignments)
425.386 Million cell updates/sec

Title: US-10-072-681-2

Perfect score: 1 PSSSHPIFRGEFVCDVS.....FIRIDTACVLSRAKAVRRA 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued Patents AA: *
1: /cgn2_6/ptodata/1/laa/5A.COMB.pep: *
2: /cgn2_6/ptodata/1/laa/5B.COMB.pep: *
3: /cgn2_6/ptodata/1/laa/6A.COMB.pep: *
4: /cgn2_6/ptodata/1/laa/6B.COMB.pep: *
5: /cgn2_6/ptodata/1/laa/PTCUS.COMB.pep: *
6: /cgn2_6/ptodata/1/laa/Dackfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	658	100.0	121	4	US-09-675-503-2
2	651	98.9	120	3	US-08-970-865-2
3	651	98.9	120	4	US-09-363-573-2
4	648	98.5	120	1	US-08-440-040-3
5	648	98.5	120	2	US-08-441-513A-3
6	648	98.5	120	3	US-08-581-662-31
7	648	98.5	120	4	US-08-845-541B-1
8	648	98.5	120	4	US-09-066-065A-1
9	648	98.5	120	4	US-09-447-356-1
10	648	98.5	120	4	US-09-664-295-31
11	648	98.5	120	5	PCT-US95-06918-3
12	648	98.5	241	1	US-08-266-0808-4
13	648	98.5	241	1	US-08-451-947-5
14	648	98.5	241	2	US-08-424-826A-5
15	648	98.5	241	2	US-08-595-043A-75
16	648	98.5	241	3	US-08-970-865-1
17	648	98.5	241	3	US-08-928-694-5
18	648	98.5	241	4	US-09-363-573-1
19	648	98.5	241	4	US-09-447-356-3
20	648	98.5	241	5	PCT-US91-06950-5
21	648	98.5	241	5	PCT-US95-05423-4
22	648	98.5	242	4	US-09-575-503-1
23	639	97.1	119	3	US-08-753-642-2
24	639	97.1	153	4	US-09-675-922-2
25	639	97.1	157	4	US-09-675-922-4
26	639	97.1	163	4	US-09-675-922-6
27	639	97.1	167	4	US-09-675-922-8

28	634	96.4	120	4	US-08-845-541B-3	Sequence 3, Appl1
29	634	96.4	120	4	US-09-066-065A-3	Sequence 3, Appl1
30	631	95.9	120	4	US-08-845-541B-4	Sequence 4, Appl1
31	631	95.9	120	4	US-09-066-065A-4	Sequence 4, Appl1
32	626	95.1	120	4	US-08-845-541B-12	Sequence 12, Appl1
33	626	95.1	120	4	US-09-066-065A-12	Sequence 12, Appl1
34	625	95.0	120	4	US-08-845-541B-17	Sequence 17, Appl1
35	625	95.0	120	4	US-08-845-541B-20	Sequence 20, Appl1
36	625	95.0	120	4	US-09-066-065A-17	Sequence 17, Appl1
37	625	95.0	120	4	US-09-066-065A-20	Sequence 20, Appl1
38	623	94.7	120	4	US-08-845-541B-18	Sequence 18, Appl1
39	623	94.7	120	4	US-08-845-541B-21	Sequence 21, Appl1
40	623	94.7	120	4	US-09-066-065A-18	Sequence 18, Appl1
41	623	94.7	120	4	US-09-066-065A-21	Sequence 21, Appl1
42	620	94.2	120	4	US-08-845-541B-13	Sequence 13, Appl1
43	620	94.2	120	4	US-08-845-541B-19	Sequence 19, Appl1
44	620	94.2	120	4	US-09-066-065A-13	Sequence 13, Appl1
45	620	94.2	120	4	US-09-066-065A-19	Sequence 19, Appl1

ALIGNMENTS

```

RESULT 1
US-09-675-503-2
; Sequence 2, Application US/09675503
; Patent No. 6423831
; GENERAL INFORMATION:
; APPLICANT: Burton, Louis E.
; APPLICANT: Schmelzer, Charles H.
; TITLE OF INVENTION: ISOLATION OF NEUROTROPINS FROM A
; TITLE OF INVENTION: MIXTURE CONTAINING OTHER PROTEINS AND NEUROTROPIN VARIANTS
; FILE REFERENCE: GENENT, 037C2
; CURRENT APPLICATION NUMBER: US/09/675,503
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/030838
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: 60/047855
; PRIOR FILING DATE: 1997-05-29
; PRIOR APPLICATION NUMBER: 08/970865
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 09/363573
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-675-503-2

Query Match          100.0%  Score 658; DB 4; Length 121;
Best Local Similarity 100.0%  Pred. No. 4, 1e-75;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSSSHPIFRGEFVCDVSVMWDKTTATDTRKKEVNVGCVINNSVPROFEETKCR 60
    |||||||
Db 1 PSSSHPIFRGEFVCDVSVMWDKTTATDTRKKEVNVGCVINNSVPROFEETKCR 60
    |||||||
QY 61 DPNPVDSGCGIDSKHNSYCTTHTFEKALTDGKQAMRFTRIDTACVLSRAKAVR 120
    |||||||
Db 61 DPNPVDSGCGIDSKHNSYCTTHTFEKALTDGKQAMRFTRIDTACVLSRAKAVR 120
    |||||||
QY 121 A 121
Db 121 A 121

RESULT 2
US-08-970-865-2
; Sequence 2, Application US/08970865

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Patent No. 6005081
GENERAL INFORMATION:
APPLICANT: Louis E. Burton, Charles H. Schmelzer, Joanne T. Beck
TITLE OF INVENTION: Purification of NGF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPalin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/970,865
FILING DATE: 14-May-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030838
FILING DATE: 11/15/1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047855
FILING DATE: 5/29/1997
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1063R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/425-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-970-865-2

Query Match          98.9%: Score 651: DB 3: Length 120:
Best Local Similarity 100.0%: Pred. No. 3.1e-74:
Matches 120: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Qy 2 SSSHPHFHREFEVSVCDSVSWVWGDKTATADIKGKEVNLGEVNINNSVFRQYFEETKCRD 61
Db 1 SSSHPHFHREFEVSVCDSVSWVWGDKTATADIKGKEVNLGEVNINNSVFRQYFEETKCRD 60
Qy 62 PNPVDSGCRGIDSKHNNSTCTTHFFVKAALTMDSGQAAHREIRIDTACVCLSKAVRA 121
Db 61 PNPVDSGCRGIDSKHNNSTCTTHFFVKAALTMDSGQAAHREIRIDTACVCLSKAVRA 120

RESULT 3
US-09-363-573-2
Sequence 2, Application US/09363573
Patent No. 6184360
GENERAL INFORMATION:
APPLICANT: Louis E. Burton, Charles H. Schmelzer, Joanne T. Beck
TITLE OF INVENTION: Purification of NGF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: WinPalin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,573
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/970,865
FILING DATE: 14-May-1997
APPLICATION NUMBER: 60/030838
FILING DATE: 11/15/1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047855
FILING DATE: 5/29/1997
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1063R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/425-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-363-573-2

Query Match          98.9%: Score 651: DB 4: Length 120:
Best Local Similarity 100.0%: Pred. No. 3.1e-74:
Matches 120: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Qy 2 SSSHPHFHREFEVSVCDSVSWVWGDKTATADIKGKEVNLGEVNINNSVFRQYFEETKCRD 61
Db 1 SSSHPHFHREFEVSVCDSVSWVWGDKTATADIKGKEVNLGEVNINNSVFRQYFEETKCRD 60
Qy 62 PNPVDSGCRGIDSKHNNSTCTTHFFVKAALTMDSGQAAHREIRIDTACVCLSKAVRA 121
Db 61 PNPVDSGCRGIDSKHNNSTCTTHFFVKAALTMDSGQAAHREIRIDTACVCLSKAVRA 120

RESULT 4
US-08-440-049-3
Sequence 3, Application US/08440049
Patent No. 5728803
GENERAL INFORMATION:
APPLICANT: Usher, Roman
APPLICANT: Presta, Leonard G.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: PANROTROPIC NEUROTROPHIC FACTORS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPalin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,049
FILING DATE: 12-May-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/253937
FILING DATE: 03-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0905C2

```

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-441-049-3

Query Match 98.5%; Score 648; DB 1; Length 120;
Best Local Similarity 99.2%; Pred. No. 7.4e-74;
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSSHPIFRHGEFVCDVSVWVGDKTTATDIDKGEVWVLEGVNINNSVFQYFFETKCD 61
DB 1 SSSHPIFRHGEFVCDVSVWVGDKTTATDIDKGEVWVLEGVNINNSVFQYFFETKCD 60
QY 62 PNPVDSGCGIDSKHNSYCTTHTFVKALTMDCQAAAFRIRIDTACVCLSRKAVRRA 121
DB 61 PNPVDSGCGIDSKHNSYCTTHTFVKALTMDCQAAAFRIRIDTACVCLSRKAVRRA 120

RESULT 5
US-08-441-513A-3
Sequence 3, Application US/08441513A
Patent No. 5981480

GENERAL INFORMATION:
APPLICANT: Ufer, Roman
APPLICANT: Presta, Leonard G.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: Pantropic Neurotrophic Factors
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,513A

FILING DATE: 15-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/253937

FILING DATE: 03-JUN-1994

ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: P0905C3

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-441-513A-3

Query Match 98.5%; Score 648; DB 2; Length 120;
Best Local Similarity 99.2%; Pred. No. 7.4e-74;
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSSHPIFRHGEFVCDVSVWVGDKTTATDIDKGEVWVLEGVNINNSVFQYFFETKCD 61
DB 1 SSSHPIFRHGEFVCDVSVWVGDKTTATDIDKGEVWVLEGVNINNSVFQYFFETKCD 60

DB 1 SSSHPIFRHGEFVCDVSVWVGDKTTATDIDKGEVWVLEGVNINNSVFQYFFETKCD 60
QY 62 PNPVDSGCGIDSKHNSYCTTHTFVKALTMDCQAAAFRIRIDTACVCLSRKAVRRA 121
DB 61 PNPVDSGCGIDSKHNSYCTTHTFVKALTMDCQAAAFRIRIDTACVCLSRKAVRRA 120

RESULT 6
US-08-581-662-31
Sequence 31, Application US/08581662
Patent No. 6121235

GENERAL INFORMATION:
APPLICANT: Gao, Wei-Qiang
TITLE OF INVENTION: Treatment of Balance Impairments
FILE REFERENCE: P0981
CURRENT APPLICATION NUMBER: US/08/581,662
CURRENT FILING DATE: 1995-12-29
NUMBER OF SEQ ID NOS: 36
SEQ ID NO 31
LENGTH: 120
TYPE: PRT
ORGANISM: Homo sapiens
US-08-581-662-31

Query Match 98.5%; Score 648; DB 3; Length 120;
Best Local Similarity 99.2%; Pred. No. 7.4e-74;
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSSHPIFRHGEFVCDVSVWVGDKTTATDIDKGEVWVLEGVNINNSVFQYFFETKCD 61
DB 1 SSSHPIFRHGEFVCDVSVWVGDKTTATDIDKGEVWVLEGVNINNSVFQYFFETKCD 60
QY 62 PNPVDSGCGIDSKHNSYCTTHTFVKALTMDCQAAAFRIRIDTACVCLSRKAVRRA 121
DB 61 PNPVDSGCGIDSKHNSYCTTHTFVKALTMDCQAAAFRIRIDTACVCLSRKAVRRA 120

RESULT 7
US-08-845-541B-1
Sequence 1, Application US/08845541B
Patent No. 6333310

GENERAL INFORMATION:
APPLICANT: Presta, Leonard

APPLICANT: Ufer, Roman

APPLICANT: Winslow, John

TITLE OF INVENTION: NGF VARIANTS

FILE REFERENCE: GENENT. 039A

CURRENT APPLICATION NUMBER: US/08/845,541B

CURRENT FILING DATE: 1995-04-25

NUMBER OF SEQ ID NOS: 38

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 120

TYPE: PRT

ORGANISM: homo sapien

US-08-845-541B-1

Query Match 98.5%; Score 648; DB 4; Length 120;
Best Local Similarity 99.2%; Pred. No. 7.4e-74;
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSSHPIFRHGEFVCDVSVWVGDKTTATDIDKGEVWVLEGVNINNSVFQYFFETKCD 61
DB 1 SSSHPIFRHGEFVCDVSVWVGDKTTATDIDKGEVWVLEGVNINNSVFQYFFETKCD 60
QY 62 PNPVDSGCGIDSKHNSYCTTHTFVKALTMDCQAAAFRIRIDTACVCLSRKAVRRA 121
DB 61 PNPVDSGCGIDSKHNSYCTTHTFVKALTMDCQAAAFRIRIDTACVCLSRKAVRRA 120

RESULT 8
US-09-066-065A-1
Sequence 1, Application US/09066065A

Patent No. 6365373
GENERAL INFORMATION:
APPLICANT: Leonard G. Presta, Roman Urfer, John W. Winslow
TITLE OF INVENTION: NGF Variants
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,065A
FILING DATE: 24-Apr-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/044918
FILING DATE: 25-Apr-1999
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1098R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-066-065A-1

Query Match 98.5% Score 648; DB 4; Length 120;
Best Local Similarity 99.2% Pred. No. 7.4e-74;
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSSHPFHRGEFVSCDSVSVWVGDKTTATDINGKKEVNLGEVININSVFROYFEETKCRD 61
DB 1 SSSHPFHRGEFVSCDSVSVWVGDKTTATDINGKKEVNLGEVININSVFROYFEETKCRD 60

QY 62 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSKQAMRFIRIDTACVCLSRKAVRA 121
DB 61 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSKQAMRFIRIDTACVCLSRKAVRA 120

RESULT 9
US-09-447-356-1
Sequence 1, Application US/09447356
Patent No. 6395513
GENERAL INFORMATION:
APPLICANT: FOSTER, KEITH ALAN
APPLICANT: DUGGAN, MICHAEL JOHN
APPLICANT: SHONE, CLIFFORD CHARLES
TITLE OF INVENTION: CLOSTRIDIAL TOXIN DERIVATIVES ABLE TO MODIFY PERIPHERAL
TITLE OF INVENTION: SENSORY AFFERENT FUNCTIONS
FILE REFERENCE: 023223/0104
CURRENT APPLICATION NUMBER: US/09/447,356
CURRENT FILING DATE: 1999-11-22
PRIOR APPLICATION NUMBER: 08/945,037
PRIOR FILING DATE: 1998-01-12
PRIOR APPLICATION NUMBER: GB 9508204.6
PRIOR FILING DATE: 1995-04-21
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 120
TYPE: PRT

ORGANISM: Murine sp.
US-09-447-356-1

Query Match 98.5% Score 648; DB 4; Length 120;
Best Local Similarity 99.2% Pred. No. 7.4e-74;
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSSHPFHRGEFVSCDSVSVWVGDKTTATDINGKKEVNLGEVININSVFROYFEETKCRD 61
DB 1 SSSHPFHRGEFVSCDSVSVWVGDKTTATDINGKKEVNLGEVININSVFROYFEETKCRD 60

QY 62 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSKQAMRFIRIDTACVCLSRKAVRA 121
DB 61 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSKQAMRFIRIDTACVCLSRKAVRA 120

RESULT 10
US-09-664-295-31
Sequence 31, Application US/09664295
Patent No. 6429196
GENERAL INFORMATION:
APPLICANT: Gao, Wei-Qiang
TITLE OF INVENTION: Treatment of Balance Impairments
FILE REFERENCE: GENENT.051C1
CURRENT APPLICATION NUMBER: US/09/664,295
CURRENT FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 08/581,662
PRIOR FILING DATE: 1995-12-29
NUMBER OF SEQ ID NOS: 37
SEQ ID NO 31
LENGTH: 120
TYPE: PRT
ORGANISM: Homo sapiens
US-09-664-295-31

Query Match 98.5% Score 648; DB 4; Length 120;
Best Local Similarity 99.2% Pred. No. 7.4e-74;
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSSHPFHRGEFVSCDSVSVWVGDKTTATDINGKKEVNLGEVININSVFROYFEETKCRD 61
DB 1 SSSHPFHRGEFVSCDSVSVWVGDKTTATDINGKKEVNLGEVININSVFROYFEETKCRD 60

QY 62 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSKQAMRFIRIDTACVCLSRKAVRA 121
DB 61 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSKQAMRFIRIDTACVCLSRKAVRA 120

RESULT 11
PCT-0595-06918-3
Sequence 3, Application PC/TU9506918
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: PANITROPIC NEUROTROPHIC FACTORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/TU95/06918
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 905PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US95-06918-3

Query Match 98.58; Score 648; DB 5; Length 120;
Best Local Similarity 99.28; Pred. No. 7,4e-74;
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSSHPFRHGEFVSVCDSVSVWGDKTATDINGKEVWVLEGVNINNSVFRQYFFETKCRD 61
DB 1 SSSHPFRHGEFVSVCDSVSVWGDKTATDINGKEVWVLEGVNINNSVFRQYFFETKCRD 60
QY 62 PNPVDSGCGIDSKHNSYCTTHTTFVAKLTMDGKQAAAFRIRIDACVCVLSRAVRA 121
DB 61 PNPVDSGCGIDSKHNSYCTTHTTFVAKLTMDGKQAAAFRIRIDACVCVLSRAVRA 120

RESULT 12
US-08-266-080B-4
Sequence 4, Application US/08266080B
Patent No. 5606031

GENERAL INFORMATION:

APPLICANT: Jack Lile
APPLICANT: Tadshiko Kohno
APPLICANT: Duane Bonam
TITLE OF INVENTION: Production of Biologically Active
TITLE OF INVENTION: Recombinant Neurotrophic Protein
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/266,080B
FILING DATE: 27-JUNE-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,122
FILING DATE: 09-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/087,912
FILING DATE: 06-JULY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/680,681
FILING DATE: 04-APRIL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/594,126
FILING DATE: 09-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/547,750
FILING DATE: 02-JULY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/505,441

ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: SYNE200C5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
FEATURE:
NAME/KEY: Inferred amino acid sequence of human NGF
US-08-266-080B-4

Query Match 98.58; Score 648; DB 1; Length 241;
Best Local Similarity 99.28; Pred. No. 1,9e-73;
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSSHPFRHGEFVSVCDSVSVWGDKTATDINGKEVWVLEGVNINNSVFRQYFFETKCRD 61
DB 122 SSSHPFRHGEFVSVCDSVSVWGDKTATDINGKEVWVLEGVNINNSVFRQYFFETKCRD 181
QY 62 PNPVDSGCGIDSKHNSYCTTHTTFVAKLTMDGKQAAAFRIRIDACVCVLSRAVRA 121
DB 182 PNPVDSGCGIDSKHNSYCTTHTTFVAKLTMDGKQAAAFRIRIDACVCVLSRAVRA 241

RESULT 13

US-08-451-947-5
Sequence 5, Application US/08451947
Patent No. 5702906

GENERAL INFORMATION:

APPLICANT: GENENTECH, INC.
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pafin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,947
FILING DATE:

CLASSIFICATION: 514

APPLICATION NUMBER: 08/426419
FILING DATE: 19-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030013
FILING DATE: 22-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 1991
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 666P2C1D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674

TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-451-947-5

Query Match 98.5%; Score 648; DB 1; Length 241;
Best Local Similarity 99.2%; Pred. No. 1.9e-73;
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSSHPFHRGEEFVSVCDSVSWVGDKTTATDIDKGEVNLGEVINNSVFQYFFETKCRD 61
DB 122 SSSHPFHRGEEFVSVCDSVSWVGDKTTATDIDKGEVNLGEVINNSVFQYFFETKCRD 181
QY 62 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSKQAAMRFIRIDTACVCLSRKAVRA 121
DB 182 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSKQAAMRFIRIDTACVCLSRKAVRA 241

RESULT 14
US-08-424-826A-5
Sequence 5; Application US/08424826A
Patent No. 5830858
GENERAL INFORMATION:
APPLICANT: Rosenthal, Arnon
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,826A
FILING DATE: 19-Apr-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240387
FILING DATE: 10-May-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-Jan-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 25-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Phd., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0666P1C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-424-826A-5

Query Match 98.5%; Score 648; DB 2; Length 241;
Best Local Similarity 99.2%; Pred. No. 1.9e-73;
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSSHPFHRGEEFVSVCDSVSWVGDKTTATDIDKGEVNLGEVINNSVFQYFFETKCRD 61
DB 122 SSSHPFHRGEEFVSVCDSVSWVGDKTTATDIDKGEVNLGEVINNSVFQYFFETKCRD 181
QY 62 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSKQAAMRFIRIDTACVCLSRKAVRA 121
DB 182 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSKQAAMRFIRIDTACVCLSRKAVRA 241

RESULT 15
US-08-595-043A-75
Sequence 75; Application US/08595043A
Patent No. 5935824
GENERAL INFORMATION:
APPLICANT: SCARLATO, GREGORY D.
TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/595,043A
FILING DATE: 31-Jan-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: SGAR-00371
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-595-043A-75

Query Match 98.5%; Score 648; DB 2; Length 241;
Best Local Similarity 99.2%; Pred. No. 1.9e-73;
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSSHPFHRGEEFVSVCDSVSWVGDKTTATDIDKGEVNLGEVINNSVFQYFFETKCRD 61
DB 122 SSSHPFHRGEEFVSVCDSVSWVGDKTTATDIDKGEVNLGEVINNSVFQYFFETKCRD 181
QY 62 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSKQAAMRFIRIDTACVCLSRKAVRA 121
DB 182 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSKQAAMRFIRIDTACVCLSRKAVRA 241

Search completed: December 2, 2002, 15:09:42
Job time : 8.36928 secs

GenCore version 5.1.3
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OK protein - protein search, using sw model

Run on: December 2, 2002, 15:08:47 : Search time 4.25557 Seconds
(without alignments)
452.778 Million cell updates/sec

Title: US-10-072-681-2

Perfect score: 658

Sequence: 1 PSSSHPIFRGSEYVCDYSV.....FIRIDTACVLSRAVRA 121

Scoring table: BLOSUM62

Searched: 102317 seqs, 15924203 residues

Total number of hits satisfying chosen parameters: 102317

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/pdata/1/pubpaa/US08_NEM_PUB.pep.*
- 2: /cgn2_6/pdata/1/pubpaa/PCT_NEM_PUB.pep.*
- 3: /cgn2_6/pdata/1/pubpaa/US06_NEM_PUB.pep.*
- 4: /cgn2_6/pdata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/pdata/1/pubpaa/US07_NEM_PUB.pep.*
- 6: /cgn2_6/pdata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/pdata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/pdata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/pdata/1/pubpaa/US09_NEM_PUB.pep.*
- 10: /cgn2_6/pdata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/pdata/1/pubpaa/US10_NEM_PUB.pep.*
- 12: /cgn2_6/pdata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/pdata/1/pubpaa/US60_NEM_PUB.pep.*
- 14: /cgn2_6/pdata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	658	100.0	121	12 US-10-072-681-2	Sequence 2, Appl1
2	648	98.5	241	8 US-08-450-842-5	Sequence 16, Appl1
3	648	98.5	241	10 US-09-822-263-16	Sequence 5, Appl1
4	648	98.5	242	12 US-10-072-681-1	Sequence 1, Appl1
5	639	97.1	153	10 US-09-798-338-2	Sequence 2, Appl1
6	639	97.1	157	10 US-09-798-338-4	Sequence 4, Appl1
7	639	97.1	163	10 US-09-798-338-6	Sequence 6, Appl1
8	639	97.1	167	10 US-09-798-338-8	Sequence 8, Appl1
9	625	95.0	121	9 US-09-813-398-9	Sequence 9, Appl1
10	594	90.3	121	12 US-10-072-681-3	Sequence 3, Appl1
11	455	69.1	142	8 US-08-450-842-52	Sequence 52, Appl1
12	387	58.8	72	10 US-09-848-664-21	Sequence 21, Appl1
13	385.5	58.6	119	10 US-09-745-032-6	Sequence 6, Appl1
14	385.5	58.6	119	10 US-09-742-600-6	Sequence 6, Appl1
15	385.5	58.6	119	10 US-09-872-090-6	Sequence 6, Appl1
16	385.5	58.6	120	10 US-09-745-032-3	Sequence 3, Appl1
17	385.5	58.6	120	10 US-09-742-600-3	Sequence 3, Appl1
18	385.5	58.6	120	10 US-09-872-090-3	Sequence 3, Appl1
19	384.5	58.4	117	10 US-09-745-032-7	Sequence 7, Appl1

20	384.5	58.4	117	10 US-09-742-600-7	Sequence 7, Appl1
21	384.5	58.4	117	10 US-09-872-090-7	Sequence 7, Appl1
22	384.5	58.4	118	10 US-09-745-032-5	Sequence 5, Appl1
23	384.5	58.4	118	10 US-09-742-600-5	Sequence 5, Appl1
24	384.5	58.4	118	10 US-09-872-090-5	Sequence 5, Appl1
25	380.5	57.8	120	10 US-09-745-032-1	Sequence 1, Appl1
26	380.5	57.8	120	10 US-09-742-600-1	Sequence 1, Appl1
27	380.5	57.8	120	10 US-09-872-090-1	Sequence 1, Appl1
28	380.5	57.8	125	8 US-08-450-842-4	Sequence 4, Appl1
29	374	56.8	120	9 US-09-813-398-11	Sequence 11, Appl1
30	371	56.4	120	12 US-10-072-681-5	Sequence 12, Appl1
31	334.5	50.8	120	10 US-09-745-032-10	Sequence 10, Appl1
32	334.5	50.8	120	10 US-09-742-600-10	Sequence 10, Appl1
33	330.5	50.2	120	10 US-09-745-032-9	Sequence 9, Appl1
34	330.5	50.2	120	10 US-09-742-600-9	Sequence 9, Appl1
35	326.5	49.6	130	8 US-08-450-842-47	Sequence 47, Appl1
36	324.5	49.3	120	10 US-09-745-032-8	Sequence 8, Appl1
37	324.5	49.3	120	10 US-09-742-600-8	Sequence 8, Appl1
38	324.5	49.3	120	8 US-08-450-842-3	Sequence 3, Appl1
39	313	47.0	132	8 US-08-450-842-51	Sequence 51, Appl1
40	309.5	46.9	130	8 US-08-450-842-23	Sequence 23, Appl1
41	308.5	46.9	119	12 US-10-072-681-4	Sequence 12, Appl1
42	307.5	46.7	130	8 US-08-450-842-22	Sequence 22, Appl1
43	307.5	46.7	131	9 US-09-813-398-12	Sequence 12, Appl1
44	307.5	46.7	168	8 US-08-450-842-6	Sequence 6, Appl1
45	307.5	46.7	210	8 US-08-450-842-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-10-072-681-2
Sequence 2, Application US/10072681
Patent No. US20020157833A1
GENERAL INFORMATION:
APPLICANT: Burton, Louis E.
APPLICANT: Beck, Joanne T.
TITLE OF INVENTION: PURIFICATION OF NGF
FILE REFERENCE: GENENT 037C3
CURRENT APPLICATION NUMBER: US/10/072,681
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/030838
PRIOR FILING DATE: 1996-11-15
PRIOR APPLICATION NUMBER: 60/047855
PRIOR FILING DATE: 1997-05-29
PRIOR APPLICATION NUMBER: 08/970865
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: 09/363573
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: 09/675,503
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 121
TYPE: PRT
ORGANISM: Homo sapien
US-10-072-681-2

Query Match 100.0%; Score 658; DB 12; Length 121;
Best Local Similarity 100.0%; Pred. No. 5,2e-69;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PSSSHPIFRGSEYVCDYSVWGKTTATDTDKGEVWVGEVWVINSVROTFETKCR 60
DB 1 PSSSHPIFRGSEYVCDYSVWVGKTTATDTDKGEVWVGEVWVINSVROTFETKCR 60
OY 61 DPAPVDSGCGSDSKHMSYCTTHTFVKALTMDCQKQAAHFRIDTACVLSRAVRA 120
DB 61 DPAPVDSGCGSDSKHMSYCTTHTFVKALTMDCQKQAAHFRIDTACVLSRAVRA 120

OY 121 A 121
DB 121 A 121

RESULT 2

US-08-450-842-5
Sequence 5, Application US/08450842
Patent No. US20020045976A1

GENERAL INFORMATION:

APPLICANT: GENENTECH, INC.
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatIn (Genentech)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,842
FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/426419

FILING DATE: 19-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/030013

FILING DATE: 22-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/648482

FILING DATE: 31-JAN

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/587707

FILING DATE: 1991

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 666P2CID3
TELEPHONE: 415/425-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-08-450-842-5

Query Match 98.5%: Score 648; DB 8; Length 241;
Best Local Similarity 99.2%: Pred. No. 1,7e-67;
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSSPIFRHGEFVSVCDSVSWVGDKTATDINGKEVNVLGSEVNNINSVFROYFEETKCRD 61
DB 122 SSSPIFRHGEFVSVCDSVSWVGDKTATDINGKEVNVLGSEVNNINSVFROYFEETKCRD 181

OY 62 PNPVDSGCRGIDSKHNSYCTTHTFVKALTDGKQAAARFIRIDTACVCLSKAVARRA 121
DB 182 PNPVDSGCRGIDSKHNSYCTTHTFVKALTDGKQAAARFIRIDTACVCLSKAVARRA 241

RESULT 3
US-09-822-263-16
Sequence 16, Application US/09822263

Patent No. US20020036598A1

GENERAL INFORMATION:

APPLICANT: Prayaga, Sudhidas
APPLICANT: Verneet, Corline
APPLICANT: Shimkels, Richard A
APPLICANT: Burgess, Catherine
APPLICANT: Szytek, Kimberly
APPLICANT: Tchiernev, Velizar T
TITLE OF INVENTION: No. US20020036598A1el Polynucleotides and Polypeptides Encoded
FILE REFERENCE: 15966-572 CIP1
CURRENT APPLICATION NUMBER: US/09/822,263
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 09/672,665
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/156,745
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 60/158,942
PRIOR FILING DATE: 1999-10-06
PRIOR APPLICATION NUMBER: 60/159,248
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/169,344
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 60/215,048
PRIOR FILING DATE: 2000-06-29
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 241
TYPE: PRT
ORGANISM: Homo sapiens

US-09-822-263-16

Query Match 98.5%: Score 648; DB 10; Length 241;
Best Local Similarity 99.2%: Pred. No. 1,7e-67;
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSSPIFRHGEFVSVCDSVSWVGDKTATDINGKEVNVLGSEVNNINSVFROYFEETKCRD 61
DB 122 SSSPIFRHGEFVSVCDSVSWVGDKTATDINGKEVNVLGSEVNNINSVFROYFEETKCRD 181

OY 62 PNPVDSGCRGIDSKHNSYCTTHTFVKALTDGKQAAARFIRIDTACVCLSKAVARRA 121
DB 182 PNPVDSGCRGIDSKHNSYCTTHTFVKALTDGKQAAARFIRIDTACVCLSKAVARRA 241

RESULT 4

US-10-072-681-1

Sequence 1, Application US/10072681

Patent No. US20020137893A1

GENERAL INFORMATION:

APPLICANT: Burton, Louis E.

APPLICANT: Schmelzer, Charles H.

TITLE OF INVENTION: PURIFICATION OF NGF

FILE REFERENCE: GENENT 037C3

CURRENT APPLICATION NUMBER: US/10/072,681

CURRENT FILING DATE: 2002-02-08

PRIOR APPLICATION NUMBER: 60/030838

PRIOR FILING DATE: 1996-11-15

PRIOR APPLICATION NUMBER: 60/047855

PRIOR FILING DATE: 1997-05-29

PRIOR APPLICATION NUMBER: 08/970665

PRIOR FILING DATE: 1997-11-14

PRIOR APPLICATION NUMBER: 09/363573

PRIOR FILING DATE: 1999-07-29

PRIOR APPLICATION NUMBER: 09/675,503

PRIOR FILING DATE: 2000-09-29

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 242

TYPE: PRT

ORGANISM: Homo sapiens

US-10-072-681-1

Query Match 98.5%: Score 648; DB 12; Length 242;
Best Local Similarity 99.2%: Pred. No. 1.7e-67;
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSSHPIFRGGEFSVCDVSVMVGDKTTATDINKGEVAVLGEVINNSVFRQYFEETKCRD 61
DB 123 SSSHPIFRGGEFSVCDVSVMVGDKTTATDINKGEVAVLGEVINNSVFRQYFEETKCRD 182
OY 62 PNPVDSGCRGIDSKHNSYCTTHTFVKALTNQKQAAAFRIIDTACVCLSRRAVR 121
DB 183 PNPVDSGCRGIDSKHNSYCTTHTFVKALTNQKQAAAFRIIDTACVCLSRRAVR 242

RESULT 5

US-09-798-338-2
Sequence 2, Application US/09798338
Patent No. US20010020086A1

GENERAL INFORMATION:
APPLICANT: Hubbell, Jeffrey A.
APPLICANT: Schense, Jason C.
APPLICANT: Sakiyama, Shelly E.
TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE
FILE REFERENCE: 87662-68879
CURRENT APPLICATION NUMBER: US/09/798,338
PRIOR APPLICATION NUMBER: 09/141,153
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 153
TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Artificial
US-09-798-338-2

Query Match 97.1%: Score 639; DB 10; Length 153;
Best Local Similarity 99.2%: Pred. No. 1.1e-66;
Matches 117; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSSHPIFRGGEFSVCDVSVMVGDKTTATDINKGEVAVLGEVINNSVFRQYFEETKCRD 61
DB 35 SSSHPIFRGGEFSVCDVSVMVGDKTTATDINKGEVAVLGEVINNSVFRQYFEETKCRD 94
OY 62 PNPVDSGCRGIDSKHNSYCTTHTFVKALTNQKQAAAFRIIDTACVCLSRRAVR 119
DB 95 PNPVDSGCRGIDSKHNSYCTTHTFVKALTNQKQAAAFRIIDTACVCLSRRAVR 152

RESULT 6

US-09-798-338-4
Sequence 4, Application US/09798338
Patent No. US20010020086A1

GENERAL INFORMATION:
APPLICANT: Hubbell, Jeffrey A.
APPLICANT: Schense, Jason C.
APPLICANT: Sakiyama, Shelly E.
TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE
FILE REFERENCE: 87662-68879
CURRENT APPLICATION NUMBER: US/09/798,338
PRIOR APPLICATION NUMBER: 09/141,153
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 157

TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Artificial
US-09-798-338-4

Query Match 97.1%: Score 639; DB 10; Length 157;
Best Local Similarity 99.2%: Pred. No. 1.1e-66;
Matches 117; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSSHPIFRGGEFSVCDVSVMVGDKTTATDINKGEVAVLGEVINNSVFRQYFEETKCRD 61
DB 39 SSSHPIFRGGEFSVCDVSVMVGDKTTATDINKGEVAVLGEVINNSVFRQYFEETKCRD 98
OY 62 PNPVDSGCRGIDSKHNSYCTTHTFVKALTNQKQAAAFRIIDTACVCLSRRAVR 119
DB 99 PNPVDSGCRGIDSKHNSYCTTHTFVKALTNQKQAAAFRIIDTACVCLSRRAVR 156

RESULT 7

US-09-798-338-6
Sequence 6, Application US/09798338
Patent No. US20010020086A1

GENERAL INFORMATION:
APPLICANT: Hubbell, Jeffrey A.
APPLICANT: Schense, Jason C.
APPLICANT: Sakiyama, Shelly E.
TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE
FILE REFERENCE: 87662-68879
CURRENT APPLICATION NUMBER: US/09/798,338
PRIOR APPLICATION NUMBER: 09/141,153
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 163
TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Artificial
US-09-798-338-6

Query Match 97.1%: Score 639; DB 10; Length 163;
Best Local Similarity 99.2%: Pred. No. 1.2e-66;
Matches 117; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSSHPIFRGGEFSVCDVSVMVGDKTTATDINKGEVAVLGEVINNSVFRQYFEETKCRD 61
DB 45 SSSHPIFRGGEFSVCDVSVMVGDKTTATDINKGEVAVLGEVINNSVFRQYFEETKCRD 104
OY 62 PNPVDSGCRGIDSKHNSYCTTHTFVKALTNQKQAAAFRIIDTACVCLSRRAVR 119
DB 105 PNPVDSGCRGIDSKHNSYCTTHTFVKALTNQKQAAAFRIIDTACVCLSRRAVR 162

RESULT 8

US-09-798-338-8
Sequence 8, Application US/09798338
Patent No. US20010020086A1

GENERAL INFORMATION:
APPLICANT: Hubbell, Jeffrey A.
APPLICANT: Schense, Jason C.
APPLICANT: Sakiyama, Shelly E.
TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE
FILE REFERENCE: 87662-68879
CURRENT APPLICATION NUMBER: US/09/798,338
PRIOR APPLICATION NUMBER: 09/141,153

PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 167
TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Artificial
US-09-798-338-8

Query Match 97.1% Score 639; DB 10; Length 167;
Best Local Similarity 99.2% Pred. No. 1.2e-66;
Matches 117; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSSHPHFHGRGFSVCDVSVVWGDKTTATDIDKGEVAVLGEVNNINSVROFFETKCRD 61
DB 49 SSSHPHFHGRGFSVCDVSVVWGDKTTATDIDKGEVAVLGEVNNINSVROFFETKCRD 108
QY 62 PNPVDSGCGIDSKHMNSCTTHTFVKALTMDSKQAMRFIRIDPACVLSRKA VR 119
DB 109 PNPVDSGCGIDSKHMNSCTTHTFVKALTMDSKQAMRFIRIDPACVLSRKA VR 166

RESULT 9
US-09-813-398-9
Sequence 9, Application US/09813398
Patent No. US20020169292A1
GENERAL INFORMATION:
APPLICANT: Bruce D. Weintraub
APPLICANT: Mariusz W. Szekulinski
TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
FILE REFERENCE: US/09/813.398
CURRENT APPLICATION NUMBER: US/09/813.398
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: PCT/US99/05908
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: PCT/US98/19772
PRIOR FILING DATE: 1998-09-22
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 121
TYPE: PRF
ORGANISM: HOMO SAPIEN
US-09-813-398-9

Query Match 95.0% Score 625; DB 9; Length 121;
Best Local Similarity 95.0% Pred. No. 3.3e-65;
Matches 115; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 PSSSHPIFHRGFSVCDVSVVWGDKTTATDIDKGEVAVLGEVNNINSVROFFETKCR 60
DB 1 PSSSHPIFHRGFSVCDVSVVWGDKTTATDIDKGEVAVLGEVNNINSVROFFETKCR 60
QY 61 DPNPVDGCGIDSKHMNSCTTHTFVKALTMDSKQAMRFIRIDPACVLSRKA VR 120
DB 61 DPNPVDGCGIDSKHMNSCTTHTFVKALTMDSKQAMRFIRIDPACVLSRKA VR 120
QY 121 A 121
DB 121 A 121

RESULT 10
US-10-072-681-3
Sequence 3, Application US/10072681
Patent No. US20020137893A1
GENERAL INFORMATION:
APPLICANT: Burton, Louis E.
APPLICANT: Schweizer, Charles H.

APPLICANT: Beck, Joanne T.
TITLE OF INVENTION: PURIFICATION OF NGF
FILE REFERENCE: GENENT.037C3
CURRENT APPLICATION NUMBER: US/10/072.681
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/030838
PRIOR FILING DATE: 1996-11-15
PRIOR APPLICATION NUMBER: 60/047855
PRIOR FILING DATE: 1997-05-29
PRIOR APPLICATION NUMBER: 08/970865
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: 09/363573
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: 09/675,503
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 121
TYPE: PRF
ORGANISM: mouse
US-10-072-681-3

Query Match 90.3% Score 594; DB 12; Length 121;
Best Local Similarity 90.8% Pred. No. 1.3e-61;
Matches 109; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 PSSSHPIFHRGFSVCDVSVVWGDKTTATDIDKGEVAVLGEVNNINSVROFFETKCR 60
DB 1 PSSSHPIFHRGFSVCDVSVVWGDKTTATDIDKGEVAVLGEVNNINSVROFFETKCR 60
QY 61 DPNPVDGCGIDSKHMNSCTTHTFVKALTMDSKQAMRFIRIDPACVLSRKA VR 120
DB 61 ASNPVDSGCGIDSKHMNSCTTHTFVKALTMDSKQAMRFIRIDPACVLSRKA VR 120

RESULT 11
US-08-450-842-52
Sequence 52, Application US/08450842
Patent No. US20020045576A1
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,842
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426419
FILING DATE: 19-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030013
FILING DATE: 22-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 1991

ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 666P2C1D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-450-842-52

Query Match 69.1%; Score 455; DB 8; Length 142;
Best Local Similarity 64.8%; Pred. No. 1,7e-45;
Matches 92; Conservative 11; Mismatches 17; Indels 22; Gaps 4;

OY 2 SSSPIRHRGEFVSVDVWGDKTATDIDKGEVNLGEVININSV----- 49
DB 1 SSSPIRHRGEFVSVDVWGDKTATDIDKGEVNLGEVININSVLEVPDAGSP 60
OY 50 FROYFETKCRDNPVD-----SSCRGIDSKHNSYCTTHFEVKALTMDCR-QAAMR 101
DB 61 LROYFETKCRDNPVD-----SSCRGIDSKHNSYCTTHFEVKALTMDCR-QAAMR 120
OY 102 FIRDPA--CVCVLSRAVRA 121
DB 121 WIRDPA--CVCVLSRAVRA 142

RESULT 12
US-09-848-664-21
Sequence 21, Application US/09848664
Patent No. US20020146414A1
GENERAL INFORMATION:
APPLICANT: Sakiyama-Elbert, Shelly E.
APPLICANT: Hubbard, Jeffrey A.
TITLE OF INVENTION: Controlled Release of No. US20020146414A1-Heparin Binding Growth
FILE REFERENCE: ETH 108
CURRENT APPLICATION NUMBER: US/09/848,664
PRIOR FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: 09/298,084
PRIOR FILING DATE: 1999-04-22
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
LENGTH: 72
TYPE: PRT
ORGANISM: Homo sapiens
US-09-848-664-21

Query Match 58.8%; Score 387; DB 10; Length 72;
Best Local Similarity 98.6%; Pred. No. 5.1e-38;
Matches 71; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSSPIRHRGEFVSVDVWGDKTATDIDKGEVNLGEVININSVFRQYFETKCRD 61
DB 1 SSSPIRHRGEFVSVDVWGDKTATDIDKGEVNLGEVININSVFRQYFETKCRD 60
OY 62 PNPVDSGCGCID 73
DB 61 PNPVDSGCGCID 72

RESULT 13
US-09-745-032-6
Sequence 6, Application US/09745032
Patent No. US20010027179A1
GENERAL INFORMATION:
APPLICANT: Boone, Thomas C.

APPLICANT: Cheung, Ellen N.
APPLICANT: Hershenson, Susan I.
APPLICANT: Young, John D.
TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS
FILE REFERENCE: A-411A US Revised 073100
CURRENT APPLICATION NUMBER: US/09/745,032
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 09/214,214
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 08/684,353
PRIOR FILING DATE: 1996-07-19
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 119
TYPE: PRT
ORGANISM: Human
US-09-745-032-6

Query Match 58.6%; Score 385.5; DB 10; Length 119;
Best Local Similarity 60.7%; Pred. No. 1.4e-37;
Matches 68; Conservative 19; Mismatches 24; Indels 1; Gaps 1;

OY 9 HRGEFVSVDVWGDKTATDIDKGEVNLGEVININSVFRQYFETKCRDNPVDSG 68
DB 7 HRGEFVSVDVWGDKTATDIDKGEVNLGEVININSVFRQYFETKCRDNPVDSG 66
OY 69 CRGIDSKHNSYCTTHFEVKALTMDCR-QAAMRFRIDPACVLSRAVR 119
DB 67 CRGIDSKHNSYCTTHFEVKALTMDCR-QAAMRFRIDPACVLSRAVR 118

RESULT 14
US-09-742-600-6
Sequence 6, Application US/09742600
Patent No. US20020010135A1
GENERAL INFORMATION:
APPLICANT: Boone, Thomas C.
APPLICANT: Cheung, Ellen N.
APPLICANT: Hershenson, Susan I.
APPLICANT: Young, John D.
TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS
FILE REFERENCE: A-411A US Revised 073100
CURRENT APPLICATION NUMBER: US/09/742,600
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 09/214,214
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 08/684,353
PRIOR FILING DATE: 1996-07-19
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 119
TYPE: PRT
ORGANISM: Human
US-09-742-600-6

Query Match 58.6%; Score 385.5; DB 10; Length 119;
Best Local Similarity 60.7%; Pred. No. 1.4e-37;
Matches 68; Conservative 19; Mismatches 24; Indels 1; Gaps 1;

OY 9 HRGEFVSVDVWGDKTATDIDKGEVNLGEVININSVFRQYFETKCRDNPVDSG 68
DB 7 HRGEFVSVDVWGDKTATDIDKGEVNLGEVININSVFRQYFETKCRDNPVDSG 66
OY 69 CRGIDSKHNSYCTTHFEVKALTMDCR-QAAMRFRIDPACVLSRAVR 119
DB 67 CRGIDSKHNSYCTTHFEVKALTMDCR-QAAMRFRIDPACVLSRAVR 118

RESULT 15
US-09-872-090-6
Sequence 6, Application US/09872090

```

; Patent No. US20020052488A1
; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C.
; APPLICANT: Cheung, Ellen Ngai Yim
; APPLICANT: Hershenson, Susan I.
; APPLICANT: Young, John D.
; TITLE OF INVENTION: Analogs of NT-3 (As Amended)
; FILE REFERENCE: A-4118
; CURRENT APPLICATION NUMBER: US/09/872,090
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 09/255,953
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: 08/684,353
; PRIOR FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 6
; LENGTH: 119
; TYPE: prt
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Analog of
; US-09-872-090-6
;
Query Match      58.6%; Score 385.5; DB 10; Length 119;
Best Local Similarity 60.7%; Pred. No. 1,4e-37;
Matches 68; Conservative 19; Mismatches 24; Indels 1; Gaps 1;
OY 9 HNGEYSVCDVSVMYGDGTTATDIDKGEVNLGEVNIINSVFQYFFETKCRDNPVDSG 68
   ||||| ||||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| |||
DB 7 HNGEYSVCDSESLWTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETKCEAPVDNG 66
   ||||| ||||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| |||
OY 69 CRGIDSKHNSYCTTHTFVKALTPD-GKQAMNFRIDTACVCLSRKAVR 119
   ||||| ||||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| |||
DB 67 CRGIDSKHNSCKTSQTYVALTSSENKLVGMNIRIDTSCVCLSRKIGR 118
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Search completed: December 2, 2002, 15:14:34
 Job time : 5.25557 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 2, 2002, 15:05:37 : Search time 24.1149 seconds
(without alignments)
668.605 Million cell updates/sec

Title: US-10-072-681-3

Perfect score: 653
Sequence: 1 PSSHPVHFHGEFVSVDVS.....FINIDPACVLSRKATRRG 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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24: /SID52/gcgdata/geneseq/geneeqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	646	98.9	120	19	AAW48887
2	646	98.9	307	5	AAW48887
3	646	98.9	307	5	AAW48887
4	646	98.9	307	5	AAW48887
5	643	98.5	120	13	AAW48887
6	643	98.5	120	13	AAW48887
7	640	98.0	23	23	AAW48887
8	639	97.9	118	13	AAW48887
9	635	97.2	118	13	AAW48887
10	633	96.9	120	13	AAW48887

11	631	96.6	120	13	AAW48887	Chimeric neurotrop
12	624	95.6	120	13	AAW48887	Chimeric neurotrop
13	622	95.3	120	13	AAW48887	Chimeric neurotrop
14	618	94.6	120	15	AAW48887	Nerve growth facto
15	611.5	93.6	121	15	AAW48887	Chimeric neurotrop
16	610	93.4	122	13	AAW48887	Chimeric neurotrop
17	608	93.1	118	13	AAW48887	Chimeric neurotrop
18	607	93.0	120	13	AAW48887	Chimeric neurotrop
19	603	92.3	120	13	AAW48887	Chimeric neurotrop
20	595	91.1	120	13	AAW48887	Chimeric neurotrop
21	591	90.5	119	10	AAW48887	Chimeric neurotrop
22	585	89.6	307	14	AAW48887	Human nerve growth
23	584	89.4	120	21	AAW48887	Nerve growth facto
24	584	89.4	120	21	AAW48887	N-term of neuro
25	584	89.4	120	22	AAW48887	Nerve growth facto
26	584	89.4	120	22	AAW48887	NGF-beta amino aci
27	584	89.4	124	13	AAW48887	Chimeric neurotrop
28	584	89.4	241	12	AAW48887	Human NGF Smat-Apa
29	584	89.4	241	12	AAW48887	Human nerve growth
30	584	89.4	241	12	AAW48887	Human nerve growth
31	584	89.4	241	12	AAW48887	Human nerve growth
32	584	89.4	241	16	AAW48887	Human nerve growth
33	584	89.4	241	16	AAW48887	Human nerve growth
34	584	89.4	241	18	AAW48887	Human nerve growth
35	584	89.4	241	19	AAW48887	Human prepro-nerve
36	584	89.4	241	20	AAW48887	Human nerve growth
37	584	89.4	241	22	AAW48887	Amino acid sequenc
38	584	89.4	241	22	AAW48887	Human NGF. Homo s
39	584	89.4	241	23	AAW48887	Human beta nerve g
40	584	89.4	241	23	AAW48887	Human beta nerve g
41	584	89.4	245	5	AAW48887	Sequence encoded b
42	584	89.4	307	14	AAW48887	Human pre-pro nerv
43	584	89.4	307	19	AAW48887	Human beta-nerve g
44	579	88.7	118	10	AAW48887	Human nerve growth
45	579	88.7	119	5	AAW48887	Sequence encoded b

ALIGNMENTS

RESULT 1	AAW48887	standard; Protein: 120 AA.
ID	AAW48887	
AC	AAW48887	
DT	12-OCT-1998	(first entry)
XX		
DE	Mouse nerve growth factor.	
KW	Neurotrophin; nerve growth factor; NGF; mouse; purification;	
KW	hydrophobic interaction chromatography.	
OS	Mus sp.	
XX		
FT	Key	Location/Qualifiers
FT	Region	58..68
FT		/note="conserved Cys-containing region involved in
FT		Cys knot motif"
FT	Region	108..110
FT		/note="conserved Cys-containing region involved in
FT		Cys knot motif"
XX		
XX	W09821234-A2.	
XX		
PD	22-MAY-1998.	
XX		
PF	14-NOV-1997;	97MO-US21068.
XX		
XX	29-MAY-1997;	97US-0047855.
PR	15-NOV-1996;	96US-0030838.
XX		
PA	(GETH) GENENTECH INC.	

```

XX Beck JT, Burton LE, Schmelzer CH:
XX WPI: 1998-322333/28.
XX
XX Isolation of neurotrophin(s) from, e.g. mis-folded or glycosylated
XX variant(s) - using hydrophobic interaction chromatography.
XX optionally in combination with high performance cation exchange
XX chromatography
XX
XX Disclosure: Page 36; 59pp: English.
XX
XX This polypeptide comprises mouse nerve growth factor (NGF) mature
XX polypeptide. Methods are provided for large-scale purification of
XX neurotrophins, including mature NGF, suitable for clinical use. A
XX claimed method comprises: (1) separating the neurotrophin from the
XX other proteins using a hydrophobic interaction chromatography resin
XX (HICR); and optionally (2) separating the neurotrophin from a
XX chemical variant by high performance cation exchange chromatography
XX (HPEC). The processes can also be used for purification of e.g.
XX human NGF (see AAM48886), brain-derived neurotrophic factor (see
XX AAM48888), neurotrophin-4/5 (see AAM48890) and neurotrophin-3 (see
XX AAM48889). The processes allow separation of neurotrophins from
XX various undesirable misprocessed, misfolded, size, glycosylated or
XX charge forms. They allow selective separation from variants and
XX other molecules, and from other polypeptides with high pI. The
XX processes are applicable to starting materials from various
XX sources, including fermentation broths or lysed bacterial or
XX mammalian cells.
XX
XX Sequence 120 AA:
XX
XX Query Match 98.9%; Score 646; DB 19; Length 120;
XX Best Local Similarity 100.0%; Pred. No. 1e-66;
XX Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 2 SSTRHPFHMGESVCSVSWWGDKTTATDIDKGEVTVLAENVNNSVFRQFEETCRA 61
XX |||||||
XX 1 SSTRHPFHMGESVCSVSWWGDKTTATDIDKGEVTVLAENVNNSVFRQFEETCRA 60
XX |||||||
XX 62 SNPEVSCRCIDSKHWNSTCTTHTFVKALTTDEKQAMRFIRIDTACVCLSKRATRG 121
XX |||||||
XX 61 SNPEVSCRCIDSKHWNSTCTTHTFVKALTTDEKQAMRFIRIDTACVCLSKRATRG 120
XX |||||||
XX
XX RESULT 2
XX AAP40036 standard; Protein: 307 AA.
XX ID AAP40036;
XX AC AAP40036;
XX
XX 25-JAN-1992 (first entry)
XX
XX Sequence encoded by the human beta-nerve growth factor (NGF) gene
XX and flanking regions on phage lambda h-beta-N8.
XX
XX Nerve damage: therapy.
XX
XX Homo sapiens.
XX
XX EP121338-A.
XX
XX 10-OCT-1984.
XX
XX 02-MAR-1984; 84EP-0301377.
XX
XX 03-MAR-1983; 83US-0471962.
XX
XX (GETH ) GENENTECH INC.
XX
XX Gray AM, Ullrich A;
XX
XX WPI: 1984-251909/41.
XX

```

```

DR N-PSDB; AAN40031.
XX
XX Human beta-nerve growth factor free from other proteins - obtd.
XX by recombinant DNA techniques for treating nerve damage
XX
XX Example: Fig 2; 42pp: English.
XX
XX The inventors claim human beta-nerve growth factor (NGF) free from
XX other proteins of human origin. Also claimed are the DNA sequence
XX encoding human beta-NGF operably linked with a DNA sequence capable
XX of effecting its expression in a recombinant host cell; a replicable
XX expression vector contg. the DNA; and host cells transformed with
XX the vector. The plasmid claimed is plasmid ph-beta-NGF trp 1. Using
XX the plasmid, larger amounts of pure beta-NGF are obtainable than by
XX extn. of natural materials, see e.g. EP-2139.
XX
XX Sequence 307 AA:
XX
XX Query Match 98.9%; Score 646; DB 5; Length 307;
XX Best Local Similarity 100.0%; Pred. No. 3.5e-66;
XX Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 2 SSTRHPFHMGESVCSVSWWGDKTTATDIDKGEVTVLAENVNNSVFRQFEETCRA 61
XX |||||||
XX 188 SSTRHPFHMGESVCSVSWWGDKTTATDIDKGEVTVLAENVNNSVFRQFEETCRA 247
XX |||||||
XX 62 SNPEVSCRCIDSKHWNSTCTTHTFVKALTTDEKQAMRFIRIDTACVCLSKRATRG 121
XX |||||||
XX 248 SNPEVSCRCIDSKHWNSTCTTHTFVKALTTDEKQAMRFIRIDTACVCLSKRATRG 307
XX |||||||
XX
XX RESULT 3
XX AAP40039 standard; Protein: 307 AA.
XX ID AAP40039;
XX AC AAP40039;
XX
XX 25-JAN-1992 (first entry)
XX
XX Sequence encoded by human prepro-beta-nerve growth factor
XX (NGF) gene.
XX
XX Nerve damage: therapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..187
XX Protein 188..307
XX
XX EP121338-A.
XX
XX 10-OCT-1984.
XX
XX 02-MAR-1984; 84EP-0301377.
XX
XX 03-MAR-1983; 83US-0471962.
XX
XX (GETH ) GENENTECH INC.
XX
XX Gray AM, Ullrich A;
XX
XX WPI: 1984-251909/41.
XX
XX N-PSDB; AAN40034.
XX
XX Human beta-nerve growth factor free from other proteins - obtd.
XX by recombinant DNA techniques for treating nerve damage
XX
XX Example: Fig 6; 42pp: English.
XX
XX The inventors claim human beta-nerve growth factor (NGF) free from
XX other proteins of human origin. Also claimed are the DNA sequence

```

CC encoding human beta-NGF operably linked with a DNA sequence capable
 CC of effecting its expression in a recombinant host cell; a replicable
 CC expression vector contg. the DNA; and host cells transformed with
 CC the vector. The plasmid claimed is plasmid ph-beta-NGF trp 1. Using
 CC the plasmid, larger amounts of pure beta-NGF are obtainable than by
 CC extrn. of natural materials, see e.g. EP-2139.

XX Sequence 307 AA;

Query Match 98.9%; Score 646; DB 5; Length 307;

Best Local Similarity 100.0%; Pred. No. 3.5e-66; Mismatches 0; Indels 0; Gaps 0;

Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 SSTRHVFHMGESVCDSSVWVGDKTTATDCKGEVTLAEVINNSVROFFETKCA 61
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 188 SSTRHVFHMGESVCDSSVWVGDKTTATDCKGEVTLAEVINNSVROFFETKCA 247
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Oy 62 SNPVESGCGIDSKHMNSCTTHTTFVKALTTDEKQAMRFIRIDPACVLSRKATRG 121
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 248 SNPVESGCGIDSKHMNSCTTHTTFVKALTTDEKQAMRFIRIDPACVLSRKATRG 307
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 4

AAR45240 standard; Protein: 307 AA.

XX AAR45240;

XX 20-JUN-1994 (first entry)

XX Cloned mouse pre-pro nerve growth factor.

XX Mature human: beta-nerve growth factor; mouse; pre-pro portion;
 XX expression; NGF; hNGF; treatment; Alzheimer's disease; murine.

XX Mus musculus.

XX Key Location/Qualifiers

XX Peptide 1..187 /note= "signal peptide"

XX Peptide 188..307 /note= "mature peptide"

XX US5722063-A.

XX 21-DEC-1993.

XX 20-JUN-1989; 89US-0383118.

XX 22-NOV-1988; 88US-0274678.

XX 20-JUL-1989; 89US-0383118.

XX (SYNT) SYNTX USA INC.

XX Baecker PA, Barnett JW, Bursztyr-Petregrew H, Chan HW, Nguyen BT;
 XX Ward C;

XX WPI; 1993-413401/51.

XX N-PSDB; AA054282.

XX Prodn. of active mature human beta-nerve growth factor in insect
 XX cells - using baculovirus expression system, and potential use of
 XX recombinant hNGF in treatment of Alzheimer's disease

XX Disclosure: Fig 1; 23pp; English.

XX The sequence is that of mouse pre-pro nerve growth factor
 CC which was used in a method of producing biologically active
 CC mature human beta-nerve growth factor in insect cells.

XX Sequence 307 AA;

Query Match 98.9%; Score 646; DB 14; Length 307;

Best Local Similarity 100.0%; Pred. No. 3.5e-66; Mismatches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 SSTRHVFHMGESVCDSSVWVGDKTTATDCKGEVTLAEVINNSVROFFETKCA 61

Db 188 SSTRHVFHMGESVCDSSVWVGDKTTATDCKGEVTLAEVINNSVROFFETKCA 247

Oy 62 SNPVESGCGIDSKHMNSCTTHTTFVKALTTDEKQAMRFIRIDPACVLSRKATRG 121

Db 248 SNPVESGCGIDSKHMNSCTTHTTFVKALTTDEKQAMRFIRIDPACVLSRKATRG 307

RESULT 5

AAR21868 standard; Protein: 120 AA.

XX AAR21868;

XX 10-JUN-1992 (first entry)

XX Chimeric neurotrophic factor S6.

XX Human BDNF; brain derived neurotrophic factor; NGF;

XX neurotrophic growth factor; Alzheimer's disease; ageing;

XX peripheral neuropathies; Parkinson's disease; Huntington's chorea;

XX amyotrophic lateral sclerosis; nervous system disorders.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..50 /note= "mouse NGF residues 1-50"

XX Peptide 51..58 /note= "human BDNF residues 51-58"

XX Peptide 59..120 /note= "mouse NGF residues 59-120"

XX WO9202620-A.

XX 20-FEB-1992.

XX 07-AUG-1991; 91WO-0505610.

XX 08-AUG-1990; 90US-0564929.

XX (REG-) REGENERON PHARM INC.

XX Shooter EM, Suter U, Ip N, Squinto SP, Furch ME, Lindsay RM;
 XX Yancopoulos GD;

XX WPI; 1992-080074/10.

XX New chimeric neurotrophic factors - useful in treating nervous
 XX conditions caused by trauma, surgery, ischemia, infection,
 XX metabolic diseases, nutritional deficiency, etc.

XX Claim 29; Fig 10; 114pp; English.

XX The sequence is that of a chimeric neurotrophic factor (NF) S6 which
 CC comprises the mouse neurotrophic growth factor (NGF) residues 1-50.

CC human brain derived growth factor (hBNF) residues 51-58 and mouse NGF
 CC residues 59-120. It may provide the activity of 2 NFs in a single mol.

CC or may serve as a superagonist of an endogenous NF thereby enabling an
 CC increased biological response at lower doses. It may also be useful in

CC targeting an active cpd. to cells responsive to NF. The design of
 CC chimeric NFs, such as S6, which retain specific biological activity

CC but which are directed to a subset of factor-responsive cells may
 CC enable treatment of neurological disorders but avoid the complications

CC of more widespread activity of parent mols. It may be used in the
 CC treatment to eliminate diseased cells, e.g. virus infected cells or

CC tumours of nervous system origin. It may also be used to treat patients
 CC whose nervous system has been damaged by trauma, surgery, ischemia,

CC infection (e.g. polio or AIDS), metabolic disease, nutritional

deficiency, malignancy or toxic agents. Also to treat e.g. Alzheimer's disease, ageing, peripheral neuropathies, Parkinson's disease, Huntington's chorea or amyotrophic lateral sclerosis. S6 or antibodies to it can also be used in the diagnosis and study of nervous system disorders. See also AAR21851-R21874 and AA022080-Q22131.

Sequence 120 AA:

Query Match 98.5%; Score 643; DB 13; Length 120;
Best Local Similarity 99.2%; Pred. No. 2,3e-66;
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSTRHVFHMGFEFSCDVSVMWGDKTATADIKGEVTVLAENVINNSVPROFEETKRA 61
DB 1 SSTRHVFHMGFEFSCDVSVMWGDKTATADIKGEVTVLAENVINNSVPROFEETKRA 60
OY 62 SNPEVSGCRGIDSKHMNSYCTTHTFVKALTTDEKQAMRFIRIDTACVCLSRKATRRG 121
DB 61 SNPEVSGCRGIDSKHMNSYCTTHTFVKALTTDEKQAMRFIRIDTACVCLSRKATRRG 120

RESULT 6
AAR21873
ID AAR21873 standard; Protein: 120 AA.

XX AAR21873;
XX
XX 10-JUN-1992 (first entry)

XX Chimeric neurotrophic factor S11.

XX Human BDNF; brain derived neurotrophic factor; NGF;
XX neurotrophic growth factor; Alzheimer's disease; ageing;
XX peripheral neuropathies; Parkinson's disease; Huntington's chorea;
XX amyotrophic lateral sclerosis; nervous system disorders.

XX Homo sapiens.

XX Key location/Qualifiers
XX Peptide 1..101 /note="mouse NGF residues 1-101"
XX Peptide 102..110 /note="human BDNF residues 103-111"
XX Peptide 111..120 /note="mouse NGF residues 111-120"

XX MO9202620-A.

XX 20-FEB-1992.

XX 07-AUG-1991; 91WO-US05610.

XX 08-AUG-1990; 90US-0564929.

XX (REGC-) REGENERON PHARM INC.

XX Shooter EM, Suter U, Ip N, Squinco SP, Furch ME, Lindsay RM;
XX Yancopoulos CD;

XX WPI: 1992-080074/10.

XX New chimeric neurotrophic factors - useful in treating nervous
XX conditions caused by trauma, surgery, ischemia, infection,
XX metabolic diseases, nutritional deficiency, etc.

XX Claim 34; Fig 10; 114pp; English.

XX The sequence is that of a chimeric neurotrophic factor (NF) S11 which
XX comprises the mouse neurotrophic growth factor (NGF) residues 1-101,
XX human brain derived growth factor (hBDNF) residues 103-111 and mouse
XX residues 111-120. It may provide the activity of 2 NFs in a single mol.
XX or may serve as a superagonist of an endogenous NF thereby enabling an
XX increased biological response at lower doses. It may also be useful in

CC targeting an active cpl. to cells responsive to NF. The design of
CC chimeric NFs, such as S11, which retain specific biological activity
CC but which are directed to a subset of factor-responsive cells may
CC enable treatment of neurological disorders but avoid the complications
CC of more widespread activity of parent mole. It may be used in the
CC treatment to eliminate diseased cells, e.g. virus infected cells or
CC tumours of nervous system origin. It may also be used to treat patients
CC whose nervous system has been damaged by trauma, surgery, ischemia,
CC infection (e.g. Polio or AIDS), metabolic disease, nutritional
CC deficiency, malignancy or toxic agents. Also to treat e.g. Alzheimer's
CC disease, ageing, peripheral neuropathies, Parkinson's disease,
CC Huntington's chorea or amyotrophic lateral sclerosis. S11 or antibodies
CC to it can also be used in the diagnosis and study of nervous system
CC disorders. See also AAR21851-R21874 and AA022080-Q22131.

Sequence 120 AA:

Query Match 98.5%; Score 643; DB 13; Length 120;
Best Local Similarity 99.2%; Pred. No. 2,3e-66;
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSTRHVFHMGFEFSCDVSVMWGDKTATADIKGEVTVLAENVINNSVPROFEETKRA 61
DB 1 SSTRHVFHMGFEFSCDVSVMWGDKTATADIKGEVTVLAENVINNSVPROFEETKRA 60
OY 62 SNPEVSGCRGIDSKHMNSYCTTHTFVKALTTDEKQAMRFIRIDTACVCLSRKATRRG 121
DB 61 SNPEVSGCRGIDSKHMNSYCTTHTFVKALTTDEKQAMRFIRIDTACVCLSRKATRRG 120

RESULT 7
AAM50845
ID AAM50845 standard; Protein: 240 AA.

XX AAM50845;

XX 01-MAY-2002 (first entry)

XX Mouse nerve growth factor.

XX Beta-nerve growth factor; NGF; mouse; neurotrophic factor; NTF;
XX Huntington's disease; Parkinson's disease; Alzheimer's disease;
XX amyotrophic lateral sclerosis; neurodegenerative disease; cancer;
XX neuroprotective; neurotropic; anticonvulsant; antiparkinsonian;
XX cyostatic; therapy.

XX Mus musculus.

XX Key location/Qualifiers
XX Peptide 1..18 /label=Signal_peptide
XX Peptide 19..121 /label=Propeptide
XX Peptide 122..240 /label=Mature_protein
XX Disulfide-bond 136..201
XX Disulfide-bond 179..229
XX Disulfide-bond 189..231

XX Modified-site 69 /note="N-glycosylated"
XX Modified-site 114 /note="N-glycosylated"

XX Misc-difference 233..240 /note="conflict, replaced by CSACRLOEPA"

XX MO200203071-A2.

XX 10-JAN-2002.

XX 05-JUL-2001; 2001WO-US21472.

XX 05-JUL-2000; 2000US-215778P.

PA (PANG-) PANGENE CORP.
 PI Bates AT:
 XX
 XX
 DR WP1: 2002-179638/23.
 XX
 PT Screening for a neurotrophic factor mimetic, useful for treating, e.g.,
 PT cancer and Alzheimer's, comprises combining a candidate mimetic with a
 PT fragment of a tyrosine kinase protein -
 XX
 XX Disclosure; Fig 5; 107pp; English.
 XX
 XX The present sequence is that of murine beta-nerve growth factor
 CC (NGF), a neurotrophic factor (NTF) that binds to TrkA receptor
 CC tyrosine kinase. The invention concerns Trks and their ligands
 CC that modulate cell growth, differentiation and survival. Trk
 CC proteins are known to mediate the activities of neurotrophins and
 CC are also known proto-oncogenes. Methods are claimed for screening
 CC for small molecule NTF mimetics, such as the cyclic peptide given
 CC in AA050844, capable of binding to a Trk protein or of modulating
 CC the binding of a neurotrophin to a Trk protein. Also claimed are
 CC medicaments comprising a small molecule NTF mimetic and their use
 CC in claimed methods for treatment of cancer or a neurodegenerative
 CC disease selected from Huntington's disease, Parkinson's disease,
 CC Alzheimer's disease and amyotrophic lateral sclerosis.
 XX
 SQ Sequence 240 AA:
 Query Match 98.0%; Score 640; DB 23; Length 240;
 Best Local Similarity 100.0%; Pred. No. 1.3e-65;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 SSTRPFFHMGESVCDVSVMGDKTTATDICKKEVTVALEVINNSVROFFETKCA 61
 DB 132 SSTRPFFHMGESVCDVSVMGDKTTATDICKKEVTVALEVINNSVROFFETKCA 161
 OY 62 SNPVESGCRGIDSKHNSYCTTHTFEVKALTTDEKQAAAFRIRIDPACVLSRKATRR 120
 DB 182 SNPVESGCRGIDSKHNSYCTTHTFEVKALTTDEKQAAAFRIRIDPACVLSRKATRR 240

RESULT 8
 ID AAR21862 standard; Protein; 132 AA.
 XX
 AC AAR21862;
 XX
 DT 10-JUN-1992 (first entry)
 XX
 DE Chimeric neurotrophic factor NM1.
 XX
 KW Human BDNF; brain derived neurotrophic factor; NGF;
 KW neurotrophic growth factor; Alzheimer's disease; ageing;
 KW peripheral neuropathies; Parkinson's disease; Huntington's chorea;
 KW amyotrophic lateral sclerosis; nervous system disorders.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 1..4
 FT Peptide /note= "mouse NGF preprosequence"
 FT 5..122
 FT Peptide /note= "mouse NGF residues 1-118"
 FT 123..132
 FT Peptide /note= "10 amino acid antigenic peptide fragment
 of human myc protein"

MO9202620-A.
 XX
 XX
 PD 20-FEB-1992.
 XX
 PF 07-AUG-1991; 91WO-US05610.
 XX

PR 08-AUG-1990; 90US-0564929.
 PA (RECE-) REGENERON PHARM INC.
 XX
 XX Shooter EM, Suter U, Ip N, Squinto SP, Furch ME, Lindsay RM;
 PI Yancopoulos GD;
 XX
 DR WP1: 1992-080074/10.
 XX
 PT New chimeric neurotrophic factors - useful in treating nervous
 PT conditions caused by trauma, surgery, ischemia, infection,
 PT metabolic diseases, nutritional deficiency, etc.
 XX
 PS Claim 46; Fig 5; 114pp; English.
 XX
 CC The sequence is that of a chimeric neurotrophic factor (NF) NM1 which
 CC comprises the preprosequence of mouse neurotrophic growth factor (NGF),
 CC residues 1-118 of mouse NGF and a 10 amino acid antigenic peptide
 CC fragment of human myc protein. It may provide the activity of 2 NFs
 CC in a single mol. or may serve as a superagonist of an endogenous NF
 CC thereby enabling an increased biological response at lower doses. It
 CC may also be useful in targeting an active cpd. to cells responsive to
 CC NF. The design of chimeric NFs, such as NM1, which retain specific
 CC biological activity but which are directed to a subset of factor-
 CC responsive cells may enable treatment of neurological disorders but
 CC avoid the complications of more widespread activity of parent mol's.
 CC It may be used in the treatment to eliminate diseased cells, e.g.
 CC virus infected cells or tumours of nervous system origin. It may also
 CC be used to treat patients whose nervous system has been damaged by
 CC trauma, surgery, ischemia, infection (e.g. polio or AIDS), metabolic
 CC disease, nutritional deficiency, malignancy or toxic agents. Also to
 CC treat e.g. Alzheimer's disease, ageing, peripheral neuropathies,
 CC Parkinson's disease, Huntington's chorea or amyotrophic lateral
 CC sclerosis. NM1 or antibodies to it can also be used in the diagnosis
 CC and study of nervous system disorders. See also AAR21851-R21874 and
 CC AA022080-Q22131.
 XX
 SQ Sequence 132 AA:
 Query Match 97.9%; Score 639; DB 13; Length 132;
 Best Local Similarity 99.2%; Pred. No. 7.5e-66;
 Matches 119; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 2 SSTRPFFHMGESVCDVSVMGDKTTATDICKKEVTVALEVINNSVROFFETKCA 61
 DB 5 SSTRPFFHMGESVCDVSVMGDKTTATDICKKEVTVALEVINNSVROFFETKCA 64
 OY 62 SNPVESGCRGIDSKHNSYCTTHTFEVKALTTDEKQAAAFRIRIDPACVLSRKATRR 121
 DB 65 SNPVESGCRGIDSKHNSYCTTHTFEVKALTTDEKQAAAFRIRIDPACVLSRKATRR 124

RESULT 9
 ID AAR29493 standard; Protein; 118 AA.
 XX
 AC AAR29493;
 XX
 DT 22-APR-1993 (first entry)
 XX
 DE NGF, mouse.
 XX
 KW Neurotrophin; NT; nerve growth factor; NGF;
 KW brain-derived neurotrophic factor; BDNF.
 XX
 OS Mus musculus.
 XX
 PN MO9220365-A.
 XX
 PD 26-NOV-1992.
 XX
 PF 20-MAY-1992; 92MO-US04266.
 XX

PR 21-MAY-1991: 91US-0703450.
 PR 12-JUL-1991: 91US-0729253.
 PR 23-JUL-1991: 91US-0734422.
 PR 28-AUG-1991: 91US-0751356.
 PR 20-SEP-1991: 91US-0762674.
 PR 14-NOV-1991: 91US-0791924.
 (REG-) REGENERON PHARM INC.
 PA Hallbook F, Ibanez Moliner CF, Persson HB, Yancopoulos GD:
 PI WPI: 1992-415468/50.
 XX Use of neurotrophin-4 for promoting growth and survival of nerve
 PT cells - useful in treating neurological, fertility and
 PT immunological disorders and in diagnosis
 PS Disclosure: Page 105-106 + Fig 4B; 180pp; English.
 CC A comparison of the mature NT-4 protein (xenopus) to the mature
 CC NGF, BDNF, and NT-3 proteins from mouse revealed 51%, 60% and 58%
 CC amino acid identity respectively. See sequences AAR29491 and
 CC AAR29493-95.
 CC
 SQ Sequence 118 AA:
 Query Match 97.2%; Score 635; DB 13; Length 118;
 Best Local Similarity 100.0%; Pred. No. 1.9e-65;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 SSTRPVFMHGEFSCVDSVWVGDKTTATDIDKKEVTVLAENVNINSVFRQYFEETCRRA 61
 DB 1 SSTRPVFMHGEFSCVDSVWVGDKTTATDIDKKEVTVLAENVNINSVFRQYFEETCRRA 60
 OY 62 SNPVESGCRGIDSKHNNSTCTTHTFVKALTTDEKQAMRFRIIDTACVLSRKATR 119
 DB 61 SNPVESGCRGIDSKHNNSTCTTHTFVKALTTDEKQAMRFRIIDTACVLSRKATR 118
 RESULT 10
 AAR21864
 ID AAR21864 standard; Protein: 120 AA.
 AC AAR21864;
 XX 10-JUN-1992 (first entry)
 DE Chimeric neurotrophic factor S2.
 XX Human BDNF; brain derived neurotrophic factor; NGF;
 KW neurotrophic growth factor; Alzheimer's disease; ageing;
 KW peripheral neuropathies; Parkinson's disease; Huntington's chorea;
 KW amyotrophic lateral sclerosis; nervous system disorders.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..9
 FT /note= "mouse NGF residues 1-9"
 FT Peptide 10..22
 FT /note= "human BDNF residues 8-20"
 FT Peptide 23..120
 FT /note= "mouse NGF residues 23-120"
 XX
 FM W09202620-A.
 XX
 PD 20-FEB-1992.
 XX
 PF 07-AUG-1991: 91MO-US05610.
 XX
 PR 08-AUG-1990: 90US-0564929.
 FT
 PA (REG-) REGENERON PHARM INC.

XX Shooter EM, Suter U, Ip N, Squinto SP, Furth ME, Lindsay RW:
 PI Yancopoulos GD;
 PI WPI: 1992-080074/10.
 DR
 XX
 PT New chimeric neurotrophic factors - useful in treating nervous
 PT conditions caused by trauma, surgery, ischemia, infection,
 PT metabolic diseases, nutritional deficiency, etc.
 PS Claim 25; Fig 10; 114pp; English.
 CC The sequence is that of a chimeric neurotrophic factor (NF) S2 which
 CC comprises the mouse neurotrophic growth factor (NGF) residues 1-9,
 CC human brain derived growth factor (hBDNF) residues 8-20 and mouse NGF
 CC residues 23-120. It may provide the activity of 2 NFs in a single mol-
 CC or may serve as a superagonist of an endogenous NF thereby enabling an
 CC increased biological response at lower doses. It may also be useful in
 CC targeting an active cpd. to cells responsive to NF. The design of
 CC chimeric NFs, such as S2, which retain specific biological activity
 CC but which are directed to a subset of factor-responsive cells may
 CC enable treatment of neurological disorders but avoid the complications
 CC of more widespread activity of parent mols. It may be used in the
 CC treatment to eliminate diseased cells, e.g. virus infected cells or
 CC tumours of nervous system origin. It may also be used to treat patients
 CC whose nervous system has been damaged by trauma, surgery, ischemia,
 CC infection (e.g. polio or AIDS), metabolic disease, nutritional
 CC deficiency, malignancy or toxic agents. Also to treat e.g. Alzheimer's
 CC disease, ageing, peripheral neuropathies, Parkinson's disease,
 CC Huntington's chorea or amyotrophic lateral sclerosis. S2 or antbodies
 CC to it can also be used in the diagnosis and study of nervous system
 CC disorders. See also AAR21851-R21874 and AAQ22080-022131.
 CC
 SQ Sequence 120 AA:
 Query Match 96.9%; Score 633; DB 13; Length 120;
 Best Local Similarity 97.5%; Pred. No. 3.3e-65;
 Matches 117; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 OY 2 SSTRPVFMHGEFSCVDSVWVGDKTTATDIDKKEVTVLAENVNINSVFRQYFEETCRRA 61
 DB 1 SSTRPVFMHGEFSCVDSVWVGDKTTATDIDKKEVTVLAENVNINSVFRQYFEETCRRA 60
 OY 62 SNPVESGCRGIDSKHNNSTCTTHTFVKALTTDEKQAMRFRIIDTACVLSRKATR 121
 DB 61 SNPVESGCRGIDSKHNNSTCTTHTFVKALTTDEKQAMRFRIIDTACVLSRKATR 120
 RESULT 11
 AAR21870
 ID AAR21870 standard; Protein: 120 AA.
 AC AAR21870;
 XX 10-JUN-1992 (first entry)
 DE Chimeric neurotrophic factor S8.
 XX Human BDNF; brain derived neurotrophic factor; NGF;
 KW neurotrophic growth factor; Alzheimer's disease; ageing;
 KW peripheral neuropathies; Parkinson's disease; Huntington's chorea;
 KW amyotrophic lateral sclerosis; nervous system disorders.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..68
 FT /note= "mouse NGF residues 1-68"
 FT Peptide 69..80
 FT /note= "human BDNF residues 69-80"
 FT Peptide 81..120
 FT /note= "mouse NGF residues 81-120"
 XX

PN M09202620-A.
 XX 20-FEB-1992.
 XX 07-AUG-1991: 91MO-US05610.
 XX 08-AUG-1990: 90US-0564929.
 XX (REG-) REGENERON PHARM INC.
 XX Shooter EM, Suter U, Ip N, Squinto SP, Furth ME, Lindsey RM;
 XX Yancopoulos GD;
 XX WPI: 1992-080074/10.
 XX New chimeric neurotrophic factors - useful in treating nervous
 XX conditions caused by trauma, surgery, ischemia, infection,
 XX metabolic diseases, nutritional deficiency, etc.
 XX Claim 31: Fig 10; 114pp; English.
 XX The sequence is that of a chimeric neurotrophic factor (NF) S8 which
 XX comprises the mouse neurotrophic growth factor (NGF) residues 1-68,
 XX human brain derived growth factor (hBDNF) residues 69-80 and mouse NGF
 XX residues 81-120. It may provide the activity of 2 NFs in a single mol.
 XX or may serve as a superagonist of an endogenous NF thereby enabling an
 XX increased biological response at lower doses. It may also be useful in
 XX targeting an active cpd. to cells responsive to NF. The design of
 XX chimeric NFs, such as S8, which retain specific biological activity
 XX but which are directed to a subset of factor-responsive cells may
 XX enable treatment of neurological disorders but avoid the complications
 XX of more widespread activity of parent moles. It may be used in the
 XX treatment to eliminate diseased cells, e.g. virus infected cells or
 XX tumors of nervous system origin. It may also be used to treat patients
 XX whose nervous system has been damaged by trauma, surgery, ischemia,
 XX infection (e.g. polio or AIDS), metabolic disease, nutritional
 XX deficiency, malignancy or toxic agents. Also to treat e.g. Alzheimer's
 XX disease, ageing, peripheral neuropathies, Parkinson's disease,
 XX Huntington's chorea or amyotrophic lateral sclerosis. S8 or antibodies
 XX to it can also be used in the diagnosis and study of nervous system
 XX disorders. See also AAR21851-R21874 and AAQ22080-Q22131.
 XX Sequence 120 AA;
 XX SO

Query Match 96.6%; Score 631; DB 13; Length 120;
 Best Local Similarity 97.5%; Pred. No. 5.6e-65;
 Matches 117; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 SSTRPVFMHGEFSCVDSVYVWGDKTTATDINKGEVTVLAEVNINNSVPROFFETKCR 61
 DB 1 SSTRPVFMHGEFSCVDSVYVWGDKTTATDINKGEVTVLAEVNINNSVPROFFETKCR 60
 OY 62 SNPEVSGCRGIDSKHNSYCTTHTFVKALTTDEKOAAMFRIRIDACVLSRKATRRG 121
 DB 61 SNPEVSGCRGIDSKHNSYCTTHTFVKALTTDEKOAAMFRIRIDACVLSRKATRRG 120

RESULT 12
 AAR21866
 ID AAR21866 standard; Protein: 120 AA.
 AC AAR21866;
 XX 10-JUN-1992 (first entry)
 XX Chimeric neurotrophic factor S4.
 XX Human BDNF: brain derived neurotrophic factor; NGF.
 XX neurotrophic growth factor; Alzheimer's disease; ageing;
 XX peripheral neuropathies; Parkinson's disease; Huntington's chorea;
 XX amyotrophic lateral sclerosis; nervous system disorders.
 XX Homo sapiens.
 XX OS

XX Key Location/Qualifiers
 XX Peptide 1..33
 XX Peptide /note- "mouse NGF residues 1-33"
 XX Peptide 34..42
 XX Peptide /note- "human BDNF residues 34-42"
 XX Peptide 43..120
 XX /note- "mouse NGF residues 43-120"
 XX M09202620-A.
 XX 20-FEB-1992.
 XX 07-AUG-1991: 91MO-US05610.
 XX 08-AUG-1990: 90US-0564929.
 XX (REG-) REGENERON PHARM INC.
 XX Shooter EM, Suter U, Ip N, Squinto SP, Furth ME, Lindsey RM;
 XX Yancopoulos GD;
 XX WPI: 1992-080074/10.
 XX New chimeric neurotrophic factors - useful in treating nervous
 XX conditions caused by trauma, surgery, ischemia, infection,
 XX metabolic diseases, nutritional deficiency, etc.
 XX Claim 27: Fig 10; 114pp; English.
 XX The sequence is that of a chimeric neurotrophic factor (NF) S4 which
 XX comprises the mouse neurotrophic growth factor (NGF) residues 1-33,
 XX human brain derived growth factor (hBDNF) residues 34-42 and mouse NGF
 XX residues 43-120. It may provide the activity of 2 NFs in a single mol.
 XX or may serve as a superagonist of an endogenous NF thereby enabling an
 XX increased biological response at lower doses. It may also be useful in
 XX targeting an active cpd. to cells responsive to NF. The design of
 XX chimeric NFs, such as S4, which retain specific biological activity
 XX but which are directed to a subset of factor-responsive cells may
 XX enable treatment of neurological disorders but avoid the complications
 XX of more widespread activity of parent moles. It may be used in the
 XX treatment to eliminate diseased cells, e.g. virus infected cells or
 XX tumors of nervous system origin. It may also be used to treat patients
 XX whose nervous system has been damaged by trauma, surgery, ischemia,
 XX infection (e.g. polio or AIDS), metabolic disease, nutritional
 XX deficiency, malignancy or toxic agents. Also to treat e.g. Alzheimer's
 XX disease, ageing, peripheral neuropathies, Parkinson's disease,
 XX Huntington's chorea or amyotrophic lateral sclerosis. S4 or antibodies
 XX to it can also be used in the diagnosis and study of nervous system
 XX disorders. See also AAR21851-R21874 and AAQ22080-Q22131.
 XX Sequence 120 AA;
 XX SO

Query Match 95.6%; Score 624; DB 13; Length 120;
 Best Local Similarity 96.7%; Pred. No. 3.6e-44;
 Matches 116; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 SSTRPVFMHGEFSCVDSVYVWGDKTTATDINKGEVTVLAEVNINNSVPROFFETKCR 61
 DB 1 SSTRPVFMHGEFSCVDSVYVWGDKTTATDINKGEVTVLEKVINNSVPROFFETKCR 60
 OY 62 SNPEVSGCRGIDSKHNSYCTTHTFVKALTTDEKOAAMFRIRIDACVLSRKATRRG 121
 DB 61 SNPEVSGCRGIDSKHNSYCTTHTFVKALTTDEKOAAMFRIRIDACVLSRKATRRG 120

RESULT 13
 AAR21871
 ID AAR21871 standard; Protein: 120 AA.
 AC AAR21871;
 XX 10-JUN-1992 (first entry)
 XX

XX Chimeric neurotrophic factor S9.

XX Human BDNF: brain derived neurotrophic factor; NGF;
XX neurotrophic growth factor; Alzheimer's disease; aging;
XX peripheral neuropathies; Parkinson's disease; Huntington's chorea;
XX amyotrophic lateral sclerosis; nervous system disorders.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..80

FT Peptide /note= "mouse NGF residues 1-80"

FT Peptide 81..91

FT Peptide /note= "human BDNF residues 81-91"

FT Peptide 92..120

FT Peptide /note= "mouse NGF residues 92-120"

XX MO9202620-A.

XX 20-FEB-1992.

XX 07-AUG-1991; 91WO-US05610.

XX 08-AUG-1990; 90US-0564929.

XX (REG-) REGENERON PHARM INC.

XX Shooter EM, Suter U, Ip N, Squinto SP, Furth ME, Lindsay RM;

XX rancopoulous GD;

XX WPI: 1992-080074/10.

XX Claim 32: Fig 10; 114pp: English.

XX The sequence is that of a chimeric neurotrophic factor (NF) S9 which

XX comprises the mouse neurotrophic growth factor (NGF) residues 1-80,

XX human brain derived growth factor (hBNDF) residues 81-91 and mouse NGF

XX residues 92-120. It may provide the activity of 2 NFs in a single mol.

XX or may serve as a superagonist of an endogenous NF thereby enabling an

XX increased biological response at lower doses. It may also be useful in

XX targeting NFs, such as S9, which retain specific biological activity

XX but which are directed to a subset of factor-responsive cells may

XX enable treatment of neurological disorders but avoid the complications

XX of more widespread activity of parent moIs. It may be used in the

XX treatment to eliminate diseased cells, e.g. virus infected cells or

XX tumours of nervous system origin. It may also be used to treat patients

XX whose nervous system has been damaged by trauma, surgery, ischemia,

XX infection (e.g. polio or AIDS), metabolic disease, nutritional

XX deficiency, malignancy or toxic agents. Also to treat e.g. Alzheimer's

XX disease, aging, peripheral neuropathies, Parkinson's disease,

XX Huntington's chorea or amyotrophic lateral sclerosis. S9 or antibodies

XX to it can also be used in the diagnosis and study of nervous system

XX disorders. See also AAR21851-R21874 and AAQ22080-Q22131.

XX Sequence 120 AA:

Query Match 95.3%; Score 622; DB 13; Length 120;

Best Local Similarity 95.8%; Pred. No. 6, 1e-64;

Matches 115; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 SSTRPVFHNKEFSVCDVSVMWGDKTTATDINGKKEVTYLAENVNINSVFROYFEETKRA 61

DB 1 SSTRPVFHNKEFSVCDVSVMWGDKTTATDINGKKEVTYLAENVNINSVFROYFEETKRA 60

OY 62 SNPEVSGCRGIDSKHNSCTTTHFFVKALTTDEKQAAARRIRIDTACVCLSRKATRRG 121

DB 61 SNPEVSGCRGIDSKHNSCTTTHFFVKALTTDEKQAAARRIRIDTACVCLSRKATRRG 120

RESULT 14

AAK54084 standard; protein; 120 AA.

AAK54084;

10-NOV-1994 (first entry)

Nerve growth factor.

Nerve growth factor; NGF; chimeric neurotrophin; neurotrophic factor;

brain-derived neurotrophic factor; BDNF; neurotrophin-3; NF-3;

TRK; TrkB; TrC; Receptor; neurological disorder;

Parkinson disease; Alzheimer disease.

Rattus sp.

MO9412539-A.

09-JUN-1994.

19-NOV-1993; 93WO-US11292.

20-NOV-1992; 92US-0979630.

(MCIN/) MCINTYRE K R.

Idanez CFM, Persson HB;

WPI: 1994-200202/24.

New chimeric neurotrophic factors and DNA - used to develop

prodcs. for use in the treatment and diagnosis of neurological

disorders

Disclousure: Page 48-49; 79pp; English.

Sequences are provided for rat nerve growth factor (AAK54084), rat

brain-derived neurotrophic factor (AAK54085) and rat neurotrophin-3

(AAK54086). Chimeric neurotrophins capable of binding TrkA, TrkB and

TrC are obtained by substituting amino acids 3-9, 28-37, 40-49,

61-66, 81-88, 94-98 or 95-97 of a neurotrophin with corresponding

amino acids from NGF, BDNF or NT-3. Recombinant chimeric

neurotrophins are used to treat e.g. Alzheimer disease and

Parkinson disease.

Sequence 120 AA:

Query Match 94.6%; Score 618; DB 15; Length 120;

Best Local Similarity 94.2%; Pred. No. 1, 8e-63;

Matches 113; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 2 SSTRPVFHNKEFSVCDVSVMWGDKTTATDINGKKEVTYLAENVNINSVFROYFEETKRA 61

DB 1 SSTRPVFHNKEFSVCDVSVMWGDKTTATDINGKKEVTYLAENVNINSVFROYFEETKRA 60

OY 62 SNPEVSGCRGIDSKHNSCTTTHFFVKALTTDEKQAAARRIRIDTACVCLSRKATRRG 121

DB 61 SNPEVSGCRGIDSKHNSCTTTHFFVKALTTDEKQAAARRIRIDTACVCLSRKATRRG 120

RESULT 15

AAK21872 standard; protein; 121 AA.

AAK21872;

10-JUN-1992 (first entry)

Chimeric neurotrophic factor S10.

DB 121 G 121
 Search completed: December 2, 2002, 15:08:38
 Job time : 25.1149 secs

KW Human BDNF; brain derived neurotrophic factor; NGF;
 KW neurotrophic growth factor; Alzheimer's disease; ageing;
 KW peripheral neuropathies; Parkinson's disease; Huntington's chorea;
 KW amyotrophic lateral sclerosis; nervous system disorders.
 OS
 XX Homo sapiens.

Key Location/Qualifiers
 FT Peptide 1..91
 FT /note="mouse NGF residues 1-91"
 FT Peptide 92..102
 FT /note="human BDNF residues 92-102"
 FT Peptide 103..121
 FT /note="mouse NGF residues 102-120"

MO9202620-A.
 20-FEB-1992.
 07-AUG-1991; 91WO-US05610.
 08-AUG-1990; 90US-0564929.
 (REGG-) REGENERON PHARM INC.
 PI Shooter EM, Suter U, Ip N, Squinto SP, Furth ME, Lindsay RM;
 PI Yencopoulos GD;
 XX WPI: 1992-080074/10.

PT New chimeric neurotrophic factors - useful in treating nervous
 PT conditions caused by trauma, surgery, ischemia, infection,
 PT metabolic diseases, nutritional deficiency, etc.

PS Claim 33: Flg 10; 114pp: English.

CC The sequence is that of a chimeric neurotrophic factor (NF) S10 which
 CC comprises the mouse neurotrophic growth factor (NGF) residues 1-91,
 CC human brain derived growth factor (hBNDF) residues 92-102 and mouse NGF
 CC residues 102-120. It may provide the activity of 2 NFs in a single mol.
 CC or may serve as a superagonist of an endogenous NF thereby enabling an
 CC increased biological response at lower doses. It may also be useful in
 CC targeting an active cpd. to cells responsive to NF. The design of
 CC chimeric NFs, such as S10, which retain specific biological activity
 CC but which are directed to a subset of factor-responsive cells may
 CC enable treatment of neurological disorders but avoid the complications
 CC of more widespread activity of parent mols. It may be used in the
 CC treatment to eliminate diseased cells, e.g. virus infected cells or
 CC tumours of nervous system origin. It may also be used to treat patients
 CC whose nervous system has been damaged by trauma, surgery, ischemia,
 CC infection (e.g. polio or AIDS), metabolic disease, nutritional
 CC deficiency, malignancy or toxic agents. Also to treat e.g. Alzheimer's
 CC disease, ageing, peripheral neuropathies, Parkinson's disease,
 CC Huntington's chorea or amyotrophic lateral sclerosis. S10 or antibodies
 CC to it can also be used in the diagnosis and study of nervous system
 CC disorders. See also AAR21851-R21874 and AAQ22080-Q22131.

CC
 XX
 SQ Sequence 121 AA:

Query Match 93.6%; Score 611.5; DB 13; Length 121;
 Best Local Similarity 95.0%; Pred. No. 1e-62;
 Matches 115; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

OY 2 SSTRPVFMHNGEFSVCDVSVMVGDKTATDIDKREVTYLAENVINNSVFQYFFETCRGA 61
 DB 1 SSTRPVFMHNGEFSVCDVSVMVGDKTATDIDKREVTYLAENVINNSVFQYFFETCRGA 60
 OY 62 SNPEVSGCGIDSKHNSCTTHTEVKALTTD-EKQAAAFIRIDRACVCVLSRKATRR 120
 DB 61 SNPEVSGCGIDSKHNSCTTHTEVKALTTDHSKRKRGIRIDRACVCVLSRKATRR 120
 OY 121 G 121
 1

GenCore version 5.1.3
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OM protein - protein search, using BW model

Run on: December 2, 2002, 15:05:43 : Search time 9.64596 Seconds
(Without alignments)
1205.921 Million cell updates/sec

Title: US-10-072-681-3

Perfect score: 653
Sequence: 1 PSSHVPVFMGEFVSCDSVS.....FIRIDTACVCLSRKATRRG 121

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5.

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	646	98.9	307	1 NGMSMG	nerve growth facto
2	636	95.9	245	2 I56570	beta-nerve growth
3	606	92.8	303	1 NGRT8A	nerve growth facto
4	593	90.8	241	2 J10097	nerve growth facto
5	584	89.4	286	1 NGHUBM	nerve growth facto
6	583	89.3	229	2 I46614	nerve growth facto
7	571	87.4	125	2 A26312	nerve growth facto
8	546	83.6	243	2 A26311	nerve growth facto
9	532	81.5	235	2 S14481	nerve growth facto
10	475	77.7	117	2 S28151	nerve growth facto
11	471	77.1	117	2 S15133	nerve growth facto
12	436.3	68.8	116	1 NGNMXI	nerve growth facto
13	432.5	66.2	116	2 A58566	nerve growth facto
14	432.5	66.2	246	2 A59218	nerve growth facto
15	390	59.7	194	2 I51709	nerve growth facto
16	378.5	58.0	257	2 C40304	neurotrophin-3 pre
17	378.5	58.0	257	2 I50400	neurotrophin-3 pre
18	378.5	58.0	258	2 S09155	neurotrophin-3 pre
19	378.5	58.0	282	2 A53781	hippocampus-derive
20	347.5	53.2	286	2 S50855	neurotrophin-6 - s
21	325.5	49.8	247	2 A40304	brain-derived neur
22	325.5	49.8	249	2 S12555	brain-derived neur
23	325.5	49.8	249	2 B40304	brain-derived neur
24	325.5	49.8	252	2 A30361	brain-derived neur
25	320.5	49.1	114	2 I84765	brain-derived neur
26	319.5	48.9	248	2 JG6183	brain-derived neur
27	313.5	48.0	114	2 I50606	brain-derived neur
28	312.5	47.9	210	2 A2687	neurotrophin-4 pre
29	311.5	47.7	269	2 I51708	brain-derived neur

30	310.5	47.5	236	2 JH0400	neurotrophin-4 pre
31	307.5	47.1	209	2 B42687	neurotrophin-4 pre
32	304.5	46.6	114	2 I51599	brain-derived neur
33	81	12.4	229	2 C69806	hypothetical prote
34	79.5	12.2	475	2 T23355	hypothetical prote
35	76	11.6	478	2 D96603	hypothetical prote
36	74.5	11.4	116	2 S50449	hypothetical prote
37	74.5	11.4	425	2 S26523	phosphoglycerate k
38	73.5	11.3	489	2 S32637	phosphoglycerate k
39	73.5	11.3	693	2 T26415	hypothetical prote
40	72	11.0	399	2 S71368	hypothetical prote
41	71.5	10.9	835	2 C97322	phosphoglycerate k
42	71	10.9	166	2 S55496	probable alpha-ara
43	71	10.9	331	1 A54932	fibrillar protein P
44	70.5	10.8	290	2 S19426	zeta-crystallin /
45	69	10.6	3083	2 AH2493	hypothetical prote

ALIGNMENTS

RESULT 1

NGMSMG nerve growth factor beta chain precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Nov-1980 #sequence-revision 19-Feb-1984 #text-change 21-Jul-2000
C:Accession: A93301; A93305; A90366; I49689; I52891; A01400; I49690
R:Scott, J.; Selby, M.; Urdew, M.; Quiroga, M.; Bell, G.I.; Rutter, W.J.
Nature 302, 538-540, 1983
A>Title: Isolation and nucleotide sequence of a cDNA encoding the precursor of mouse
A:Reference number: A93301; M01D:83167518; PMID:6336309
A:Accession: A93301
A:Molecule type: mRNA
A:Residues: 1-307 <SCD>
A:Cross-references: GB:V00836; M1D:953364; P1D:CA24221.1; P1D:953365
R:Ullrich, A.; Gray, A.; Berman, C.; Dull, T.J.
Nature 303, 821-825, 1983
A>Title: Human beta-nerve growth factor gene sequence highly homologous to that of mo
A:Reference number: A93305; M01D:83244969; PMID:6688123
A:Accession: A93305
A:Molecule type: mRNA
A:Residues: 1-307 <ULD>
A:Cross-references: GB:K01759; M1D:920051; P1D:AAA39620.1; P1D:9387495
A:Note: These authors believe that Met-67 is probably the amino-terminal residue and
R:Angelletti, R.H.; Herndon, M.A.; Bradshaw, R.A.
Biochemistry 12, 100-115, 1973
A>Title: Amino acid sequences of mouse 2.5S nerve growth factor. II. Isolation and ch
A:Reference number: A90366; M01D:73075048; PMID:4566923
A:Accession: A90366
A:Molecule type: protein
A:Residues: 188-216, 'N', 218-305 <ANG>
R:Selby, M.J.; Edwards, R.; Sharp, F.; Rutter, W.J.
Mol. Cell. Biol. 7, 3057-3064, 1987
A>Title: Mouse nerve growth factor gene: Structure and expression.
A:Reference number: I49689; M01D:88038855; PMID:3670305
A:Accession: I49689
A>Status: preliminary; translated from GB/EML/DDBJ
A:Molecule type: DNA
A:Residues: 1-307 <RES>
A:Cross-references: GB:M17298; M1D:9193493; P1D:AAA37687.1; P1D:9467311
R:Ullrich, A.; Gray, A.; Berman, C.H.; Coussens, L.; Dull, T.J.
Cold Spring Harb. Symp. Quant. Biol. 48, 435-442, 1983
A>Title: Sequence homology of human and mouse beta-NGF subunit genes.
A:Reference number: I52891; M01D:84205655; PMID:6327169
A:Accession: I52891
A>Status: preliminary; translated from GB/EML/DDBJ
A:Molecule type: mRNA
A:Residues: 1-307 <RB3>
A:Cross-references: GB:M14805; M1D:920053; P1D:AAA38821.1; P1D:920054
C:Comment: The active molecule is a dimer of identical chains associated by noncovalent
C:Comment: Nerve growth factor is found in submaxillary gland in large quantities and
C:Genetics: nic sensory ganglia in vivo and in vitro and to increase cellular neurotubule levels

A:Gene: NGFB
 A:Introns: 21/2: 62/3
 C:Superfamily: nerve growth factor beta chain
 C:Keywords: glycoprotein; growth factor; homodimer
 E:11-187/Domain: signal sequence and propeptide status predicted <SIG>
 F:188-305/Product: nerve growth factor beta chain status experimental <MAT>
 F:135-180/Binding site: carbohydrate (Asn) (covalent) status predicted
 F:202-267,245-295,255-297/Disulfide bonds: status experimental
 F:233/Binding site: carbohydrate (Asn) (covalent) status absent

Query Match 98.9%: Score 646; DB 1; Length 307;
 Best Local Similarity 100.0%: Pred. No. 1,8e-59;
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSTRPVPFHMGESVCDSSVWVGDKTTATDIDKREVTYLAENVINNSVPROFEETKCA 61
 DB 188 SSTRPVPFHMGESVCDSSVWVGDKTTATDIDKREVTYLAENVINNSVPROFEETKCA 247
 OY 62 SNPEVSGCGIDSKHNSYCTTHTFVKALTTDEKQAAAFIRIDTACVLSRKATRRG 121
 DB 248 SNPEVSGCGIDSKHNSYCTTHTFVKALTTDEKQAAAFIRIDTACVLSRKATRRG 307

RESULT 2
 156570
 beta-nerve growth factor - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
 C:Accession: 156570
 R:Whittemore, S.R.; Friedman, P.L.; Larhammar, D.G.; Persson, H.; Gonzalez-Carvajal, M.; J. Neurosci. Res. 20, 403-410, 1988
 A:Title: Rat beta-nerve growth factor sequence and site of synthesis in the adult hippo
 A:Reference number: 156570; MUID:89037223; PMID:3184206
 A:Accession: 156570
 A:Structure: preliminary; translated from 68/EMBL/DBJ
 A:Residues: 1-245 <RES>
 A:Cross-references: GR:M36589; NID:9205691; PIDN:AAA1697.1; PID:9205692
 C:Superfamily: nerve growth factor beta chain

Query Match 95.9%: Score 626; DB 2; Length 245;
 Best Local Similarity 95.8%: Pred. No. 1.7e-57;
 Matches 115; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 SSTRPVPFHMGESVCDSSVWVGDKTTATDIDKREVTYLAENVINNSVPROFEETKCA 61
 DB 126 SSTRPVPFHMGESVCDSSVWVGDKTTATDIDKREVTYLAENVINNSVPROFEETKCA 185
 OY 62 SNPEVSGCGIDSKHNSYCTTHTFVKALTTDEKQAAAFIRIDTACVLSRKATRRG 121
 DB 186 SNPEVSGCGIDSKHNSYCTTHTFVKALTTDEKQAAAFIRIDTACVLSRKATRRG 245

RESULT 3
 NGFB
 nerve growth factor beta chain precursor - multimammate rat (Mastomys natalensis)
 C:Species: Mastomys natalensis
 C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 18-Jun-1999
 C:Accession: J0343
 R:Fahnestock, M.; Bell, R.A.
 Gene 69, 257-264, 1988
 A:Title: Molecular cloning of a cDNA encoding the nerve growth factor precursor from Ma
 A:Reference number: J0343; MUID:89172070; PMID:3224767
 A:Accession: J0343
 A:Molecule type: mRNA
 A:Residues: 1-303 <PNA>
 A:Cross-references: GB:M22748; NID:9202514; PIDN:AAA0599.1; PID:9202515
 A:Note: It is uncertain whether Met-1 or Met-63 is the initiator
 C:Superfamily: nerve growth factor beta chain
 C:Keywords: glycoprotein; growth factor; homodimer; submaxillary gland
 F:184-301/Product: nerve growth factor beta chain status predicted <MAT>
 F:131,176,228/Binding site: carbohydrate (Asn) (covalent) status predicted
 F:198-263,241-293/Disulfide bonds: status predicted

Query Match 92.8%: Score 606; DB 1; Length 303;
 Best Local Similarity 92.5%: Pred. No. 2.5e-55;
 Matches 111; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 2 SSTRPVPFHMGESVCDSSVWVGDKTTATDIDKREVTYLAENVINNSVPROFEETKCA 61
 DB 184 SSTRPVPFHMGESVCDSSVWVGDKTTATDIDKREVTYLAENVINNSVPROFEETKCA 243
 OY 62 SNPEVSGCGIDSKHNSYCTTHTFVKALTTDEKQAAAFIRIDTACVLSRKATRRG 121
 DB 244 SNPEVSGCGIDSKHNSYCTTHTFVKALTTDEKQAAAFIRIDTACVLSRKATRRG 303

RESULT 4
 J0097
 nerve growth factor beta chain precursor - guinea pig
 C:Species: Cavia porcellus (guinea pig)
 C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 15-Mar-1996
 C:Accession: J0097
 R:Schwarz, M.A.; Fisher, D.; Bradshaw, R.A.; Jackson, P.J.
 J. Neurochem. 52, 1203-1209, 1989
 A:Title: Isolation and sequence of a cDNA clone of beta-nerve growth factor from the
 A:Reference number: J0097; MUID:89177243; PMID:2926397
 A:Accession: J0097
 A:Molecule type: mRNA
 A:Residues: 1-241 <SCH>
 A:Note: The authors translated the codon GCU for residue 214 as Asp
 C:Genetic9:
 A:Gene: Beta-NGF
 C:Superfamily: nerve growth factor beta chain
 C:Keywords: glycoprotein; growth factor; hormone
 F:112-241/Domain: propeptide status predicted <PRO>
 F:122-241/Product: nerve growth factor beta chain status predicted <MAT>
 F:146-154/Region: receptor binding status predicted
 F:69,114/Binding site: carbohydrate (Asn) (covalent) status predicted

Query Match 90.8%: Score 593; DB 2; Length 241;
 Best Local Similarity 90.0%: Pred. No. 4.4e-54;
 Matches 108; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 2 SSTRPVPFHMGESVCDSSVWVGDKTTATDIDKREVTYLAENVINNSVPROFEETKCA 61
 DB 122 SSTRPVPFHMGESVCDSSVWVGDKTTATDIDKREVTYLAENVINNSVPROFEETKCA 181
 OY 62 SNPEVSGCGIDSKHNSYCTTHTFVKALTTDEKQAAAFIRIDTACVLSRKATRRG 121
 DB 182 SNPEVSGCGIDSKHNSYCTTHTFVKALTTDEKQAAAFIRIDTACVLSRKATRRG 241

RESULT 5
 NGFB
 nerve growth factor beta chain precursor - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 18-Jun-1999
 C:Accession: A01399; S10253
 R:Ullrich, A.; Gray, A.; Berman, C.; Dull, T.J.
 Nature 303, 821-825, 1983
 A:Title: Human beta-nerve growth factor gene sequence, highly homologous to that of mo
 A:Reference number: A93305; MUID:83244569; PMID:6688123
 A:Accession: A01399
 A:Molecule type: DNA
 A:Residues: 1-286 <ULL>
 R:Boersant, G.; Pizutti, A.; Rugerli, E.L.; Fallin, A.; Siliati, V.; Sidoli, A.; Scarla
 Nucleic Acids Res. 18, 4020, 1990
 A:Title: cDNA sequence of human beta-NGF.
 A:Reference number: S10253; MUID:90326556; PMID:2374737
 A:Accession: S10253
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 46-286 <BOB>
 A:Cross-references: EMBL:X52599; NID:929476; PIDN:CAA36837.1; PID:929477
 C:Comment: Nerve growth factor is found in submaxillary gland in large quantities and

ntic sensory ganglia in vivo and in vitro and to increase cellular neurotubule levels may

C:Comment: Nerve growth factor stimulates neurite outgrowth from sympathetic and embr

C:Superfamily: nerve growth factor beta chain

C:Keywords: growth factor; homodimer; seminal vesicle

F:5-125/Product: nerve growth factor #status predicted <MAT>

F:20-85,63-113,73-115/Disulfide bonds: #status predicted

Query Match 87.4%; Score 571; DB 2; Length 125;

Best Local Similarity 87.4%; Pred. No. 4,1e-52;

Matches 104; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

2 SSTRPVRHMGESVCDSSVWVGDKTTATDIDKGEVTVLAENVINNSVPROFFETKCR 61

6 SSSHPVHRGSESVCDSSVWVGDKTTATDIDKGEVTVLAENVINNSVPROFFETKCR 65

62 SNPVESGCRGIDSKHNSCTTHTFVKALTTDEKQAAFRIRIDPACVLSRKATRR 120

66 PNPVDSGCRGIDSKHNSCTTHTFVKALTTDEKQAAFRIRIDPACVLSRKATRR 124

RESULT 8

nerve growth factor beta chain precursor - chicken (fragment)

C:Species: Gallus gallus (chicken)

C>Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 21-Jul-2000

C:Accession: A26311; A24837; S00127; S12332

R:Bandal, T.; Lathamar, D.; Persson, H.

EMBO J. 5, 1483-1487, 1986

A:Title: Structure and expression of the chicken beta nerve growth factor gene.

A:Reference number: A26311; MUID:86300646; PMID:3017695

A:Accession: A26311

A:Molecule type: mRNA

A:Residues: 1-243 <MB>

A:Cross-references: GB:X4003; NID:963697; PIDN:CAA27633.1; PID:91334740

R:Kiloh, D.; Perrele, C.; Frechin, N.; Keller, A.; Behar, G.; Brachet, P.; Aufray, C.

EBBS Lett. 203, 82-86, 1986

A:Title: Molecular cloning of the avian beta-nerve growth factor gene: transcription

A:Reference number: A24837; MUID:86248129; PMID:3720959

A:Accession: A24837

A:Molecule type: DNA

A:Residues: 118-243 <MIO>

A:Cross-references: GB:D00010; GB:N00010; GB:X4067; NID:9222440; PIDN:BA00008.1; PI

R:Meier, R.; Becker-Andre, M.; Goetz, R.; Heumann, R.; Shaw, A.; Thoenen, H.

EMBO J. 5, 1489-1493, 1986

A:Title: Molecular cloning of bovine and chick nerve growth factor (NGF): delineation

A:Reference number: A26312; MUID:86300647; PMID:2427334

A:Accession: S00127

A:Molecule type: DNA

A:Residues: 121-243 <MEI>

A:Cross-references: GB:M26810; NID:9212446; PIDN:AAA8984.1; PID:9212447

R:Bandal, T.; Lathamar, D.; Persson, H.

EMBO J. 9, 1477-1483, 1990

A:Title: Structure-function studies of nerve growth factor: functional importance of

A:Reference number: S12532; MUID:90228346; PMID:2328722

A:Accession: S12532

A:Molecule type: Preliminary

A:Status: preliminary

A:Residues: 126-243 <IBA>

A:Superfamily: nerve growth factor beta chain

C:Keywords: growth factor

F:1-125/Domain: signal sequence #status predicted <SIG>

F:126-243/Product: nerve growth factor beta chain #status predicted <MAT>

Query Match 83.6%; Score 546; DB 2; Length 243;

Best Local Similarity 84.6%; Pred. No. 3,3e-49;

Matches 99; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

3 STHPRVHMGESVCDSSVWVGDKTTATDIDKGEVTVLAENVINNSVPROFFETKCR 62

126 TAAHPVLRGSESVCDSSVWVGDKTTATDIDKGEVTVLAENVINNSVPROFFETKCR 185

63 SNPVESGCRGIDSKHNSCTTHTFVKALTTDEKQAAFRIRIDPACVLSRKATRR 119

119 PNPVDSGCRGIDSKHNSCTTHTFVKALTTDEKQAAFRIRIDPACVLSRKATRR 119

RESULT 7

A26312

nerve growth factor beta chain precursor - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C>Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 16-Jul-1999

C:Accession: A26312

R:Meier, R.; Becker-Andre, M.; Goetz, R.; Heumann, R.; Shaw, A.; Thoenen, H.

EMBO J. 5, 1489-1493, 1986

A:Title: Molecular cloning of bovine and chick nerve growth factor (NGF): delineation of

A:Reference number: A26312; MUID:86300647; PMID:2427334

A:Accession: A26312

A:Molecule type: mRNA

A:Residues: 1-125 <MEI>

A:Cross-references: GB:M26809; NID:9163419; PIDN:AAA3066.1; PID:9163420

DB 186 RPVSSGCGIDAKHNSYCTTHTFVKALTMESGQAAMRFIRIDPACVLSRSGR 242

RESULT 9

S14401

nerve growth factor beta chain precursor - African clawed frog

C:Species: *Xenopus laevis* (African clawed frog)

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Jul-1999

C:Accession: S14401

R:Carriero, F.; Campion, M.; Cardinale, B.; Pierandrei-Amaldi, P.

Submitted to the EMBL Data Library, October 1990

A:Description: Structure and expression of the nerve growth gene in *Xenopus oocyte* and

A:Reference number: S14401

A:Accession: S14401

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-235 <CAR>

A:Cross-references: EMBL:X55716; NID:664914; PIDD:CAA39249.1; PID:664915

C:Superfamily: nerve growth factor beta chain

Query Match 81.5%: Score 532; DB 2; Length 235;

Best Local Similarity 84.2%: Pred. No. 9.2e-48;

Matches 96; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

OY 3 STHPVFMHGEFSVCDVSVWVGDKTTATDIDKKEVTLAEVINNSVFRQFFETKCRAS 62

DB 119 TVHPLHKGESVCDVSVWVGDKTTATDIDKKEVTLAEVINNSVFRQFFETKCRDP 178

OY 63 NPVSGCGIDSKHNSYCTTHTFVKALTTDEKQAAMRFIRIDPACVLSRK 116

DB 179 KPVSSGCGIDAKHNSYCTTHTFVKALTMESGQAAMRFIRIDPACVLSRK 232

RESULT 10

S28161

nerve growth factor beta chain - Russell's viper

C:Species: *Vipera russelli* (Russell's viper)

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997

C:Accession: S28161

R:Koyama, J.; Inoue, S.; Ikeda, K.; Hayashi, K.

Biochem. Biophys. Acta 1160, 287-292, 1992

A:Title: Purification and amino-acid sequence of a nerve growth factor from the venom of

A:Reference number: S28161; MUID:93120151; PMID:1477101

A:Accession: S28161

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-117 <KOY>

C:Superfamily: nerve growth factor beta chain

Query Match 72.7%: Score 475; DB 2; Length 117;

Best Local Similarity 73.2%: Pred. No. 3.6e-42;

Matches 82; Conservative 17; Mismatches 13; Indels 0; Gaps 0;

OY 5 HPVFMHGEFSVCDVSVWVGDKTTATDIDKKEVTLAEVINNSVFRQFFETKCRASNP 64

DB 1 HNVHMGESVCDVSVWVGDKTTATDIDKKEVTLAEVINNSVFRQFFETKCRNP 60

OY 65 VESGCGIDSKHNSYCTTHTFVKALTTDEKQAAMRFIRIDPACVLSRK 116

DB 61 VPSGCGIDAKHNSYCTTHTFVKALTMESGQAAMRFIRIDPACVLSRK 112

RESULT 11

S15193

nerve growth factor precursor - many-banded krait

C:Species: *Bungarus multicinctus* (many-banded krait)

C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999

C:Accession: S15193

R:Danse, J.M.; Garnier, J.M.

Growth Factors 8, 77-86, 1993

A:Title: Molecular cloning of a cDNA encoding a nerve growth factor precursor from the

A:Reference number: S15193; MUID:93192074; PMID:7916740

A:Accession: S15193

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-243 <DAN>

A:Cross-references: GB:S56212; NID:9266298; PIDD:AA835729.1; PID:9266299

C:Superfamily: nerve growth factor beta chain

Query Match 72.1%: Score 471; DB 2; Length 243;

Best Local Similarity 72.2%: Pred. No. 2.1e-41;

Matches 83; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

OY 2 STHPVFMHGEFSVCDVSVWVGDKTTATDIDKKEVTLAEVINNSVFRQFFETKCR 61

DB 125 NHPVFMHGEFSVCDVSVWVGDKTTATDIDKKEVTLAEVINNSVFRQFFETKCRN 184

OY 62 NPVSGCGIDSKHNSYCTTHTFVKALTTDEKQAAMRFIRIDPACVLSRK 116

DB 185 RPVSSGCGIDSKHNSYCTTHTFVKALTMESGQAAMRFIRIDPACVLSRK 239

RESULT 12

NGNXXI

nerve growth factor - Indian cobra

C:Species: *Naja naja* (Indian cobra)

C>Date: 30-Nov-1980 #sequence_revision 25-Apr-1997 #text_change 17-Mar-2000

C:Accession: S13927; A01401

R:Inoue, S.; Oda, T.; Koyama, J.; Ikeda, K.; Hayashi, K.

FEBS Lett. 279, 38-40, 1991

A:Title: Amino acid sequences of nerve growth factors derived from cobra venoms.

A:Reference number: S13927; MUID:9118755; PMID:1995338

A:Accession: S13927

A:Molecule type: protein

A:Residues: 1-116 <INO>

A:Experimental source: venom

A:Note: the source is designated as *Naja naja* and referred to as Indian cobra, so ve

R:Hoque-Angeletti, R.A.; Frazier, W.A.; Jacobs, J.M.; Nall, H.D.; Bradshaw, R.A.

Biochemistry 15, 26-34, 1976

A:Title: Purification, characterization, and partial amino acid sequence of nerve gro

A:Reference number: A01401; MUID:76114772; PMID:1247508

A:Accession: A01401

A:Molecule type: protein

A:Residues: 1-11, 'P', 13-14, 'B', 16, 'TBR', 20-21, 'GV', 23-27, 'N', 29-31, 'AS', 34, 'S', 36-48,

15-116 <NO>

A:Experimental source: venom

A:Note: the source is designated as *Naja naja* and referred to as Indian cobra, so ve

C:Comment: Nerve growth factor is necessary for the development of embryonic symphat

C:Complex: homodimer

C:Superfamily: nerve growth factor beta chain

C:Keywords: growth factor; homodimer; venom

F14-78,56-106,66-108/Disulfide bonds: #status predicted

Query Match 66.8%: Score 436.5; DB 1; Length 116;

Best Local Similarity 69.6%: Pred. No. 3.6e-38;

Matches 78; Conservative 14; Mismatches 19; Indels 1; Gaps 1;

OY 5 HPVFMHGEFSVCDVSVWVGDKTTATDIDKKEVTLAEVINNSVFRQFFETKCRASNP 64

DB 3 HNVHMGESVCDVSVWVGDKTTATDIDKKEVTLAEVINNSVFRQFFETKCRNP 61

OY 65 VESGCGIDSKHNSYCTTHTFVKALTTDEKQAAMRFIRIDPACVLSRK 116

DB 62 EPSGCGIDSKHNSYCTTHTFVKALTMESGQAAMRFIRIDPACVLSRK 113

RESULT 13

A58566

nerve growth factor - Chinese cobra

C:Species: *Naja naja atra* (Chinese cobra)

C>Date: 16-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 25-Apr-1997

C:Accession: A58566

R:Oda, T.; Ohta, M.; Inoue, S.; Ikeda, K.; Furukawa, S.; Hayashi, K.

Biochem. Int. 19, 909-917, 1989

A:Title: Amino acid sequence of nerve growth factor purified from the venom of the Fo

A:Reference number: A58566; MUID:90147847; PMID:2619756

A:Accession: A58566
 A:Molecule type: protein
 A:Residues: 1-116 <ODA>
 A:Experimental source: Venom
 C:Comment: Nerve growth factor is necessary for the development of embryonic sympathetic
 C:Complex: homodimer
 C:Superfamily: nerve growth factor beta chain
 C:Keywords: growth factor; homodimer; venom
 F:14-78,56-106,66-108/Disulfide bonds: #status predicted

Query Match 66.2% Score 432.5; DB 2; Length 116;
 Best Local Similarity 68.8%; Pred. No. 9,2e-38;
 Matches 77; Conservative 15; Mismatches 19; Indels 1; Gaps 1;

OY 5 HPMHGFESVCDVSVWVGDKTATDIDKGEVTVLAEVNINNSVFRQYFETKCRASNP 64
 DB 3 HPMHNLGHSHSVCDVSVWVGDKTATDIDKGNVTYVENVNLDNKKYKQYFETKCKNPNP 61

OY 65 VESGCRGIDSKHNSYCTTHTFVKALTTDEKQAMRFIRIDTACVCLSRK 116
 DB 62 EPSCGRGIDSKHNSYCTTHTFVKALTTDEKQAMRFIRIDTACVCLSRK 113

RESULT 14

A:Accession: A59218
 A:Molecule type: mRNA
 C:Species: Naja naja kaouthia, Naja naja siamensis (monocled cobra)
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000
 C:Accession: A59218; S13965
 R:Salby, M.J.; Edwards, R.H.; Rutter, W.J.
 J. Neurosci. Res. 18, 293-298, 1987

A:Title: Cobra nerve growth factor: structure and evolutionary comparison.
 A:Reference number: A59218; MUID:88090976; PMID:3694712

A:Accession: A59218
 A:Molecule type: mRNA

A:Residues: 1-246 <SEL>

R:Inoue, S.; Oda, T.; Koyama, J.; Ikeda, K.; Hayashi, K.

FEBS Lett. 279, 38-40, 1991

A:Title: Amino acid sequences of nerve growth factors derived from cobra venoms.

A:Reference number: S13927; MUID:91138755; PMID:1995338

A:Accession: S13965

A:Molecule type: protein

A:Residues: 131-246 <INO>

A:Experimental source: Venom

C:Comment: Nerve growth factor is necessary for the development of embryonic sympathetic

C:Complex: homodimer

C:Superfamily: nerve growth factor beta chain

C:Keywords: growth factor; homodimer; venom

F:1-23/Domain: signal sequence #status predicted <SIG>

F:131-246/Product: nerve growth factor beta chain #status experimental <MAT>

F:144-208,186-236,196-238/Disulfide bonds: #status predicted

Query Match 66.2% Score 432.5; DB 2; Length 246;
 Best Local Similarity 68.8%; Pred. No. 2.1e-37;
 Matches 77; Conservative 15; Mismatches 19; Indels 1; Gaps 1;

OY 5 HPMHGFESVCDVSVWVGDKTATDIDKGEVTVLAEVNINNSVFRQYFETKCRASNP 64
 DB 133 HPMHNLGHSHSVCDVSVWVGDKTATDIDKGNVTYVENVNLDNKKYKQYFETKCKNPNP 191

OY 65 VESGCRGIDSKHNSYCTTHTFVKALTTDEKQAMRFIRIDTACVCLSRK 116
 DB 192 EPSCGRGIDSKHNSYCTTHTFVKALTTDEKQAMRFIRIDTACVCLSRK 243

RESULT 15
 151709
 nerve growth factor beta chain precursor - southern platyfish
 C:Species: xiphophorus maculatus (southern platyfish)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
 C:Accession: 151709; S26674
 R:Gotz, R.; Raulf, F.; Schartzl, M.
 J. Neurochem. 59, 433-442, 1992

A:Title: Brain-derived neurotrophic factor is more highly conserved in structure and
 A:Reference number: 151708; MUID:92333301; PMID:1629719

A:Accession: 151709

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-194 <GOR>

A:Cross-references: EMBL:X59941; NID:965277; PIDN:CAA42566.1; PID:965278

C:Genetics: NGF

C:Superfamily: nerve growth factor beta chain

C:Keywords: glycoprotein; growth factor

F:1-13/Domain: signal sequence #status predicted <SIG>

F:15-79/Domain: propeptide #status predicted <PRO>

F:80-194/Product: nerve growth factor beta chain #status predicted <MAT>

F:90-155,133-183,143-185/Disulfide bonds: #status predicted

F:99/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 59.7% Score 390; DB 2; Length 194;
 Best Local Similarity 66.1%; Pred. No. 4.2e-33;
 Matches 72; Conservative 13; Mismatches 24; Indels 0; Gaps 0;

OY 9 HMGESVCDVSVWVGDKTATDIDKGEVTVLAEVNINNSVFRQYFETKCRASNPVPSG 68
 DB 83 HRGVSVCDVSVWVGDKTATDIDKGEVTVLAEVNINNSVFRQYFETKCRASNPVPSG 142

OY 69 CNGISKIMNSYCTTHTFVKALTTDEKQAMRFIRIDTACVCLSRK 117
 DB 143 CIGIDARHNSHCTNSHTFVALTSSENQVAMRLIRINACVCLSRK 191

Search completed: December 2, 2002, 15:13:58
 Job time: 9.64596 secs

GenCore version 5.1.3
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OH protein - protein search, using sw model

Run on: December 2, 2002, 15:05:43 : Search time 4.96483 seconds
(without alignments)
1010.837 Million cell updates/sec

Title: US-10-072-681-3

Sequence: 1 PSSHPHFVMEGFSVCDSVS.....FIRIDACVCLSRKATRRG 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	666	98.9	241 1	NGF_MOUSE
2	626	95.9	241 1	NGF_RAT
3	606	92.8	241 1	NGF_PRAWA
4	593	90.8	241 1	NGF_CAVPO
5	584	89.4	241 1	NGF_HUMAN
6	583	88.3	229 1	NGF_PIG
7	564	86.4	231 1	NGF_BOVIN
8	566	83.6	231 1	NGF_CHICK
9	532	81.5	231 1	NGF_XENLA
10	475	72.1	117 1	NGF_DABRR
11	471	72.1	243 1	NGF_BUNMU
12	433.5	66.4	116 1	NGF_NAJNA
13	429.5	65.8	116 1	NGF_NAJNA
14	390	59.7	194 1	NGF_XIPMA
15	379.5	58.1	140 1	NGF_CYPCA
16	378.5	58.0	257 1	NGF_CHICK
17	378.5	58.0	257 1	NGF_CHICK
18	378.5	58.0	258 1	NGF_HUMAN
19	378.5	58.0	258 1	NGF_MOUSE
20	377.5	57.8	260 1	NT3_RAT
21	374.5	57.4	233 1	NT3_XENLA
22	374.5	57.4	233 1	NT3_XENLA
23	374.5	57.4	255 1	NT3_XENLA
24	374.5	57.4	255 1	NT3_XENLA
25	374.5	57.4	255 1	NT3_XENLA
26	374.5	57.4	255 1	NT3_XENLA
27	374.5	57.4	255 1	NT3_XENLA
28	374.5	57.4	255 1	NT3_XENLA
29	374.5	57.4	255 1	NT3_XENLA
30	374.5	57.4	255 1	NT3_XENLA
31	374.5	57.4	255 1	NT3_XENLA
32	374.5	57.4	255 1	NT3_XENLA
33	374.5	57.4	255 1	NT3_XENLA

34	319.5	48.9	270 1	BDNF_CYPCA	090322 cyprinus ca
35	318.5	48.8	246 1	BDNF_CHICK	P25429 gallus gall
36	312.5	47.9	210 1	NT5_HUMAN	P34130 homo sapien
37	311.5	47.7	269 1	BDNF_XIPMA	000193 xiphophorus
38	310.5	47.5	236 1	NT4_XENLA	P24131 xenopus lae
39	307.5	47.1	209 1	NT5_RAT	P34131 xenopus lae
40	304.5	46.6	114 1	BDNF_XENLA	P25432 xenopus lae
41	229	35.1	257 1	NT6B_HUMAN	P34133 homo sapien
42	224	34.3	186 1	NT6G_HUMAN	P34133 homo sapien
43	222	34.0	257 1	NT6A_HUMAN	P34132 homo sapien
44	165	25.3	42 1	NGF_VIPLE	P25428 vipera lebe
45	130	19.9	43 1	NT3_RATCL	P25434 rana clavat

ALIGNMENTS

RESULT 1	NGF_MOUSE	STANDARD:	PRT:	241 AA.
AC	P01339: 063864:			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-JAN-1990 (Rel. 13, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Beta-nerve growth factor precursor (Beta-NGF).			
GN	NGFB.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-83167518: PubMed-6336309;			
RA	Scott J., Selby M.J., Urdan M.S., Quiroga M., Bell G.I., Rutter W.J.;			
RT	*Isolation and nucleotide sequence of a cDNA encoding the precursor			
RL	of mouse nerve growth factor.*;			
RL	Nature 302:538-540(1983).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-63244969: PubMed-6688123;			
RA	Ullrich A., Gray A., Berman C., Dull T.J.;			
RT	*Human beta-nerve growth factor gene sequence highly homologous to			
RL	that of mouse.*;			
RL	Nature 303:821-825(1983).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-84206565: PubMed-6337169;			
RA	Ullrich A., Gray A., Berman C., Coussens L., Dull T.J.;			
RT	*Sequence homology of human and mouse beta-NGF subunit genes.*;			
RL	Cold Spring Harb. Symp. Quant. Biol. 48:435-442(1983).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-CS7BL/6; TISSUE-Submaxillary gland;			
RX	MEDLINE-88038855: PubMed-3670305;			
RA	Selby M.J., Edwards R., Sharp F., Rutter W.J.;			
RT	*Mouse nerve growth factor gene: structure and expression.*;			
RL	Mol. Cell. Biol. 7:3057-3064(1987).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-93264918: PubMed-1284621;			
RA	Yamamoto T., Yamakuni T., Okabe N., Amano T.;			
RT	*Production and secretion of nerve growth factor by clonal striated			
RL	muscle cell line, G8-1.*;			
RL	Neurochem. Int. 21:251-258(1992).			
RN	[6]			
RP	SEQUENCE OF 122-239.			
RX	MEDLINE-73075048: PubMed-4566923;			
RA	Angelini R.H., Hermodson M.A., Bradshaw R.A.;			
RT	*Amino acid sequences of mouse 2.5S nerve growth factor. II.			
RL	Isolation and characterization of the thermolytic and peptic peptides			
RL	and the complete covalent structure.*;			
RL	Biochemistry 12:100-115(1973).			
RN	[7]			

RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE-92065986; PubMed-1956407;
 RA McDonald N.O., Lapatto R., Murrey-Rust J., Gunning J., Nlodawer A.,
 BLundell T.L.;
 RT "New protein fold revealed by a 2.3-A resolution crystal structure of
 RT nerve growth factor.";
 RL Nature 354:411-414(1991).
 RM [8]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE-94260545; PubMed-8201620;
 RA Holland D.R., Cousens L.S., Meng W., Matthews B.W.;
 RT "Nerve growth factor in different crystal forms displays structural
 RT flexibility and reveals zinc binding sites.";
 RL J. Mol. Biol. 239:385-400(1994).
 RM [9]
 RP X-RAY CRYSTALLOGRAPHY (3.15 ANGSTROMS) OF 7S COMPLEX.
 RC STRAIN-SVANS Webster; TISSUE-SUBMAXILLARY gland;
 RX MEDLINE-98035451; PubMed-9351801;
 RA Bax B., Blundell T.L., Murray-Rust J., McDonald N.O.;
 RT "Structure of mouse 7S NGF: a complex of nerve growth factor with
 RT four binding proteins.";
 RL Structure 5:1275-1285(1997).
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 CC EMBRYONIC SENSOR NEURONS.
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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 CC -----
 DR EMBL: M35075; AAA39818.1; ALT_INIT.
 DR EMBL: V00836; CAA24221.1; ALT_INIT.
 DR EMBL: K01759; AAA39820.1; ALT_INIT.
 DR EMBL: M14805; AAA39821.1; ALT_INIT.
 DR EMBL: M17298; AAA37687.1; ALT_INIT.
 DR EMBL: M17296; AAA37687.1; JOINED.
 DR EMBL: M17297; AAA37687.1; JOINED.
 DR EMBL: S62089; CAB32081.2; ALT_SEQ.
 DR PIR: A01400; NCMSMG.
 DR PDB: 1BET; 31-MAY-94.
 DR PDB: 1BTG; 08-MAR-96.
 DR PDB: 1SGF; 27-MAY-98.
 DR MGD: MGI:97321; NGFp.
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF; 1.
 DR PRINTS: PR00268; NGF.
 DR PRODOM: PD002052; NGF; 1.
 DR SMART: SM00140; NGF; 1.
 DR PROSITE: PS00248; NGF; 1; 1.
 DR PROSITE: PS50270; NGF; 2; 1.
 KM Growth factor; Signal; 3D-structure.
 FT SIGNAL 1 18 POTENTIAL.
 FT PROPEP 19 121
 FT CHAIN 122 241 BETA-NERVE GROWTH FACTOR.
 FT DISULFID 136 201
 FT DISULFID 179 229
 FT DISULFID 189 231
 FT CARBOHYD 69 69
 FT CARBOHYD 114 114 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CONFLICT 233 241 LSKATIRRG->CSAGRQDEEA (IN REF. 5).
 SQ SEQUENCE 241 AA; 27076 MW; 164465EDC550081 CRC64;

Query Match 98.9%; Score 646; DB 1; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.5e-62;
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSTRPVFMKEEFSVCDSSVWVGDKRTATDIDKREVTVAEVLNINSVPROYFFETKCA 61
 DB 122 SSTHPFHFHKEEFSVCDSSVWVGDKRTATDIDKREVTVAEVLNINSVPROYFFETKCA 181
 OY 62 SNPVESGCGIDSKHNSYCTTTFVVALTTDDKOAAMFPIIDACVCVLSRRATRG 121
 DB 182 SNPVESGCGIDSKHNSYCTTTFVVALTTDDKOAAMFPIIDACVCVLSRRATRG 241
 RESULT 2
 NGF RAT
 ID NGF RAT STANDARD: PRT: 241 AA.
 AC P25427;
 DT 01-MAY-1997 (Rel. 22, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Beta-nerve growth factor precursor (Beta-NGF).
 GN NGFB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid-10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-89037223; PubMed-3184206;
 RA Whittemore S.R., Friedman P.L., Larhammar D.G., Persson H.,
 RA Gonzalez-Carvajal M., Holets V.R.;
 RT "Rat beta-nerve growth factor sequence and site of synthesis in the
 RT adult hippocampus.";
 RL J. Neurosci. Res. 20:403-410(1988).
 RM [2]
 RP SEQUENCE OF 178-219 FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE-Liver;
 RX MEDLINE-9122573; PubMed-2025430;
 RA Hallboeek F., Idanez C.F., Persson H.;
 RT "Evolutionary studies of the nerve growth factor family reveal a
 RT novel member abundantly expressed in Xenopus ovary.";
 RL Neuron 6:845-858(1991).
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 CC EMBRYONIC SENSOR NEURONS.
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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 CC -----
 DR EMBL: M3589; AAA41697.1; ALT_INIT.
 DR HSSP: P01139; 1BET.
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF; 1.
 DR PRINTS: PR00268; NGF.
 DR PRODOM: PD002052; NGF; 1.
 DR SMART: SM00140; NGF; 1.
 DR PROSITE: PS00248; NGF; 1; 1.
 DR PROSITE: PS50270; NGF; 2; 1.
 KM Growth factor; Signal; 1.
 FT SIGNAL 1 18 POTENTIAL.
 FT PROPEP 19 121
 FT CHAIN 122 241 BETA-NERVE GROWTH FACTOR.
 FT DISULFID 136 201
 FT DISULFID 179 229
 FT DISULFID 189 231 BY SIMILARITY.
 FT CARBOHYD 69 69 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 114 114 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 241 AA; 27009 MW; 665F42371553213D CRC64;

Query Match 95.9%; Score 626; DB 1; Length 241;
 Best Local Similarity 95.8%; Pred. No. 2, 1e-60;
 Matches 111; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 SSTRPFHMGESVCDSSVWVGDKTTATDIDKREVTYLAEVNINNSVPROFFETKRA 61
 |||||
 DB 122 SSTRPFHMGESVCDSSVWVGDKTTATDIDKREVTYLAEVNINNSVPROFFETKRA 181
 OY 62 SNPVSGCGRGIDSKHNSYCTTHTFVKALTTDEKQAAAFRIIDPACVCLSRATRRG 121
 |||||
 DB 182 PNPVSGCGRGIDSKHNSYCTTHTFVKALTTDEKQAAAFRIIDPACVCLSRATRRG 241

RESULT 3

NGF_PRANA STANDARD; PRT; 241 AA.
 AC P20675;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Beta-nerve growth factor precursor (Beta-NGF).
 GN NGF.
 OS *Proxymys natalensis* (African soft-furred rat) (*Mastomys natalensis*).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 OC *Mastomys*.
 RN NCBI_TaxID=10112;
 RP SEQUENCE FROM N.A.
 RA MEDLINE=89172070; PubMed=3234767;
 RX Faminestock M., Bell R.A.;
 RT "Molecular cloning of a cDNA encoding the nerve growth factor precursor from *Mastomys natalensis*."
 RL Gene 69:257-264(1988).
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND EMBRYONIC SENSORY NEURONS.
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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 CC -----
 DR EMBL: M22748; AAA40599.1; ALT_INIT.
 DR PIR: J70343; NCRTBA.
 DR HSSP: P01139; 1BTG.
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF.1.
 DR PRINTS: PR00268; NGF.1.
 DR PRODOM: PD002052; NGF.1.
 DR SMART: SM00140; NGF.1.
 DR PROSITE: PS00248; NGF.1;
 DR PROSITE: PS50270; NGF.2; 1.
 KW Growth factor; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 121
 FT CHAIN 122 241
 FT DISULFID 136 201
 FT DISULFID 179 229
 FT DISULFID 189 231
 FT CARBOHYD 69 69
 FT CARBOHYD 114 114
 FT CARBOHYD 166 166
 FT SEQUENCE 241 AA; 27035 MW; 8BFB207A1FB2EF CIRC64;

Query Match 92.8%; Score 606; DB 1; Length 241;

Best Local Similarity 92.5%; Pred. No. 3e-58;
 Matches 111; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 2 SSTRPFHMGESVCDSSVWVGDKTTATDIDKREVTYLAEVNINNSVPROFFETKRA 61
 |||||
 DB 122 SSTRPFHMGESVCDSSVWVGDKTTATDIDKREVTYLAEVNINNSVPROFFETKRA 181
 OY 62 SNPVSGCGRGIDSKHNSYCTTHTFVKALTTDEKQAAAFRIIDPACVCLSRATRRG 121
 |||||
 DB 182 PNPVSGCGRGIDSKHNSYCTTHTFVKALTTDEKQAAAFRIIDPACVCLSRATRRG 241

RESULT 4

NGF_CAVPO STANDARD; PRT; 241 AA.
 AC P19093;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Beta-nerve growth factor precursor (Beta-NGF).
 GN NGF.
 OS *Cavia porcellus* (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 RN NCBI_TaxID=10141;
 RP SEQUENCE FROM N.A.
 RC TISSUE=prostate;
 RX MEDLINE=89177243; PubMed=2926397;
 RA Schwarz M.A., Fisher D., Bradshaw R.A., Isackson P.J.;
 RT "Isolation and sequence of a cDNA clone of beta-nerve growth factor from the guinea pig prostate gland."
 RL J. Neurochem. 52:1203-1209(1989).
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND EMBRYONIC SENSORY NEURONS.
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
 CC PIR: J10097; J10097.
 DR HSSP: P01139; 1BET.
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF.1.
 DR PRINTS: PR00268; NGF.1.
 DR PRODOM: PD002052; NGF.1.
 DR SMART: SM00140; NGF.1.
 DR PROSITE: PS00248; NGF.1;
 DR PROSITE: PS50270; NGF.2; 1.
 KW Growth factor; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 121
 FT CHAIN 122 241
 FT DISULFID 136 201
 FT DISULFID 179 229
 FT DISULFID 189 231
 FT CARBOHYD 69 69
 FT CARBOHYD 114 114
 FT SEQUENCE 241 AA; 26821 MW; 2F4E26B197804BF4 CIRC64;

Query Match 90.8%; Score 593; DB 1; Length 241;
 Best Local Similarity 90.0%; Pred. No. 7.7e-57;
 Matches 108; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 2 SSTRPFHMGESVCDSSVWVGDKTTATDIDKREVTYLAEVNINNSVPROFFETKRA 61
 |||||
 DB 122 SSTRPFHMGESVCDSSVWVGDKTTATDIDKREVTYLAEVNINNSVPROFFETKRA 181
 OY 62 SNPVSGCGRGIDSKHNSYCTTHTFVKALTTDEKQAAAFRIIDPACVCLSRATRRG 121
 |||||
 DB 182 PNPVSGCGRGIDSKHNSYCTTHTFVKALTTDEKQAAAFRIIDPACVCLSRATRRG 241

RESULT 5

FT DISULFID 177 219 BY SIMILARITY.
 FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 229 AA; 25275 MW; FE8890771CBA189 CRC64.

Query Match 89.3%; Score 583; DB 1; Length 229;
 Best Local Similarity 90.8%; Pred. No. 8.7e-56;
 Matches 108; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 2 SSTRPVFMGEFSVCDVSVMGDKTATDIDKKEVYLAEVNINSVPROFFETKRA 61
 DB 110 SSSHPVLRHGEFSVCDVSVMGDKTATDIDKKEVYLAEVNINSVPROFFETKCRD 169
 OY 62 SNPVESGCRGIDSKHNSYCTTHTFEVKALTDKQAAFRIRIDPACVLSRKATR 120
 DB 170 PNPVDSGCRGIDSKHNSYCTTHTFEVKALTDKQAAFRIRIDPACVLSRKAGR 228

RESULT 7
 NGF_BOVIN STANDARD; PRT: 231 AA.
 AC P13600; 018969;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Beta-nerve growth factor precursor (Beta-NGF) (Fragment).
 GN NGFB.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_Taxid=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=97430845; PubMed=9284944;
 RA Elounga C., Laurent P., Hayes H., Rodellar C., Levezuel H.,
 RA Zaragoza P.;
 RT "Assignment of the beta-nerve growth factor (NGFB) to bovine
 RT chromosome 3 band q23 by in situ hybridization.";
 RL Cytogenet. Cell Genet. 77:306-307(1997).
 RN [2]
 RP SEQUENCE OF 107-231 FROM N.A.
 RX MEDLINE=86300647; PubMed=2427334;
 RA Weller R., Becker-Andre M., Gotz R., Heumann R., Shaw A., Thoenen H.;
 RT "Molecular cloning of bovine and chick nerve growth factor (NGF):
 RT delineation of conserved and unconserved domains and their
 RT relationship to the biological activity and antigenicity of NGF.";
 RL EMBO J. 5:1489-1493(1986).
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 CC EMBRYONIC SENSORY NEURONS.
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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 CC -----
 CC EMBL: Y09566; CAA70759.1; -;
 CC EMBL: M26809; AAA30666.1; -;
 CC PIR: A26312; A26312.
 CC HSSP: P01139; IRET.
 CC InterPro: IPR002072; NGF.
 CC Pfam: PF00243; NGF; 1.
 CC PRODOM: PD002052; NGF; 1.
 CC SMART: SM00140; NGF; 1.

DR PROSITE: PS00248; NGF_1; 1.
 DR PROSITE: PS00270; NGF_2; 1.
 KW Growth factor; Signal.
 FT MON_TER 1
 FT SIGNAL <1 8
 FT PROPEP 9 111
 FT CHAIN 112 231
 FT DISULFID 126 191
 FT DISULFID 169 219
 FT DISULFID 179 221
 FT CARBOHYD 156 156
 FT CARBOHYD 158 158
 FT CONFLICT 161 161
 FT CONFLICT 230 231
 SQ SEQUENCE 231 AA; 25437 MW; 01605099291AA46C CRC64;

Query Match 86.4%; Score 564; DB 1; Length 231;
 Best Local Similarity 89.6%; Pred. No. 9.9e-54;
 Matches 103; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 2 SSTRPVFMGEFSVCDVSVMGDKTATDIDKKEVYLAEVNINSVPROFFETKRA 61
 DB 112 SSSHPVLRHGEFSVCDVSVMGDKTATDIDKKEVYLAEVNINSVPROFFETKCRD 171
 OY 62 SNPVESGCRGIDSKHNSYCTTHTFEVKALTDKQAAFRIRIDPACVLSRK 116
 DB 172 PNPVDSGCRGIDSKHNSYCTTHTFEVKALTDKQAAFRIRIDPACVLSRK 226

RESULT 8
 NGF_CHICK STANDARD; PRT: 243 AA.
 AC P05200;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Beta-nerve growth factor precursor (Beta-NGF).
 GN NGFB.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_Taxid=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86300646; PubMed=3017695;
 RA Eberhardt T., Larhammar D., Persson H.;
 RT "Structure and expression of the chicken beta nerve growth factor
 RT gene.";
 RL EMBO J. 5:1483-1487(1986).
 RN [2]
 RP SEQUENCE OF 118-243 FROM N.A.
 RX MEDLINE=86248129; PubMed=3720959;
 RA Wion D., Perret C., Frechlin N., Keller A., Behar G., Brechet P.,
 RA Auffray C.;
 RT "Molecular cloning of the avian beta-nerve growth factor gene:
 RT transcription in brain.";
 RL FEBS Lett. 203:82-86(1986).
 RN [3]
 RP SEQUENCE OF 121-243 FROM N.A.
 RX MEDLINE=86300647; PubMed=2427334;
 RA Weller R., Becker-Andre M., Gotz R., Heumann R., Shaw A., Thoenen H.;
 RT "Molecular cloning of bovine and chick nerve growth factor (NGF):
 RT delineation of conserved and unconserved domains and their
 RT relationship to the biological activity and antigenicity of NGF.";
 RL EMBO J. 5:1489-1493(1986).
 RN [4]
 RP SEQUENCE OF 181-222 FROM N.A.
 RX MEDLINE=9122573; PubMed=2025430;
 RA Hallboeck F., Ibanez C.F., Persson H.;
 RT "Evolutionary studies of the nerve growth factor family reveal a
 RT novel member abundantly expressed in Xenopus ovary.";
 RL Neuron 6:845-858(1991).

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CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS.
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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CC -----
CC EMBL; X04003; CAA27633.1; ALT_INIT.
CC EMBL; X04067; CAA27703.1; -
CC EMBL; M26810; AAA48984.1; -
CC PIR; A24857; A24857.
CC PIR; A26311; A26311.
CC HSSP; P01139; 1BET.
CC InterPro: IPR002072; NGF.
CC Pfam; PF00243; NGF_1.
CC PRINTS; PR00268; NGF.
CC PRODOM; PD002052; NGF_1.
CC SMART; SM00140; NGF_1; 1.
CC PROSITE; PS00248; NGF_1; 1.
CC PROSITE; PS50270; NGF_2; 1.
CC Growth factor; Signal.
CC SIGNAL; 1 22 POTENTIAL.
CC PROPEP 23 125 BETA-NERVE GROWTH FACTOR.
CC CHAIN 126 243 BY SIMILARITY.
CC DISULFID 139 204 BY SIMILARITY.
CC DISULFID 182 232 BY SIMILARITY.
CC DISULFID 192 234 BY SIMILARITY.
CC SEQUENCE 243 AA; 27138 MW; 74C306CB2079DA07 CRC64;

Query Match 83.6%; Score 546; DB 1; Length 243;
Best Local Similarity 84.6%; Pred. No. 9, 2e-52;
Matches 99; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 3 STRPVFMHGEFSVCDVSVMVGDKTTATNDIKGEVTVLAEVNINNSVFNQYFETKCRAS 62
DB 126 TAPHYLRHREEFVCDVSVMVGDKTTATNDIKGEVTVLAEVNINNSVFNQYFETKCRAP 185
QY 63 NPVSSGRCGIDSKHNSYCTTHTFVKALTTDEKQANRRIRIDTACVLSKRR 119
DB 186 RPVSSGRCGIDSKHNSYCTTHTFVKALTTDEKQANRRIRIDTACVLSKRR 242

RESULT 9
NGF_XENLA STANDARD: PRT: 231 AA.
ID NGF_XENLA
AC P1617;
DT 01-MAY-1991 (Rel. 18, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Nerve growth factor precursor (NGF).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91362944; PubMed=1888511;
RA Carriero F., Campioni M., Cardinali B., Pierandrei-Amaldi P.;
RT "Structure and expression of the nerve growth factor gene in Xenopus
RT oocytes and embryos."
RL Mol. Reprod. Dev. 29:313-322(1991).
RN [2]
RP SEQUENCE OF 170-211 FROM N.A.
RC TISSUE=Liver;

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RX MEDLINE=9122573; PubMed=2025430;
RA Hallboeck F., Ibanez C.F., Persson H.;
RT "Evolutionary studies of the nerve growth factor family reveal a
RT novel member abundantly expressed in Xenopus ovary."
RL Neuron 6:845-858(1991).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS.
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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CC -----
CC EMBL; X5716; CAA39249.1; ALT_INIT.
CC PIR; S1481; S1481.
CC HSSP; P01139; 1BET.
CC InterPro: IPR002072; NGF.
CC Pfam; PF00243; NGF_1.
CC PRINTS; PR00268; NGF.
CC PRODOM; PD002052; NGF_1.
CC SMART; SM00140; NGF_1; 1.
CC PROSITE; PS00248; NGF_1; 1.
CC PROSITE; PS50270; NGF_2; 1.
CC Growth factor; Signal.
CC SIGNAL; 1 18 POTENTIAL.
CC PROPEP 19 114 NERVE GROWTH FACTOR.
CC CHAIN 115 231 BY SIMILARITY.
CC DISULFID 128 193 BY SIMILARITY.
CC DISULFID 171 223 BY SIMILARITY.
CC DISULFID 181 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 107 107 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 231 AA; 26416 MW; 72A04E7D008B58C5 CRC64;

Query Match 81.5%; Score 532; DB 1; Length 231;
Best Local Similarity 84.2%; Pred. No. 2, 8e-50;
Matches 96; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 3 STRPVFMHGEFSVCDVSVMVGDKTTATNDIKGEVTVLAEVNINNSVFNQYFETKCRAS 62
DB 115 TAPHYLRHREEFVCDVSVMVGDKTTATNDIKGEVTVLAEVNINNSVFNQYFETKCRAP 174
QY 63 NPVSSGRCGIDSKHNSYCTTHTFVKALTTDEKQANRRIRIDTACVLSKRR 116
DB 175 KPVSSGRCGIDSKHNSYCTTHTFVKALTTDEKQANRRIRIDTACVLSKRR 228

RESULT 10
NGF_DABRR STANDARD: PRT: 117 AA.
ID NGF_DABRR
AC P30894;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Nerve growth factor (NGF).
OS Dabolia russelli russelli (Russell's viper) (Vipera russelli russelli).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Viperinae; Dabolia.
OX NCBI_TaxID=31159;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=93120151; PubMed=1477101;
RA Koyama T.-I., Inoue S., Ikeda K., Hayashi K.;

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RT      "Purification and amino-acid sequence of a nerve growth factor from
RL      the venom of Vipera russelli russelli."
CC      Blochm. Biophys. Acta 1160:287-292(1992).
CC      -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC      MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC      STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC      EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
CC      NEURONS IN THE BRAIN.
CC      -1- SUBUNIT: HOMODIMER.
CC      -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
DR      PIR: S28161; S28161.
DR      HSSP: P01139; 187.
DR      InterPro: IPR002072; NGF.
DR      Pfam: PF00243; NGF; 1.
DR      PRINTS: PR00268; NGF.
DR      ProDom: PD002052; NGF; 1.
DR      SMART: SM00140; NGF; 1.
DR      PROSITE: PS00248; NGF_1; 1.
DR      PROSITE: PS0270; NGF_2; 1.
DR      GlycoProtein: Growth factor.
KW      DISULFID 12
FT      DISULFID 55 105
FT      DISULFID 65 107
FT      CARBOHYD 21 21
SQ      SEQUENCE 117 AA; 13283 MW; A64559C5EC11F66 CRC64;

Query Match      72.7%; Score 475; DB 1; Length 117;
Best Local Similarity 73.2%; Pred. No. 1.9e-44;
Matches 82; Conservative 17; Mismatches 13; Indels 0; Gaps 0;

Oy      5 HPVHMGESFSDSVSWVGDKTTATDICKREYVLAEVNINNSVPROYFETCKRASP 64
Db      1 HPVHMGESFSDSVSWVGDKTTATDICKREYVLAEVNINNSVPROYFETCKRASP 60

Oy      65 VESGCRGIDSKHNSCTTHTFVKALTTDEQAAMRFIRIDACVLSRK 116
Db      61 VPSGCRGIDSKHNSCTTHTFVKALTTDEQAAMRFIRIDACVLSRK 112

RESULT 11
NGF_BUNMU
ID      NGF_BUNMU      STANDARD;      PRT;      243 AA.
AC      P3128;
DT      01-FEB-1994 (Rel. 28, Created)
DT      01-FEB-1994 (Rel. 28, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Nerve growth factor precursor (NGF).
OS      Bungarus multicinctus (Many-banded krait).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Lepidosaurs; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC      Elapidae; Bungarinae; Bungarus.
OX      NCBI_TaxID=8616;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Venom gland;
RA      MEDLINE=93192074; PubMed=7916740;
RA      Danse J.M., Garnier J.M.;
RT      "Molecular cloning of a cDNA encoding a nerve growth factor precursor
RT      from the krait, Bungarus multicinctus."
RL      Growth factors 8:77-86(1993).
CC      -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC      MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC      STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC      EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
CC      NEURONS IN THE BRAIN.
CC      -1- SUBUNIT: HOMODIMER.
CC      -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: S56212; AB25729.1; -.
DR      HSSP: P01139; 187.
DR      InterPro: IPR002072; NGF.
DR      Pfam: PF00243; NGF; 1.
DR      PRINTS: PR00268; NGF.
DR      ProDom: PD002052; NGF; 1.
DR      SMART: SM00140; NGF; 1.
DR      PROSITE: PS00248; NGF_1; 1.
DR      PROSITE: PS0270; NGF_2; 1.
KW      Growth factor; Signal.
FT      SIGNAL 1 18
FT      PROPEP 19 125
FT      CHAIN 126 243
FT      DISULFID 139 204
FT      DISULFID 182 232
FT      DISULFID 192 234
SQ      SEQUENCE 243 AA; 27514 MW; E33F64B142179A08 CRC64;

Query Match      72.1%; Score 473; DB 1; Length 243;
Best Local Similarity 72.2%; Pred. No. 1.1e-43;
Matches 83; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

Oy      2 STHPVEHMGESFSDSVSWVGDKTTATDICKREYVLAEVNINNSVPROYFETCKRA 61
Db      125 NENHVEHMGESFSDSVSWVGDKTTATDICKREYVLAEVNINNSVPROYFETCKRN 184

Oy      62 SPVSGCRGIDSKHNSCTTHTFVKALTTDEQAAMRFIRIDACVLSRK 116
Db      185 PBPVSGCRGIDSKHNSCTTHTFVKALTTDEQAAMRFIRIDACVLSRK 239

RESULT 12
NGF_NAJNA
ID      NGF_NAJNA      STANDARD;      PRT;      116 AA.
AC      P01140;
DT      21-JUL-1986 (Rel. 01, Created)
DT      01-MAY-1991 (Rel. 18, Last sequence update)
DT      01-JUL-1993 (Rel. 26, Last annotation update)
DE      Nerve growth factor (NGF).
OS      Naja naja (Indian cobra).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Lepidosaurs; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC      Elapidae; Elapinae; Naja.
OX      NCBI_TaxID=35670;
RN      [1]
RP      SEQUENCE.
RC      TISSUE=Venom;
RA      MEDLINE=91138755; PubMed=1995338;
RA      Inoue S., Oda T., Koyama J., Ikeda K., Hayashi K.;
RT      "Amino acid sequences of nerve growth factors derived from cobra
RT      venoms."
RT      FEBS Lett. 279:38-40(1991).
RN      [2]
RP      PRELIMINARY SEQUENCE.
RC      TISSUE=Venom;
RA      MEDLINE=76114772; PubMed=1247508;
RA      Hogue-Angelietti R.A., Frazier W.A., Jacobs J.W., Nall H.D.,
RA      Bradshaw R.A.;
RT      "Purification, characterization, and partial amino acid sequence of
RT      nerve growth factor from cobra venom."
RT      Biochemistry 15:26-34(1976).
CC      -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC      MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC      STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC      EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
CC      NEURONS IN THE BRAIN.
CC      -1- SUBUNIT: HOMODIMER.
CC      -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC      PIR: A01401; NGNXXI.
CC      PIR: S13927; S13927.

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FT CHAIN 80 194 NERVE GROWTH FACTOR.
 FT DISULFID 90 155 BY SIMILARITY.
 FT DISULFID 133 183 BY SIMILARITY.
 FT DISULFID 143 185 BY SIMILARITY.
 SQ SEQUENCE 194 AA: 21596 MW: 03690FA51147AE CRC64;

Query Match 59.7%; Score 390; DB 1; Length 194;
 Best Local Similarity 66.1%; Pred. No. 4, 9e-35;
 Matches 72; Conservative 13; Mismatches 24; Indels 0; Gaps 0;

QY 9 HMGESVCDSSVYWGDKTTATDINGKKEVTVLAEVNINSVFRQYFEETKCRASNPVSG 68
 DB 83 HMGESVCDSSVYWGDKTTATDINGKKEVTVLAEVNINSVFRQYFEETKCRASNPVSG 68
 QY 69 CNGIDSKHNSYCTTHTFVKALTTDEKQAMRFRTIDTACVLSRKA 117
 DB 143 CNGIDSKHNSYCTTHTFVKALTTDEKQAMRFRTIDTACVLSRKA 117

RESULT 15

NT7_CYPCA
 ID NT7_CYPCA STANDARD: PRT: 140 AA.

AC 093474:
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neurotrophin-7 precursor (NT-7) (Fragment).
 GN NTF7 OR NT7 OR NNT.
 OS Cyprinus carpio (Common carp).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Cyprinus.
 OX NCBI_TaxID=7962;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=9618228;
 RA Lai K.-O., Fu W.-Y., Ip F.C.F., Ip N.Y.;
 RT Cloning and expression of a novel neurotrophin, NT-7, from carp.;
 RL Mol. Cell. Neurosci. 11:64-76(1998).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
 CC -----
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 CC -----
 DR EMBL: U94949; AAC2632.1; -
 DR HSSP: P01139; 1SGF.
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF.1.
 DR PRINTS: PR00268; NGF.
 DR PRODOM: PD002052; NGF.1.
 DR SMART: SM00140; NGF.1.
 DR PROSITE: PS00248; NGF_1; 1.
 DR PROSITE: PS0270; NGF_2; 1.
 KW Growth factor.
 FT NON_TER 1
 FT PROSEP 7
 FT CHAIN 8 140 BY SIMILARITY.
 FT DISULFID 21 101 NEUTROTROPHIN-7.
 FT DISULFID 64 129 BY SIMILARITY.
 FT DISULFID 89 131 BY SIMILARITY.
 FT VARIANT 70 70 I -> V.
 FT VARIANT 95 95 E -> K.
 SQ SEQUENCE 140 AA: 15855 MW: 3F5F0BCE2601B0FC CRC64;

Query Match 58.1%; Score 379.5; DB 1; Length 140;
 Best Local Similarity 56.3%; Pred. No. 4, 7e-34;
 Matches 71; Conservative 14; Mismatches 26; Indels 15; Gaps 1;

QY 9 HMGESVCDSSVYWGDKTTATDINGKKEVTVLAEVNINSVFRQYFEETKCRASNPVSG 65
 DB 14 HMGESVCDSSVYWGDKTTATDINGKKEVTVLAEVNINSVFRQYFEETKCRASNPVSG 65
 QY 66 -----ESGCRGIDSKHNSYCTTHTFVKALTTDEKQAMRFRTIDTACVLSRKA 113
 DB 74 KPGQGVGVKAGTSSCGIDNEHNSYCTNHTFVRLTYSKQIAMRFRTINACVYL 133
 QY 114 SRKATR 119
 DB 134 SRNSMR 139

Search completed: December 2, 2002, 15:12:43
 Job time: 5.96483 secs

GenCore version 5.1.3
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OK protein - protein search, using sw model

Run on: December 2, 2002, 15:05:42 : Search time 18.7245 Seconds
(without alignments)
1331.501 Million cell updates/sec

Title: US-10-072-681-3

Perfect score: 653
Sequence: 1 PSSSTPVPFMGEFSVCDSVS.....FIRIDTACVCLSRKATRRG 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL21.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_ricent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriopl:*
17: sp_archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	584	89.4	241	4	Q9P208
2	584	89.4	241	4	Q9UKL8
3	584	89.4	241	6	Q9N2F1
4	584	89.4	241	6	Q9N2F0
5	584	89.4	241	6	Q9N2E9
6	577	88.4	294	11	Q91XB4
7	576	88.2	241	4	Q96P60
8	522	79.9	217	6	Q9N1B3
9	478	73.2	241	13	Q90W38
10	471	72.1	241	13	Q9DEZ9
11	424	64.9	87	6	Q9N2C3
12	416	63.7	86	4	Q9P224
13	347.5	53.2	286	13	Q9N198
14	335.5	51.4	241	6	Q9N1B2
15	325.5	49.8	153	11	Q9CYL3
16	325.5	49.8	247	6	Q97759

17	325.5	49.8	249	11	Q9VNH4	Q9VNH4 mus musc
18	320.5	49.1	246	13	Q9G76	Q9G76 japalura sp
19	319.5	48.9	270	13	Q9YH42	Q9YH42 brachydanto
20	318.5	48.8	177	13	Q91BL2	Q91BL2 poephila gu
21	318.5	48.8	246	13	Q9G74	Q9G74 cyclophiops
22	314.5	48.2	246	13	Q9G75	Q9G75 phrynocep
23	305	46.7	247	13	Q9G77	Q9G77 tylocorrio
24	296.5	45.4	101	6	Q9N22	Q9N22 macaca fusc
25	270	41.3	324	13	Q9N25	Q9N25 lampetra fl
26	262.5	40.2	186	12	Q945D9	Q945D9 fowilpox vir
27	227	34.8	85	6	Q92790	Q92790 macropus fu
28	221	33.8	85	6	Q91314	Q91314 isodon mac
29	221	33.8	85	6	Q91312	Q91312 tarsipes ro
30	221	33.8	85	6	Q92795	Q92795 ornithorhyn
31	221	33.8	85	6	Q92798	Q92798 petaurus br
32	221	33.8	85	6	Q91304	Q91304 cetartetes
33	221	33.8	85	6	Q92792	Q92792 notoryctes
34	221	33.8	85	6	Q91305	Q91305 dasyrodides
35	221	33.8	85	6	Q92801	Q92801 tachyglossu
36	220	33.7	85	6	Q92803	Q92803 trichosurus
37	197	30.2	42	6	Q92794	Q92794 ornithorhyn
38	195	29.9	42	6	Q92802	Q92802 tachyglossu
39	194	29.7	42	6	Q92802	Q92802 trichosurus
40	161	24.7	185	11	Q99NV9	Q99NV9 pedetes cep
41	160	24.5	184	6	Q9BRT5	Q9BRT5 tupia mino
42	160	24.5	185	6	Q9BRT6	Q9BRT6 talpa alai
43	160	24.5	185	6	Q9BRT5	Q9BRT5 condyura c
44	160	24.5	186	6	Q9BRT3	Q9BRT3 choleopus h
45	160	24.5	186	6	Q9BRT2	Q9BRT2 choleopus d

ALIGNMENTS

RESULT 1

ID	Q9P208	PRELIMINARY:	PRT:	241 AA.
AC	Q9P208:			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	Beta-nerve growth factor (Fragment).			
GN	BETA-NGF.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RA	SEQUENCE FROM N.A.			
RP	Kitano T., Kobayakawa H., Saitou N.;			
RT	*Silver Project.*			
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBD databases.			
DR	EMBL: AB037517; BAA90437.1; -			
DR	HSSP: P01139; 1BET.			
DR	InterPro: IPR002072; NGF.			
DR	Pfam: PF00243; NGF. 1.			
DR	PRINTS: PR00268; NGF.			
DR	ProDom: PD002052; NGF. 1.			
DR	SMART: SM00140; NGF. 1.			
DR	PROSITE: PS00246; NGF_1; 1.			
DR	PROSITE: PS0270; NGF_2; 1.			
FT	NON_TER 241 241			
SO	SEQUENCE 241 AA; 26998 MW; D5531ED825D9C14 CRC64;			
Query Match	89.4%; Score 584; DB 4; Length 241;			
Best Local Similarity	89.9%; Pred. No. 1,le-58;			
Matches 107; Conservative 4; Mismatches 8; Indels 0; Gaps 0;				
QY	2 SSTRPVPFMGEFSVCDSVWVGDKTTATDIKKEVTLAEVNNVSFROYFFETCKRA 61			
DB	122 SSSHPFIFRGEFSVCDSVWVGDKTTATDIKKEVTLAEVNNVSFROYFFETCKRD 181			
OY	62 SNPVEGCGIDSKHNSYCTTHTFYKALTDEKQAAFRIRIDTACVCLSRKATRR 120			

DB 182 PNPVDSGCRGIDSKHMNSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRKAVRR 240

RESULT 2

ID 09N2F0 PRELIMINARY: PRT: 241 AA.

AC 09N2F0: 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

GN Nerve growth factor B.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RM SEQUENCE FROM N.A.

RP MEDLINE=99256269; PubMed=10322959;

RA Tong Y., Wang H., Chen W.;

RT "Cloning and sequencing of the gene for premature beta nerve growth

factor.";

RT Chung Kuo Ying Yung Sheng Li Hsueh Tsa Chih 13:316-318(1997).

RM SEQUENCE FROM N.A.

RA Tong Y., Wang H.;

RT Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.

DR EMBL: AF150960; AAD55975.1; -

DR HSP: P01139; 1BET.

DR InterPro: IPR002072; NCF.

DR Pfam: PF00243; NCF. 1.

DR PRINTS: PR00268; NCF.

DR ProDom: PD002052; NCF. 1.

DR SMART: SM00140; NCF. 1.

DR PROSITE: PS00248; NCF. 1; 1.

DR PROSITE: PS50270; NCF. 2; 1.

SO SEQUENCE 241 AA; 26959 MW; 619DFC65E83B0671 CRC64;

Query Match 89.4%; Score 584; DB 4; Length 241;

Best Local Similarity 89.9%; Pred. No. 1.1e-58;

Matches 107; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 SSTRPFFHMGESVCDVSVMVGDKTTATDIDKKEVTLAEVNNNSVFQYFEETKCA 61

DB 122 SSSHPFFHMGESVCDVSVMVGDKTTATDIDKKEVTLAEVNNNSVFQYFEETKCD 181

QY 62 SNPVESGCRGIDSKHMNSYCTTHTFVKALTTDEKQAMRFIRIDTACVLSRKATR 120

DB 182 PNPVDSGCRGIDSKHMNSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRKAVRR 240

RESULT 3

ID 09N2F1 PRELIMINARY: PRT: 241 AA.

AC 09N2F1: 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

GN Beta-nerve growth factor (fragment).

OS Pan troglodytes (Chimpanzee).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.

OX NCBI_TaxID=9598;

RM SEQUENCE FROM N.A.

RP STRAIN=CHMP-220;

RA Kikano T., Kobayakawa H., Saitou N.;

RT "Silver Project."

RT Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL: AB037518; BAA90438.1; -

DR HSP: P01139; 1BET.

DR InterPro: IPR002072; NCF.

DR Pfam: PF00243; NCF. 1.

DR PRINTS: PR00268; NCF.

DR ProDom: PD002052; NCF. 1.

DR SMART: SM00140; NCF. 1.

DR PROSITE: PS00248; NCF. 1; 1.

DR PROSITE: PS50270; NCF. 2; 1.

FT NON-TER 241

SO SEQUENCE 241 AA; 26868 MW; B39FA8912C00A0B CRC64;

Query Match 89.4%; Score 584; DB 6; Length 241;

Best Local Similarity 89.9%; Pred. No. 1.1e-58;

Matches 107; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 SSTRPFFHMGESVCDVSVMVGDKTTATDIDKKEVTLAEVNNNSVFQYFEETKCA 61

DB 122 SSSHPFFHMGESVCDVSVMVGDKTTATDIDKKEVTLAEVNNNSVFQYFEETKCD 181

QY 62 SNPVESGCRGIDSKHMNSYCTTHTFVKALTTDEKQAMRFIRIDTACVLSRKATR 120

DB 182 PNPVDSGCRGIDSKHMNSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRKAVRR 240

RESULT 4

ID 09N2F0 PRELIMINARY: PRT: 241 AA.

AC 09N2F0: 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

GN Beta-nerve growth factor (fragment).

OS Gorilla gorilla (gorilla).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.

OX NCBI_TaxID=9593;

RM SEQUENCE FROM N.A.

RP STRAIN=GORILLA-U1;

RA Kikano T., Kobayakawa H., Saitou N.;

RT "Silver Project."

RT Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL: AB037519; BAA90439.1; -

DR HSP: P01139; 1BET.

DR InterPro: IPR002072; NCF.

DR Pfam: PF00243; NCF. 1.

DR PRINTS: PR00268; NCF.

DR ProDom: PD002052; NCF. 1.

DR SMART: SM00140; NCF. 1.

DR PROSITE: PS00248; NCF. 1; 1.

DR PROSITE: PS50270; NCF. 2; 1.

FT NON-TER 241

SO SEQUENCE 241 AA; 26915 MW; 6F54D163C384B834 CRC64;

Query Match 89.4%; Score 584; DB 6; Length 241;

Best Local Similarity 89.9%; Pred. No. 1.1e-58;

Matches 107; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 SSTRPFFHMGESVCDVSVMVGDKTTATDIDKKEVTLAEVNNNSVFQYFEETKCA 61

DB 122 SSSHPFFHMGESVCDVSVMVGDKTTATDIDKKEVTLAEVNNNSVFQYFEETKCD 181

QY 62 SNPVESGCRGIDSKHMNSYCTTHTFVKALTTDEKQAMRFIRIDTACVLSRKATR 120

DB 182 PNPVDSGCRGIDSKHMNSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRKAVRR 240

RESULT 5

ID 09N2E9 PRELIMINARY: PRT: 241 AA.

AC 09N2E9: 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

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DE 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE Beta-nerve growth factor (Fragment).
GN BETA-NGF.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pongo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ORAN-U1.
RA Kitano T., Kobayakawa H., Saitou N.;
RT "Silver Project."
RU Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB037520; BAA90440.1; -.
DR HSSP: P01139; 1BET.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF. 1.
DR PRINTS: PR00268; NGF.
DR ProDom: PD002052; NGF. 1.
DR SMART: SM00140; NGF. 1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS50270; NGF_2; 1.
FT NON_TER 241
SQ SEQUENCE 241 AA; 26876 MW; DFC168E7E4E01F15 CRC64;

Query Match 89.4%; Score 584; DB 6; Length 241;
Best Local Similarity 89.9%; Pred. No. 1.1e-58;
Matches 107; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 2 SSTRPVHMGESVCDVSVVWGDKTTATDINGKREVTVAEYNNINSVFRQYFFETKRA 61
DB 122 SSTRPVHMGESVCDVSVVWGDKTTATDINGKREVTVAEYNNINSVFRQYFFETKRD 181
OY 62 SNPESGCGRIGDSKHNSTCTTHTFVKALTDEKQAAAFRIIDPACVCSRRARR 120
DB 182 PNPVDSGCGRIGDSKHNSTCTTHTFVKALTMGKQAAAFRIIDPACVCSRRARR 240

RESULT 6
OY 091XB4 PRELIMINARY; PRT; 294 AA.
ID 091XB4
AC 091XB4;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE Similar to nerve growth factor, beta.
GN NGFB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary Gland;
RA Strausberg R.;
RU Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC011123; AAH11123.1; -.
DR MGI: MGI:97321; Ngfb.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF. 1.
DR ProDom: PD002052; NGF. 1.
DR PROSITE: PS00248; NGF_1; UNKNOWN_1.
DR PROSITE: PS50270; NGF_2; 1.
FT NON_TER 294
SQ SEQUENCE 294 AA; 33326 MW; 9EE7402DAC899229 CRC64;

Query Match 88.4%; Score 577; DB 11; Length 294;
Best Local Similarity 100.0%; Pred. No. 9e-58;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSTRPVHMGESVCDVSVVWGDKTTATDINGKREVTVAEYNNINSVFRQYFFETKRA 61
DB 188 SSTRPVHMGESVCDVSVVWGDKTTATDINGKREVTVAEYNNINSVFRQYFFETKRA 247

OY 62 SNPESGCGRIGDSKHNSTCTTHTFVKALTDEKQAAAFRIIDPACVCSRRARR 108
DB 248 SNPESGCGRIGDSKHNSTCTTHTFVKALTDEKQAAAFRIIDPACVCSRRARR 294

RESULT 7
OY 096P60 PRELIMINARY; PRT; 241 AA.
ID 096P60
AC 096P60;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, last annotation update)
DE Nerve growth factor beta.
GN NGFB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Zhang B., Zhou Y., Peng X., Yuan J., Qiang B.;
RU Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF411526; AL05874.1; -.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF. 1.
DR ProDom: PD002052; NGF. 1.
DR PROSITE: PS00248; NGF_1; UNKNOWN_1.
DR PROSITE: PS50270; NGF_2; 1.
FT NON_TER 241
SQ SEQUENCE 241 AA; 26964 MW; 745216485C21E558 CRC64;

Query Match 88.2%; Score 576; DB 4; Length 241;
Best Local Similarity 88.2%; Pred. No. 9.2e-58;
Matches 105; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 2 SSTRPVHMGESVCDVSVVWGDKTTATDINGKREVTVAEYNNINSVFRQYFFETKRA 61
DB 122 SSTRPVHMGESVCDVSVVWGDKTTATDINGKREVTVAEYNNINSVFRQYFFETKRD 181
OY 62 SNPESGCGRIGDSKHNSTCTTHTFVKALTDEKQAAAFRIIDPACVCSRRARR 120
DB 182 PNPVDSGCGRIGDSKHNSTCTTHTFVKALTMGKQAAAFRIIDPACVCSRRARR 240

RESULT 8
OY 09N1B3 PRELIMINARY; PRT; 217 AA.
ID 09N1B3
AC 09N1B3;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE Beta nerve growth factor (fragment).
OS Macaca fasciata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9542;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA MEDLINE-99270338; PubMed-10340513;
RA Okuno H., Tokuyama W., Li Y.X., Hashimoto T., Miyashita Y.;
RT "Quantitative evaluation of neurotrophin and c-fos mRNA expression in
RT visual and limbic areas along the occipito-temporo-hippocampal pathway
RT in adult macaque monkeys."
RN J. Comp. Neurol. 408:378-398(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Okuno H., Tokuyama W., Li Y.X., Hashimoto T., Miyashita Y.;
RU Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF222682; AAF33790.1; -.
DR HSSP: P01139; 1BET.
DR InterPro: IPR002072; NGF.
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DR PFam: P000243; NGF; 1.
DR PRINTS: PR00268; NGF; 1.
DR PRODOM: PD002052; NGF; 1.
DR SMART: SM00140; NGF; 1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS50270; NGF_2; 1.
FT NON_TER 1
FT SEQUENCE 217 AA; 24240 MW; 36A5A201DFCD8DC CRC64;
SO QUERY MATCH 79.9%; Score 522; DB 6; Length 217;
Best Local Similarity 89.6%; Pred. No. 1.2e-31;
Matches 95; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
OY 2 STHPVFKGEFSCVDSVYVGGDTTATDIDKREYVLAENVINNSVFRQYFETKCRPA 61
DB 112 SSSHPIFHNGEFSCVDSVYVGGDTTATDIDKREYVLAENVINNSVFRQYFETKCRD 171
OY 62 SAPVESGCGRIDSKHNSYCTTHTFYKALTDEKQAMRFIRIDT 107
DB 172 PNPVDSGCRGIDSKHNSYCTTHTFYKALTMDGKQAMRFIRIDT 217
RESULT 9
O90W38 PRELIMINARY; PRT; 241 AA.
AC 090W38:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Putative neurotrophic growth factor.
GN NGF.
OS Botryops jararacussu (Jararacussu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8726;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=VENOM GLAND;
RA Kashima S., Pereira J.O., Astolfi Filho S., Soares A.M.,
RA Cincta A.C.O., Giglio J.R., Franca S.C.;
RT Molecular cloning and cDNA sequence of a nerve growth factor
RT precursor from Bothrops jararacussu venomous gland.
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY007318; AAC12169.1;
DR InterPro: IPR002072; NGF.
DR PFam: PF00243; NGF; 1.
DR PRODOM: PD002052; NGF; 1.
DR PROSITE: PS00248; NGF_1; UNKNOWN_1.
DR PROSITE: PS50270; NGF_2; 1.
SQ SEQUENCE 241 AA; 27161 MW; AC57F724A6531A8F CRC64;
Query Match 73.2%; Score 478; DB 13; Length 241;
Best Local Similarity 74.1%; Pred. No. 1.5e-46;
Matches 83; Conservative 17; Mismatches 12; Indels 0; Gaps 0;
OY 5 HPVFHNGEFSCVDSVYVGGDTTATDIDKREYVLAENVINNSVFRQYFETKCRASP 64
DB 125 HPVHNGEFSCVDSVYVGGDTTATDIDKREYVLAENVINNSVFRQYFETKCRNP 184
OY 65 VESGCGRIDSKHNSYCTTHTFYKALTDEKQAMRFIRIDTACVCYSRK 116
DB 185 VPTGCGRIDARHNSYCTTHTFYKALTMEGQNSMRFIRIDTACVCYSRK 236
RESULT 10
O9DE29 PRELIMINARY; PRT; 241 AA.
AC 09DE29:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
```

```
DE Nerve growth factor.
OS Crotalus durissus terrificus (South American rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Crotalus.
OX NCBI_TaxID=8732;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=VENOM GLAND;
RA Hayashi M.A.F., Radle-Baptista G., Ymane T., Canargo A.C.M.;
RT Cloning and sequence of a cDNA coding for a rattlesnake (Crotalus
RT durissus terrificus) nerve growth factor.
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF306533; AAG30924.1;
DR HSSP: P01139; 1BET.
DR InterPro: IPR002072; NGF.
DR PFam: PF00243; NGF; 1.
DR PRINTS: PR00268; NGF; 1.
DR PRODOM: PD002052; NGF; 1.
DR SMART: SM00140; NGF; 1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS50270; NGF_2; 1.
SQ SEQUENCE 241 AA; 27118 MW; 4A261F42C5D6EF3F CRC64;
Query Match 72.1%; Score 471; DB 13; Length 241;
Best Local Similarity 73.2%; Pred. No. 9.4e-46;
Matches 82; Conservative 17; Mismatches 13; Indels 0; Gaps 0;
OY 5 HPVFHNGEFSCVDSVYVGGDTTATDIDKREYVLAENVINNSVFRQYFETKCRASP 64
DB 125 HPVHNGEFSCVDSVYVGGDTTATDIDKREYVLAENVINNSVFRQYFETKCRNP 184
OY 65 VESGCGRIDSKHNSYCTTHTFYKALTDEKQAMRFIRIDTACVCYSRK 116
DB 185 VPTGCGRIDARHNSYCTTHTFYKALTMEGQNSMRFIRIDTACVCYSRK 236
RESULT 11
O9TTC3 PRELIMINARY; PRT; 87 AA.
AC 09TTC3:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Beta nerve growth factor (fragment).
GN NGF.
OS Cervus elaphus scoticus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=109627;
RN [1]
RP SEQUENCE FROM N.A.
RA Robertson T.M., Stanton J.L., Clark D.E., Sheard P.W., Harris A.J.,
RA Suttle J.M.;
RT "NGF expression in Antler."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF145043; AAF17235.1;
DR HSSP: P01139; 1BET.
DR InterPro: IPR002072; NGF.
DR PFam: PF00243; NGF; 1.
DR PRINTS: PR00268; NGF; 1.
DR PRODOM: PD002052; NGF; 1.
DR SMART: SM00140; NGF; 1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS50270; NGF_2; 1.
FT NON_TER 1
FT SEQUENCE 87 AA; 9876 MW; 17E06E49AF7A0A4 CRC64;
Query Match 64.9%; Score 424; DB 6; Length 87;
Best Local Similarity 88.5%; Pred. No. 6.5e-41;
Matches 77; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
```


FT NON_TER 1 1
 SEQUENCE 241 AA: 27803 MW: AB95E457C7B07113 CRC64:
 SO

Query Match 51.44: Score 335.5: DB 6: Length 241:
 Best Local Similarity 58.08: Pred. No. 3e-30: 21: Indels 1: Gaps 1:
 Matches 58: Conservative 20: Mismatches 201

OY 9 HNGEFSVCDVSVMVGDKTATDIDKREVTYLAEVNINNSVPROYFEETKCRASNPVSG 68
 DB 142 HNGEVSVCSESLWTKSSAIDIRGHQVTLGEIKTGNSPVKOYFEETKCRARPVKMG 201
 OY 69 CRGIDSKHNSCTTHTFEVKALITD-EKQAAAFRIIDT 107
 DB 202 CRGIDSKHNSCTTHTFEVKALITD-EKQAAAFRIIDT 241

RESULT 15
 ID 09CYL3 PRELIMINARY: PRT: 153 AA.

AC 01-JUN-2001 (TEMBLrel. 17, Created)
 DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
 DE Brain derived neurotrophic factor.
 GN BDNF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN
 RP
 RC STRAIN=C57BL/6J; TISSUE=EMBryo;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanae I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gasterland T., Gissi C., King B., Kochava H.,
 RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Ohido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Marzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsaki S.,
 RA Hayashizaki Y.;
 RA
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL: AK017559; BAB30805.1; -.
 DR HSSP: P23560; 188M.
 DR MGD: MGI:88145; Bdnf.
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF. 1.
 DR PRINTS: PR00268; NGF.
 DR PRODOM: PD002052; NGF. 1.
 DR SMART: SM00140; NGF. 1.
 DR PROSITE: PS00248; NGF. 1; 1.
 DR PROSITE: PS50270; NGF. 2; 1.
 SO SEQUENCE 153 AA: 17519 MW: CA8E8B944CE5B37 CRC64:

Query Match 49.8%: Score 325.5: DB 11: Length 153;
 Best Local Similarity 54.58: Pred. No. 2.4e-29;
 Matches 61: Conservative 16: Mismatches 33: Indels 3: Gaps 2;

OY 11 GEFVCSVSVWV--GKTTATDIDKREVTYLAEVNINNSVPROYFEETKCRASNPVSG 68
 DB 42 GELSVCSISWVTAADKRTAVDMSGVTYVLEKVPVSKGOLKQYFEETKCRPKGTMEG 101

OY 69 CRGIDSKHNSCTTHTFEVKALITD-EKQAAAFRIIDTACVLSRATR 119
 DB 102 CRGIDSKHNSCTTHTFEVKALITD-EKQAAAFRIIDTACVLSRATR 153

Search completed: December 2, 2002, 15:12:01
 Job time: 18.7245 secs

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OM protein - protein search, using sw model

Run on: December 2, 2002, 15:05:42 : Search time 8.16928 Seconds
(without alignments)
425.386 Million cell updates/sec

Title: US-10-072-681-3

Perfect score: 653

Sequence: 1 PESTHVFHMGESVCDVS.....FRIDACVLSRKATRRG 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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6: /cgn2_6/ptodata/1/laa/Deckfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	653	100.0	121	4	US-09-675-503-3
2	646	98.9	120	1	US-08-440-049-1
3	646	98.9	120	2	US-08-441-513A-1
4	646	98.9	120	3	US-08-970-865-3
5	646	98.9	120	4	US-09-363-573-3
6	646	98.9	120	5	PCT-US93-08918-1
7	618	94.6	120	1	US-07-979-630-1
8	618	94.6	120	5	PCT-US93-11292-1
9	594	91.0	121	4	US-09-675-503-2
10	587	89.9	120	3	US-08-970-865-2
11	587	89.9	120	4	US-09-363-573-2
12	584	89.4	120	1	US-08-440-049-3
13	584	89.4	120	2	US-08-441-513A-3
14	584	89.4	120	3	US-08-581-662-31
15	584	89.4	120	4	US-08-845-541B-1
16	584	89.4	120	4	US-09-066-065A-1
17	584	89.4	120	4	US-09-447-356-1
18	584	89.4	120	4	US-09-664-295-31
19	584	89.4	120	5	PCT-US93-06918-3
20	584	89.4	241	1	US-08-266-080B-4
21	584	89.4	241	1	US-08-451-947-5
22	584	89.4	241	1	US-08-424-826A-5
23	584	89.4	241	2	US-08-595-043A-75
24	584	89.4	241	3	US-08-970-865-1
25	584	89.4	241	3	US-08-928-694-5
26	584	89.4	241	4	US-09-363-573-1
27	584	89.4	241	4	US-09-447-356-3

28	584	89.4	241	5	PCT-US91-06950-5	Sequence 5, Appl1
29	584	89.4	241	5	PCT-US93-05423-4	Sequence 4, Appl1
30	584	89.4	242	4	US-09-675-503-1	Sequence 1, Appl1
31	579	88.7	119	3	US-08-753-642-2	Sequence 2, Appl1
32	579	88.7	153	4	US-09-675-922-2	Sequence 2, Appl1
33	579	88.7	157	4	US-09-675-922-4	Sequence 4, Appl1
34	579	88.7	163	4	US-09-675-922-6	Sequence 6, Appl1
35	579	88.7	167	4	US-09-675-922-8	Sequence 8, Appl1
36	570	87.3	120	4	US-08-845-541B-3	Sequence 3, Appl1
37	570	87.3	120	4	US-09-066-065A-3	Sequence 3, Appl1
38	567	86.8	120	4	US-08-845-541B-4	Sequence 4, Appl1
39	567	86.8	120	4	US-09-066-065A-4	Sequence 4, Appl1
40	562	86.1	120	4	US-08-845-541B-12	Sequence 12, Appl1
41	562	86.1	120	4	US-09-066-065A-12	Sequence 12, Appl1
42	561	85.9	120	4	US-08-845-541B-17	Sequence 17, Appl1
43	561	85.9	120	4	US-08-845-541B-20	Sequence 20, Appl1
44	561	85.9	120	4	US-09-066-065A-17	Sequence 17, Appl1
45	561	85.9	120	4	US-09-066-065A-20	Sequence 20, Appl1

ALIGNMENTS

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RESULT 1
US-09-675-503-3
; Sequence 3, Application US/09675503
; Patent No. 6423831
; GENERAL INFORMATION:
; APPLICANT: Burton, Louis E.
; APPLICANT: Schmeltzer, Charles H.
; TITLE OF INVENTION: ISOLATION OF NEUROROPHINS FROM A
; TITLE OF INVENTION: MIXTURE CONTAINING OTHER PROTEINS AND NEUROROPHIN VARIANTS
; FILE REFERENCE: GENE 037C2
; CURRENT APPLICATION NUMBER: US/09/675,503
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/030838
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: 60/047855
; PRIOR FILING DATE: 1997-05-29
; PRIOR APPLICATION NUMBER: 08/970865
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 09/363573
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: mouse
US-09-675-503-3
; Sequence 1, Application US/08440049
; Sequence 1, Application US/08440049
```

Patent No. 5728803
GENERAL INFORMATION:
APPLICANT: Ureter, Roman
APPLICANT: Presta, Leonard G.
APPLICANT: Winslow, John M.
TITLE OF INVENTION: PANTHROPIC NEUTROTROPHIC FACTORS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Minipain (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,049
FILING DATE: 12-May-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/253937
FILING DATE: 03-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0905C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-440-049-1
Query Match 98.9%; Score 646; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.5e-72;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SSTRPFFHMGESVCDVSVMVGDKTTATDIDKGEVTVLAENVNINSVFROYFEETKRA 61
DB 1 SSTRPFFHMGESVCDVSVMVGDKTTATDIDKGEVTVLAENVNINSVFROYFEETKRA 60
QY 62 SNVESGCGKIDSKHNSYCTTHTFVAKLTDEKQAAAMRIRIDTACVLSRKATRRG 121
DB 61 SNVESGCGKIDSKHNSYCTTHTFVAKLTDEKQAAAMRIRIDTACVLSRKATRRG 120
RESULT 3
US-08-441-513A-1
Sequence 1, Application US/08441513A
GENERAL INFORMATION:
APPLICANT: Ureter, Roman
APPLICANT: Presta, Leonard G.
APPLICANT: Winslow, John M.
TITLE OF INVENTION: Panthropic Neutrotrophic Factors
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Minipain (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,513A
FILING DATE: 15-May-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/253937
FILING DATE: 03-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, P.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0905C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-441-513A-1
Query Match 98.9%; Score 646; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.5e-72;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SSTRPFFHMGESVCDVSVMVGDKTTATDIDKGEVTVLAENVNINSVFROYFEETKRA 61
DB 1 SSTRPFFHMGESVCDVSVMVGDKTTATDIDKGEVTVLAENVNINSVFROYFEETKRA 60
QY 62 SNVESGCGKIDSKHNSYCTTHTFVAKLTDEKQAAAMRIRIDTACVLSRKATRRG 121
DB 61 SNVESGCGKIDSKHNSYCTTHTFVAKLTDEKQAAAMRIRIDTACVLSRKATRRG 120
RESULT 4
US-08-970-865-3
Sequence 3, Application US/08970865
Patent No. 6005081
GENERAL INFORMATION:
APPLICANT: Louis E. Burton, Charles H. Schmeizer, Joanne T. Beck
TITLE OF INVENTION: Purification of NGF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Minipain (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/970,865
FILING DATE: 14-No. 6005081-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030838
FILING DATE: 11/15/1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047855
FILING DATE: 5/29/1997
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, P.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1063R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 120 amino acids
: TYPE: Amino Acid
: TOPOLOGY: Linear
US-08-970-865-3

Query Match 98.9%; Score 646; DB 3; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.5e-72;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSTRPVEFHMGERSVCDSSVWVGDKTTATDIDKGEVTVLAEVNINNSVPROFFETKRA 61
DB 1 SSTRPVEFHMGERSVCDSSVWVGDKTTATDIDKGEVTVLAEVNINNSVPROFFETKRA 60
QY 62 SNPVESGCGIDSKHNSYCTTHTFVKALTTDEKQAAHFRIDPACVLSRKATRG 121
DB 61 SNPVESGCGIDSKHNSYCTTHTFVKALTTDEKQAAHFRIDPACVLSRKATRG 120

RESULT 5

US-09-363-573-3
: Sequence 3, Application US/09363573
: Patent No. 6184360

GENERAL INFORMATION:
: APPLICANT: Louis E. Burton, Charles H. Schmelzer, Joanne T. Beck
: TITLE OF INVENTION: Purification of NGF
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/363,573

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/970,865

FILING DATE: 14-No. 6184360-1997

APPLICATION NUMBER: 60/030838

FILING DATE: 11/15/1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/047855

FILING DATE: 5/29/1997

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Ph.D., Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: P1063R2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-09-363-573-3

Query Match 98.9%; Score 646; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.5e-72;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSTRPVEFHMGERSVCDSSVWVGDKTTATDIDKGEVTVLAEVNINNSVPROFFETKRA 61
DB 1 SSTRPVEFHMGERSVCDSSVWVGDKTTATDIDKGEVTVLAEVNINNSVPROFFETKRA 60

DB 1 SSTRPVEFHMGERSVCDSSVWVGDKTTATDIDKGEVTVLAEVNINNSVPROFFETKRA 60
QY 62 SNPVESGCGIDSKHNSYCTTHTFVKALTTDEKQAAHFRIDPACVLSRKATRG 121
DB 61 SNPVESGCGIDSKHNSYCTTHTFVKALTTDEKQAAHFRIDPACVLSRKATRG 120

RESULT 6

PCT-US95-06918-1
: Sequence 1, Application PC/TUS9506918
: Patent No. 5488099

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

TITLE OF INVENTION: PANTROPIC NEUROTROPHIC FACTORS

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/06918

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: 905PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-8674

TELEFAX: 910/371-7168

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acids

TYPE: amino acid

TOPOLOGY: linear

PCT-US95-06918-1

Query Match 98.9%; Score 646; DB 5; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.5e-72;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSTRPVEFHMGERSVCDSSVWVGDKTTATDIDKGEVTVLAEVNINNSVPROFFETKRA 61
DB 1 SSTRPVEFHMGERSVCDSSVWVGDKTTATDIDKGEVTVLAEVNINNSVPROFFETKRA 60
QY 62 SNPVESGCGIDSKHNSYCTTHTFVKALTTDEKQAAHFRIDPACVLSRKATRG 121
DB 61 SNPVESGCGIDSKHNSYCTTHTFVKALTTDEKQAAHFRIDPACVLSRKATRG 120

RESULT 7

US-07-979-630-1

: Sequence 1, Application US/07979630

: Patent No. 5488099

GENERAL INFORMATION:

APPLICANT: Person, et al

TITLE OF INVENTION: Multifunctional Neurotrophic Factors

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Regeneron Pharmaceuticals, Inc.

STREET: 777 Old Saw Mill River Road

CITY: Tarrytown

STATE: New York
COUNTRY: U.S.A.
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/979,630
FILING DATE: 20-NOV-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,369
FILING DATE: 06-MAR-1992
NAME:
ATTORNEY/AGENT INFORMATION:
NAME: Kempier Ph.D., Gail M.
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG 41
TELEPHONE: 914-347-7000
TELEFAX: 914-347-2113
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-07-979-630-1

Query Match
Best Local Similarity 94.6%; Score 618; DB 1; Length 120;
Matches 113; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 2 SSTRPVEFHMGESVCDSSVWVGDKTTATDIDKGEVYLAEVNINNSVFRQYFEETKCR 61
DB 1 SSTRPVEFHMGESVCDSSVWVGDKTTATDIDKGEVYLAEVNINNSVFRQYFEETKCR 60
OY 62 SNPEVSGCGIDSKHNSCTTHTFVKALTTDEKQAMRIRIDTACVCLSRKAAVRG 121
DB 61 PNPEVSGCGIDSKHNSCTTHTFVKALTTDDKQAMRIRIDTACVCLSRKAAVRG 120

RESULT 8
PCT-US93-11292-1
Sequence 1, Application PC/TUS9311292
GENERAL INFORMATION:
APPLICANT: Persson, et al.
TITLE OF INVENTION: Multifunctional Neurotrophic Factors
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11292
FILING DATE: 19-NOV-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,369
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Kempier Ph.D., Gail M.

REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG 41
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-347-7000
TELEFAX: 914-347-2113
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US93-11292-1

Query Match
Best Local Similarity 94.6%; Score 618; DB 5; Length 120;
Matches 113; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 2 SSTRPVEFHMGESVCDSSVWVGDKTTATDIDKGEVYLAEVNINNSVFRQYFEETKCR 61
DB 1 SSTRPVEFHMGESVCDSSVWVGDKTTATDIDKGEVYLAEVNINNSVFRQYFEETKCR 60
OY 62 SNPEVSGCGIDSKHNSCTTHTFVKALTTDEKQAMRIRIDTACVCLSRKAAVRG 121
DB 61 PNPEVSGCGIDSKHNSCTTHTFVKALTTDDKQAMRIRIDTACVCLSRKAAVRG 120

RESULT 9
US-09-675-503-2
Sequence 2, Application US/09675503
Patent No. 6423831
GENERAL INFORMATION:
APPLICANT: Burton, Louis E.
APPLICANT: Beck, Joanne T.
TITLE OF INVENTION: ISOLATION OF NEUROTROPHINS FROM A
MIXTURE CONTAINING OTHER PROTEINS AND NEUROTROPHIN VARIANTS
FILE REFERENCE: GENE 037C2
CURRENT APPLICATION NUMBER: US/09/675,503
CURRENT FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/030838
PRIOR FILING DATE: 1996-11-15
PRIOR APPLICATION NUMBER: 60/047855
PRIOR FILING DATE: 1997-05-29
PRIOR APPLICATION NUMBER: 08/970865
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: 09/363573
PRIOR FILING DATE: 1999-07-29
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 121
TYPE: PRT
ORGANISM: Homo sapien
US-09-675-503-2

Query Match
Best Local Similarity 91.0%; Score 594; DB 4; Length 121;
Matches 109; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 1 PSSTRPVEFHMGESVCDSSVWVGDKTTATDIDKGEVYLAEVNINNSVFRQYFEETKCR 60
DB 1 PSSSTRPVEFHMGESVCDSSVWVGDKTTATDIDKGEVYLAEVNINNSVFRQYFEETKCR 60
OY 61 ASNPESGCGIDSKHNSCTTHTFVKALTTDEKQAMRIRIDTACVCLSRKAAVR 120
DB 61 DNPVDSGCGIDSKHNSCTTHTFVKALTTDDKQAMRIRIDTACVCLSRKAAVR 120

RESULT 10
US-08-970-865-2
Sequence 2, Application US/08970865

```
Patent No. 6005081
GENERAL INFORMATION:
APPLICANT: Louis E. Burton, Charles H. Schmeltzer, Joanne T. Beck
TITLE OF INVENTION: Purification of NGF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/970,865
FILING DATE: 14-NOV-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030838
FILING DATE: 11/15/1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047855
FILING DATE: 5/29/1997
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1063R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-9861
TELEFAX: 650/952-8674
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-970-865-2

Query Match      89.9%; Score 587; DB 3; Length 120;
Best Local Similarity 90.8%; Pred. No. 3e-65;
Matches 108; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 SSTRPVHMGESVYCDVSVWVGDKTTATDCKEYVLAEVNINSVPROFFETKRA 61
    ||:|||||
DB 1 SSSHPHFHMGESVYCDVSVWVGDKTTATDCKEYVLAEVNINSVPROFFETKRD 60
    ||:|||||
QY 62 SPPVSGCGRIGDSKHMNSYCTTHTFVKALTTDEKQAAFRIRIDTACVLSRAVRR 120
    ||:|||||
DB 61 PNPVDSGCGRIGDSKHMNSYCTTHTFVKALTTDEKQAAFRIRIDTACVLSRAVRR 119
    ||:|||||

RESULT 11
US-09-363-573-2
Sequence 3, Application US/09363573
Patent No. 6184360
GENERAL INFORMATION:
APPLICANT: Louis E. Burton, Charles H. Schmeltzer, Joanne T. Beck
TITLE OF INVENTION: Purification of NGF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
```

```
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,573
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/970,865
FILING DATE: 14-NOV-1997
APPLICATION NUMBER: 60/030838
FILING DATE: 11/15/1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047855
FILING DATE: 5/29/1997
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1063R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-9861
TELEFAX: 650/952-8674
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-363-573-2

Query Match      89.9%; Score 587; DB 4; Length 120;
Best Local Similarity 90.8%; Pred. No. 3e-65;
Matches 108; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 SSTRPVHMGESVYCDVSVWVGDKTTATDCKEYVLAEVNINSVPROFFETKRA 61
    ||:|||||
DB 1 SSSHPHFHMGESVYCDVSVWVGDKTTATDCKEYVLAEVNINSVPROFFETKRD 60
    ||:|||||
QY 62 SPPVSGCGRIGDSKHMNSYCTTHTFVKALTTDEKQAAFRIRIDTACVLSRAVRR 120
    ||:|||||
DB 61 PNPVDSGCGRIGDSKHMNSYCTTHTFVKALTTDEKQAAFRIRIDTACVLSRAVRR 119
    ||:|||||

RESULT 12
US-08-440-049-3
Sequence 3, Application US/08440049
Patent No. 5728603
GENERAL INFORMATION:
APPLICANT: Uffer, Roman
APPLICANT: Presta, Leonard G.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: PANROTROPIC NEUROTROPHIC FACTORS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,049
FILING DATE: 12-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/253937
FILING DATE: 03-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0905C2
```

```
TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-8674
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 120 amino acids
: TYPE: Amino Acid
: TOPOLOGY: Linear
:
US-08-440-049-3

Query Match      89.4%; Score 584; DB 1; Length 120;
Best Local Similarity 89.9%; Pred. No. 7.2e-65;
Matches 107; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 2 SSTRPVFMGEFVSVCDSVSWVGDKTTATDIDKGEVTVLAEVNINNSVFRQYFETKRA 61
DB 1 SSSHPHFHRCGFVSVCDSVSWVGDKTTATDIDKGEVTVLAEVNINNSVFRQYFETKCRD 60

OY 62 SNPVESGCRGIDSKHNSYCTTHTFVKALTTDEKQAMRFIRIDTACVCLSKRAVR 120
DB 61 PNPVDSGCRGIDSKHNSYCTTHTFVKALTTMDGKQAMRFIRIDTACVCLSKRAVR 119

RESULT 13
US-08-441-513A-3
: Sequence 3, Application US/08441513A
: Patent No. 5981480
: GENERAL INFORMATION:
: APPLICANT: Ufer, Leonard G.
: APPLICANT: Presta, Leonard G.
: TITLE OF INVENTION: 'Pantropic Neurotrophic Factors
: NUMBER OF SEQUENCES: 20
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/441,513A
: FILING DATE: 15-May-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/253937
: FILING DATE: 03-JUN-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Torchia, Ph.D., Timothy E.
: REGISTRATION NUMBER: 36,700
: REFERENCE/DOCKET NUMBER: P0905C3
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-8674
: TELEFAX: 650/952-9881
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 120 amino acids
: TYPE: Amino Acid
: TOPOLOGY: Linear
:
US-08-441-513A-3

Query Match      89.4%; Score 584; DB 2; Length 120;
Best Local Similarity 89.9%; Pred. No. 7.2e-65;
Matches 107; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 2 SSTRPVFMGEFVSVCDSVSWVGDKTTATDIDKGEVTVLAEVNINNSVFRQYFETKRA 61
DB 1 SSSHPHFHRCGFVSVCDSVSWVGDKTTATDIDKGEVTVLAEVNINNSVFRQYFETKCRD 60
```

```
DB 1 SSSHPHFHRCGFVSVCDSVSWVGDKTTATDIDKGEVTVLAEVNINNSVFRQYFETKCRD 60
OY 62 SNPVESGCRGIDSKHNSYCTTHTFVKALTTDEKQAMRFIRIDTACVCLSKRAVR 120
DB 61 PNPVDSGCRGIDSKHNSYCTTHTFVKALTTMDGKQAMRFIRIDTACVCLSKRAVR 119

RESULT 14
US-08-581-662-31
: Sequence 31, Application US/08581662
: Patent No. 6121235
: GENERAL INFORMATION:
: APPLICANT: Gao, Wei-Oiang
: TITLE OF INVENTION: Treatment of Balance Impairments
: FILE REFERENCE: P0981
: CURRENT APPLICATION NUMBER: US/08/581,662
: CURRENT FILING DATE: 1995-12-29
: NUMBER OF SEQ ID NOS: 36
: SEQ ID NO 31
: LENGTH: 120
: TYPE: PRT
: ORGANISM: Homo sapiens
:
US-08-581-662-31

Query Match      89.4%; Score 584; DB 3; Length 120;
Best Local Similarity 89.9%; Pred. No. 7.2e-65;
Matches 107; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 2 SSTRPVFMGEFVSVCDSVSWVGDKTTATDIDKGEVTVLAEVNINNSVFRQYFETKRA 61
DB 1 SSSHPHFHRCGFVSVCDSVSWVGDKTTATDIDKGEVTVLAEVNINNSVFRQYFETKCRD 60

OY 62 SNPVESGCRGIDSKHNSYCTTHTFVKALTTDEKQAMRFIRIDTACVCLSKRAVR 120
DB 61 PNPVDSGCRGIDSKHNSYCTTHTFVKALTTMDGKQAMRFIRIDTACVCLSKRAVR 119

RESULT 15
US-08-845-541B-1
: Sequence 1, Application US/08845541B
: Patent No. 633310
: GENERAL INFORMATION:
: APPLICANT: Presta, Leonard
: APPLICANT: Ufer, Roman
: APPLICANT: Winslow, John
: TITLE OF INVENTION: NGF VARIANTS
: FILE REFERENCE: GENENT-039A
: CURRENT APPLICATION NUMBER: US/08/845,541B
: CURRENT FILING DATE: 1999-04-25
: NUMBER OF SEQ ID NOS: 38
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 120
: TYPE: PRT
: ORGANISM: homo sapien
:
US-08-845-541B-1

Query Match      89.4%; Score 584; DB 4; Length 120;
Best Local Similarity 89.9%; Pred. No. 7.2e-65;
Matches 107; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 2 SSTRPVFMGEFVSVCDSVSWVGDKTTATDIDKGEVTVLAEVNINNSVFRQYFETKRA 61
DB 1 SSSHPHFHRCGFVSVCDSVSWVGDKTTATDIDKGEVTVLAEVNINNSVFRQYFETKCRD 60

OY 62 SNPVESGCRGIDSKHNSYCTTHTFVKALTTDEKQAMRFIRIDTACVCLSKRAVR 120
DB 61 PNPVDSGCRGIDSKHNSYCTTHTFVKALTTMDGKQAMRFIRIDTACVCLSKRAVR 119

Search completed: December 2, 2002, 15:09:43
Job time : 9.36928 secs
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 2, 2002, 15:08:47 | Search time 4.25557 Seconds
(without alignments)
452.778 Million cell updates/sec

Title: US-10-072-681-3

Perfect score: 653

Sequence: 1 PSSSTHPVFHMGFVSCDSVS.....PFRIDACVLSRKATRRG 121

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 102317 seqs, 15924203 residues

Total number of hits satisfying chosen parameters: 102317

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PTCT_NEM_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	653	100.0	121	12 US-10-072-681-3	Sequence 3, Appl1
2	584	91.0	121	12 US-10-072-681-2	Sequence 2, Appl1
3	584	89.4	241	8 US-08-450-842-5	Sequence 5, Appl1
4	584	89.4	241	10 US-09-822-263-16	Sequence 16, Appl1
5	584	89.4	242	12 US-10-072-681-1	Sequence 1, Appl1
6	579	88.7	153	10 US-09-798-338-2	Sequence 2, Appl1
7	579	88.7	153	10 US-09-798-338-4	Sequence 4, Appl1
8	579	88.7	153	10 US-09-798-338-6	Sequence 6, Appl1
9	579	88.7	167	10 US-09-798-338-8	Sequence 8, Appl1
10	573	87.7	121	9 US-09-813-398-9	Sequence 9, Appl1
11	435	66.6	142	8 US-08-450-842-52	Sequence 52, Appl1
12	378.5	58.0	120	10 US-09-745-032-1	Sequence 1, Appl1
13	378.5	58.0	120	10 US-09-742-600-1	Sequence 1, Appl1
14	378.5	58.0	120	10 US-09-872-090-1	Sequence 1, Appl1
15	378.5	58.0	257	8 US-08-450-842-4	Sequence 4, Appl1
16	377.5	57.8	119	10 US-09-745-032-6	Sequence 6, Appl1
17	377.5	57.8	119	10 US-09-742-600-6	Sequence 6, Appl1
18	377.5	57.8	119	10 US-09-872-090-6	Sequence 6, Appl1
19	377.5	57.8	120	10 US-09-745-032-3	Sequence 3, Appl1

20	377.5	57.8	120	10 US-09-742-600-3	Sequence 3, Appl1
21	377.5	57.8	120	10 US-09-872-090-3	Sequence 3, Appl1
22	375.5	57.5	117	10 US-09-745-032-7	Sequence 7, Appl1
23	375.5	57.5	117	10 US-09-742-600-7	Sequence 7, Appl1
24	375.5	57.5	117	10 US-09-872-090-7	Sequence 7, Appl1
25	375.5	57.5	118	10 US-09-745-032-5	Sequence 5, Appl1
26	375.5	57.5	118	10 US-09-742-600-5	Sequence 5, Appl1
27	375.5	57.5	118	10 US-09-872-090-5	Sequence 5, Appl1
28	370.5	56.7	120	9 US-09-813-398-11	Sequence 11, Appl1
29	368.5	56.4	120	12 US-10-072-681-5	Sequence 5, Appl1
30	345	52.8	72	10 US-09-848-664-21	Sequence 21, Appl1
31	326.5	50.0	130	8 US-08-450-842-47	Sequence 8, Appl1
32	325.5	49.8	120	10 US-09-745-032-8	Sequence 8, Appl1
33	325.5	49.8	120	10 US-09-745-032-10	Sequence 10, Appl1
34	325.5	49.8	120	10 US-09-742-600-8	Sequence 8, Appl1
35	325.5	49.8	120	10 US-09-742-600-10	Sequence 10, Appl1
36	325.5	49.8	247	8 US-08-450-842-3	Sequence 47, Appl1
37	324.5	49.7	120	10 US-09-745-032-9	Sequence 9, Appl1
38	324.5	49.7	120	10 US-09-742-600-9	Sequence 9, Appl1
39	319.5	48.9	120	9 US-09-813-398-10	Sequence 10, Appl1
40	314.5	48.2	130	8 US-08-450-842-23	Sequence 23, Appl1
41	312.5	47.9	130	8 US-08-450-842-22	Sequence 22, Appl1
42	312.5	47.9	131	9 US-09-813-398-12	Sequence 12, Appl1
43	312.5	47.9	168	8 US-08-450-842-6	Sequence 6, Appl1
44	312.5	47.9	210	8 US-08-450-842-2	Sequence 2, Appl1
45	311.5	47.7	130	8 US-08-450-842-60	Sequence 60, Appl1

ALIGNMENTS

RESULT 1

US-10-072-681-3

Sequence 3, Application US/10072681

Patent No. US20020137893A1

GENERAL INFORMATION:

APPLICANT: Burton, Louis E.

APPLICANT: Beck, Joanne T.

APPLICANT: Schmelzer, Charles H.

TITLE OF INVENTION: PURIFICATION OF NGF

FILE REFERENCE: GENENT.037C3

CURRENT APPLICATION NUMBER: US/10/072,681

CURRENT FILING DATE: 2002-02-08

PRIOR APPLICATION NUMBER: 60/030838

PRIOR FILING DATE: 1996-11-15

PRIOR APPLICATION NUMBER: 60/047855

PRIOR FILING DATE: 1997-05-29

PRIOR APPLICATION NUMBER: 08/970865

PRIOR FILING DATE: 1997-11-14

PRIOR APPLICATION NUMBER: 09/363573

PRIOR FILING DATE: 1999-07-29

PRIOR APPLICATION NUMBER: 09/675,503

PRIOR FILING DATE: 2000-09-29

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSeq for Windows version 4.0

SEQ ID NO: 3

LENGTH: 121

TYPE: PRT

ORGANISM: mouse

US-10-072-681-3

Query Match 100.0% Score 653 DB 12 Length 121

Best Local Similarity 100.0% Pred. No. 5, 1e-68

Matches 121: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSSSTHPVFHMGFVSCDSVSVMWGDKTTATDIDKREVTVALEVININSVTFROFEETKCR 60

DB 1 PSSSTHPVFHMGFVSCDSVSVMWGDKTTATDIDKREVTVALEVININSVTFROFEETKCR 60

QY 61 ASNPVSGCGIDSKHNSYCTTTRTFYKALTTDEKOAAMFFIRIDACVLSRKATRR 120

DB 61 ASNPVSGCGIDSKHNSYCTTTRTFYKALTTDEKOAAMFFIRIDACVLSRKATRR 120

OY 121 G 121
Db 121 G 121

RESULT 2

US-10-072-681-2
Sequence 2, Application US/10072681
Patent No. US20020137893A1
GENERAL INFORMATION:
APPLICANT: Burton, Louis E.
APPLICANT: Schmelzer, Charles H.
APPLICANT: Beck, Joanne T.
TITLE OF INVENTION: PURIFICATION OF NCF
FILE REFERENCE: GENENT-037C3
CURRENT APPLICATION NUMBER: US/10/072.681
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/030838
PRIOR FILING DATE: 1996-11-15
PRIOR APPLICATION NUMBER: 60/047855
PRIOR FILING DATE: 1997-05-29
PRIOR APPLICATION NUMBER: 08/970865
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: 09/363573
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: 09/675.503
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 121
TYPE: PRT
ORGANISM: Homo sapien
US-10-072-681-2

Query Match
Best Local Similarity 91.0%; Score 594; DB 12; Length 121;
Pred. No. 3e-61; Mismatches 3; Indels 8; Gaps 0;
Matches 109; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 1 PSSHTPVFMHGEFSCVDSVYWGDKTTATDTDKGKAVTVLAENVINNSVFQYFETKCR 60
Db 1 PSSHPHFHNGEFSVCDSSVWVGDKTTATDTDKGKAVTVLAENVINNSVFQYFETKCR 60
OY 61 ASNVESGCGIDSKHNSYCTTHTTFVKALTTDEKQAAAFRIIDTACVCLSRKATRR 120
Db 61 DPNVDSGCGIDSKHNSYCTTHTTFVKALTTDEKQAAAFRIIDTACVCLSRKAVRR 120

RESULT 3

US-08-450-842-5
Sequence 5, Application US/08450842
Patent No. US20020045576A1
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUTROPHILIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25 Inch, 360 Kb floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Palin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,842
FILING DATE:
CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/426419
FILING DATE: 19-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030013
FILING DATE: 22-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 1991
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,770
REFERENCE/DOCKET NUMBER: 666P2C1D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: Linear
US-08-450-842-5

Query Match
Best Local Similarity 89.4%; Score 584; DB 8; Length 241;
Pred. No. 9.4e-60; Mismatches 4; Indels 8; Gaps 0;
Matches 107; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 2 STHPVFMHGEFSCVDSVWVGDKTTATDTDKGKAVTVLAENVINNSVFQYFETKCR 61
Db 122 SSSHPHFHNGEFSVCDSSVWVGDKTTATDTDKGKAVTVLAENVINNSVFQYFETKCR 181
OY 62 SNPVESGCGIDSKHNSYCTTHTTFVKALTTDEKQAAAFRIIDTACVCLSRKATRR 120
Db 182 DPNVDSGCGIDSKHNSYCTTHTTFVKALTTDEKQAAAFRIIDTACVCLSRKAVRR 240

RESULT 4

US-03-822-263-16
Sequence 16, Application US/09822263
Patent No. US20020036598A1
GENERAL INFORMATION:
APPLICANT: Prayaga, Sudhirdas
APPLICANT: Vernet, Corine
APPLICANT: Shinkets, Richard A
APPLICANT: Burgess, Catherine
APPLICANT: Szytek, Kimberly
APPLICANT: Tchernev, Velizar T
TITLE OF INVENTION: No. US20020036598A1el Polynucleotides and Polypeptides Encoded
FILE REFERENCE: 15966-572 CIP1
CURRENT APPLICATION NUMBER: US/09/822,263
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 09/672,665
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/156,745
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 60/158,942
PRIOR FILING DATE: 1999-10-06
PRIOR APPLICATION NUMBER: 60/159,248
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/169,344
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 60/215,048
PRIOR FILING DATE: 2000-06-29
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 16
LENGTH: 241
TYPE: PRT
ORGANISM: Homo sapiens

FILE REFERENCE: 87662-68879
CURRENT APPLICATION NUMBER: US/09/798.338
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 09/141.153
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 6
LENGTH: 163
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Artificial
US-09-798-338-6

Query Match 88.7% Score 579; DB 10; Length 163;
Best Local Similarity 89.8% Pred. No. 2.2e-59;
Matches 106; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 SSTRPVFMGEFVSVCDSVYWGDKTTATDINGKREYVLAEVNINNSVFRQYFEETCR 61
DB 45 SSSHPHFHRCFVSVCDSVYWGDKTTATDINGKREYVLAEVNINNSVFRQYFEETCR 104
QY 62 SNPEVSGCRGIDSKHNSYCTTHTFVKALTTDERQAMRFRIDTACVCLSKRAVR 119
DB 105 PNPVDSGCRGIDSKHNSYCTTHTFVKALTDGQAMRFRIDTACVCLSKRAVR 162

RESULT 9
US-09-798-338-8
Sequence 8, Application US/09798338
Patent No. US20010020086A1
GENERAL INFORMATION:
APPLICANT: Hubbell, Jeffrey A.
APPLICANT: Schense, Jason C.
APPLICANT: Sakiyama, Shelly E.
TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE
FILE REFERENCE: 87662-68879
CURRENT APPLICATION NUMBER: US/09/798.338
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 09/141.153
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 8
LENGTH: 167
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Artificial
US-09-798-338-8

Query Match 88.7% Score 579; DB 10; Length 167;
Best Local Similarity 89.8% Pred. No. 2.3e-59;
Matches 106; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 SSTRPVFMGEFVSVCDSVYWGDKTTATDINGKREYVLAEVNINNSVFRQYFEETCR 61
DB 49 SSSHPHFHRCFVSVCDSVYWGDKTTATDINGKREYVLAEVNINNSVFRQYFEETCR 108
QY 62 SNPEVSGCRGIDSKHNSYCTTHTFVKALTTDERQAMRFRIDTACVCLSKRAVR 119
DB 109 PNPVDSGCRGIDSKHNSYCTTHTFVKALTDGQAMRFRIDTACVCLSKRAVR 166

RESULT 10
US-09-813-398-9
Sequence 9, Application US/09813398
Patent No. US20020169292A1
GENERAL INFORMATION:

APPLICANT: Bruce D. Weintraub
APPLICANT: Mariusz W. Szuljanski
APPLICANT: University of Maryland
TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
FILE REFERENCE: UOFPD.003C1
CURRENT APPLICATION NUMBER: US/09/813.398
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: PCT/US99/05908
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: PCT/US98/19772
PRIOR FILING DATE: 1998-09-22
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 121
TYPE: PRT
ORGANISM: HOMO SAPIEN
US-09-813-398-9

Query Match 87.7% Score 573; DB 9; Length 121;
Best Local Similarity 87.3% Pred. No. 7.6e-59;
Matches 105; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 PSSTPVFMGEFVSVCDSVYWGDKTTATDINGKREYVLAEVNINNSVFRQYFEETCR 60
DB 1 PSSHPHFHRCFVSVCDSVYWGDKTTATDINGKREYVLAEVNINNSVFRQYFEETCR 60
QY 61 ASNPESGCRGIDSKHNSYCTTHTFVKALTTDERQAMRFRIDTACVCLSKRAVR 120
DB 61 DNPVDSGCRGIDSKHNSYCTTHTFVKALTDGQAMRFRIDTACVCLSKRAVR 120

RESULT 11
US-08-450-842-52
Sequence 52, Application US/08450842
Patent No. US20020045576A1
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 Inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patcin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450.842
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426419
FILING DATE: 19-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030013
FILING DATE: 22-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 1991
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 66622C1D3

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/953-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-450-842-52

Query Match	66.6%	Score 435;	DB 8;	Length 142;
Best Local Similarity	61.7%	Pred. NO. 6.2e-43;		
Matches	87;	Conservative	12;	Mismatches 20;
			Indels	22;
			Gaps	4;

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0y      2 SSTPFFVFMKPEFSCDVSVMVGDKTATDIDKGEVTYLAEVNINSV----- 49
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Db      1 SSSHPIFHKGEEFSVDCSVSMVGDKTTATDIDKGEVMVLGVNINNSVLTGEVPAGGSP 60

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50 FROFFETCKRASNPVE-----SGCRGIDSKHNSYCTTHTEFKALITD-EKQAAVR 101
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 61 LRQFFETCKADNNEGGPCAGGGGCGRCDRHNVSECKAKQSIYRALTADAGRGVR 120

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Oy      102 FIRIDTA--CVCVLSRKATR 120
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Db      121 WIRIDTACVCVCVLSRKAVR 141

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RESULT 12
US-09-745-032-1
; Sequence 1, Application US/09745032
; Patent No. US20110027179A1

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? GENERAL INFORMATION:
? APPLICANT: Boone, Thomas C.
? APPLICANT: Cheung, Ellen N.
? APPLICANT: Herzhenshon, Susan I.
? APPLICANT: Young, John D.
? TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS
? FILE REFERENCE: A-411A US Revised 073100
? CURRENT APPLICATION NUMBER: US/09/745,032
? PRIOR FILING DATE: 2000-12-19
? PRIOR APPLICATION NUMBER: 09/214,214
? PRIOR FILING DATE: 1998-12-23
? PRIOR APPLICATION NUMBER: US 08/684,353
? PRIOR FILING DATE: 1996-07-19
? NUMBER OF SEQ. ID NOS: 12
? SOFTWARE: PatentIn Ver. 2.1
? SEQ. ID NO. 1
? LENGTH: 120
? TYPE: PRT
? ORGANISM: Human
? OS-09-745-032-1

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Query Match	58.0%	Score 378.5	DB 10	Length 120
Best Local Similarity	58.9%	Pred. No. 1.5e-36		
Matches 66; Conservative	21	Mismatches 24	Indels 1	Gaps 1

Dc

Qy 69 CRGIDSKHNSYCITTHIFVALTLD-EKQAWRFIRIDTACVLSRKATR 119
 ||||| ||||| - :
 Db 68 CRGIDSKHNSOCKTSOTIVFALTSNNKLVGWRWIRIDTSCVALSRKIGR 119

RESULT 13
US-09-742-600-1

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: Sequence 1, Application US/09742600
: Patent No. US20020010135A1
:
: GENERAL INFORMATION:
:
: APPLICANT: Boone, Thomas C.
:
: APPLICANT: Cheung, Ellen N.

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Query Match	58.0%	Score 378.5;	DB 10;	Length 120;
Best Local Similarity	58.9%	Pred. No. 1.5e-36;		
Matches 66;	Conservative 21;	Mismatches 24;	Indels 1;	Gaps 1

Db 8 HRGELSYCDSESLWYTDKSSAIDIRGHQVYVLGSEIKTGNSPVQYFYETRECKEARPVKNG 67

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07 CRGIDSKHWNSTCTTHTFVKALTTD-EKQAAHFIRIDTACVCLSRKATR 119
    ||||| ||||| : : : : ||| : : ||||| : ||| |
Db CRGIDDKHWNSTCTTHTFVKALTTD-EKQAAHFIRIDTACVCLSRKATR 119
    ||||| ||||| : : : : ||| : : ||||| : ||| |
68 CRGIDDKHWNSTCTTHTFVKALTTD-EKQAAHFIRIDTACVCLSRKATR 119
    ||||| ||||| : : : : ||| : : ||||| : ||| |

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RESULT 14
US-09-872-090-1
; Sequence 1, Application US/09872090

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Query Match	58.0%	Score 378.5;	DB 10;	Length 120;
Best Local Similarity	58.9%	Pred. No.1.5e-36;		
Matches 66; Conservative	21;	Mismatches 24;	Indels 1;	Gaps 1.

QY HMGEEFSCDSVWVGDKTTATDIDKRETVTLAEVINNSVFROYEFETIKRASNPEVSG 68
| | : | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
Db HRGEIYSCDSLSLMTDRSSAIDIRGHQTVLGLGIKTGNSPVKQFYETRECKEARPVKNG 67

QY 69 CRGIDSKHWNXCCTTHTFVKAULTD-EKQAMRFIRIDTACVLSRKATR 119
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 Db 68 CRGIDDKHWNXCCTTSQTIVKALTSENKLVGRWRIRIDTSCVCALSRKIGR 119

RESULT 15
US-08-450-842-4
; Sequence 4, Application US/08450842
; Patent No. US20020045576a1

RESULT 15
US-08-450-842-4
; Sequence 4, Application US/08450842
; Patent No. US20020045576a1

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Page 6

GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUTROPHILIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,842
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426419
FILING DATE: 19-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030013
FILING DATE: 22-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 1991
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 656P2C1D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/852-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-450-842-4

Query Match 58.0%; Score 378.5; DB 8; Length 257;
Best Local Similarity 58.9%; Pred. No. 3.8e-36;
Matches 66; Conservative 21; Mismatches 24; Indels 1; Gaps 1;

Oy 9 HMGFSVCDVSVMVCDKATATDICKKVTVAEVNINSVFRQFFETKCRASNPVPSG 68
DB 145 HRGEYSVCDSESLMTWDKSSALDIRGHQTVLGEIKTGSPPVKKQYFETRCKEAPVYKNG 204
Oy 69 CRGIDSKHMSYCTTHTFYKATTD-EKQAAHFRIRIDTACVCYLKRATR 119
DB 205 CRGIDSKHMSYCTTHTFYKATTD-EKQAAHFRIRIDTACVCYLKRATR 256

Search completed: December 2, 2002, 15:14:34
Job time : 4.25557 secs

XX
PA (GETH) GENENTECH INC.

XX Beck JT, Burton LE, Schmelzer CH;
PI WPI: 1998-322333/28.
DR
XX
XX Isolation of neurotrophin(s) from, e.g. mla-folded or glycosylated
PT variant(s) - using hydrophobic interaction chromatography,
PT optionally in combination with high performance cation exchange
PT chromatography
PS
XX Disclosure: page 37: 59pp: English.
CC
XX This polypeptide comprises brain-derived neurotrophic factor
CC (BDNF). Methods are provided for large-scale purification of
CC neurotrophins, including mature BDNF, suitable for clinical use. A
CC claimed method comprises: (1) separating the neurotrophin from the
CC other proteins using a hydrophobic interaction chromatography resin
CC (HICR); and optionally (2) separating the neurotrophin from a
CC chemical variant by high performance cation exchange chromatography
CC (HPEC). The processes can also be used for purification of e.g.
CC human nerve growth factor (NGF) (see AAM48886), mouse NGF (see
CC AAM48887), neurotrophin-4/5 (see AAM48890) and neurotrophin-3 (see
CC AAM48889). The processes allow separation of neurotrophins from
CC various undesirable misprocessed, misfolded, size, glycosylated or
CC charge forms. They allow selective separation from variants and
CC other molecules, and from other polypeptides with high pI. The
CC processes are applicable to starting materials from various
CC sources, including fermentation broths or lysed bacterial or
CC mammalian cells.
SQ Sequence 118 AA:
Query Match 98.9%; Score 633; DB 19; Length 118;
Best Local Similarity 100.0%; Pred. No. 5.4e-62;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 HSDPARGELSDSISEVNTAADKKTAVDMSGCTVTVLEKVPVSKGLKQYFETKCNP 61
DB 1 HSDPARGELSDSISEVNTAADKKTAVDMSGCTVTVLEKVPVSKGLKQYFETKCNP 60
QY 62 MGYTKECRGIDIRHNNNSOCRTTOSYVRALTMDSKKRIGMRIRIDTSCVLTIRGR 119
DB 61 MGYTKECRGIDIRHNNNSOCRTTOSYVRALTMDSKKRIGMRIRIDTSCVLTIRGR 118
RESULT 2
AAB29114
ID AAB29114 standard; Protein: 118 AA.
XX
XX AAB29114:
AC
XX
XX 02-FEB-2001 (first entry)
DT
XX
XX Brain derived neurotrophic factor.
DE
XX
XX Neurotrophin: trkB; trkC; ototoxicity-related balance impairment;
XX Meniere's syndrome; myringitis; otitis media;
XX acute vestibular neuronitis; herpes zoster oticus; labyrinthitis;
XX middle; labyrinthine tumour; petrositis; otosclerosis; bacteria.
XX
XX Homo sapiens.
OS
XX
XX US6121235-A.
PN
XX
XX 19-SEP-2000.
PD
XX
XX 29-DEC-1995; 95US-0581662.
PF
XX
XX 29-DEC-1995; 95US-0581662.
PR
XX
XX (GETH) GENENTECH INC.
PA
XX
XX Gao W;
PI

XX
DR WPI: 2000-618200/59.
XX
XX Treating ototoxin-induced neuronal-related balance impairment and
PT promoting vestibular ganglion neuron survival prior to, upon or after
PT exposure to an ototoxin, comprises administering a trkB or trkC agonist
PT
PS Disclosure: Column 49-50; 40pp: English.
XX
XX The present invention relates to treating ototoxin-induced
CC neuronal-related balance impairment in a mammal by administering a
CC trkB or trkC agonist, particularly neurotrophin-4/5 (NT-4/5).
CC ototoxicity-related balance impairments include Meniere's syndrome,
CC myringitis, otitis media, acute vestibular neuronitis, herpes zoster
CC oticus, labyrinthitis, middle or labyrinthine tumour, petrositis and
CC otosclerosis. NT-4/5 may also be used to treat diseases
CC induced by gram positive, gram negative and acid-fast bacteria. The
CC present sequence is a protein used in the invention.
SQ Sequence 118 AA:
Query Match 98.9%; Score 633; DB 21; Length 118;
Best Local Similarity 100.0%; Pred. No. 5.4e-62;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 HSDPARGELSDSISEVNTAADKKTAVDMSGCTVTVLEKVPVSKGLKQYFETKCNP 61
DB 1 HSDPARGELSDSISEVNTAADKKTAVDMSGCTVTVLEKVPVSKGLKQYFETKCNP 60
QY 62 MGYTKECRGIDIRHNNNSOCRTTOSYVRALTMDSKKRIGMRIRIDTSCVLTIRGR 119
DB 61 MGYTKECRGIDIRHNNNSOCRTTOSYVRALTMDSKKRIGMRIRIDTSCVLTIRGR 118
RESULT 3
AAR29494
ID AAR29494 standard; Protein: 119 AA.
XX
XX AAR29494:
AC
XX
XX 22-APR-1993 (first entry)
DT
XX
XX BDNF, mouse.
DE
XX
XX Neurotrophin; NT: nerve growth factor; NGF;
XX Brain-derived neurotrophic factor; BDNF.
XX
XX Mus musculus.
OS
XX
XX WO9220365-A.
PN
XX
XX 26-NOV-1992.
PD
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XX 20-MAY-1992; 92MO-0504266.
PF
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XX 21-MAY-1991; 91US-0703450.
PR
XX 12-JUL-1991; 91US-0729253.
PR 23-JUL-1991; 91US-0734422.
PR 28-AUG-1991; 91US-0751356.
PR 20-SEP-1991; 91US-0762674.
PR 14-NOV-1991; 91US-0791924.
XX
XX (REGG-) REGENERON PHARM INC.
XX
XX Halibook F, Ibanez Moliner CF, Persson HB, Yancopoulos GD;
PI WPI: 1992-415468/50.
DR
XX
XX Use of neurotrophin-4 for promoting growth and survival of nerve
PT cells - useful in treating neurological, fertility and
PT immunological disorders and in diagnosis
XX

PS Disclosure; Page 106 + Fig 4B; 180pp; English.
XX A comparison of the mature NT-4 protein (Xenopus) to the mature
CC NTF, BDNF, and NT-3 proteins from mouse revealed 51%, 60% and 58%
CC amino acid identity respectively. See sequences AAB39491 and
CC AAB39493-95.
XX

Sequence 119 AA:

Query Match 97.3%; Score 622.5; DB 13; Length 119;
Best Local Similarity 99.2%; Pred. No. 7,8e-61;
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARRGELSYVCDISSEVNTADKKTAVDMSGCTVLEKVPVSKGOLKQYFETKCNP 61
DB 1 HSDPARRGELSYVCDISSEVNTADKKTAVDMSGCTVLEKVPVSKGOLKQYFETKCNP 60
OY 62 MGYTKEGCGIDKRHMNSOCRTTOSYVRLTMDSKKRIGMRIRIDTSCV-TLTIKRGR 119
DB 61 MGYTKEGCGIDKRHMNSOCRTTOSYVRLTMDSKKRIGMRIRIDTSCV-TLTIKRGR 119

RESULT 4

AAB76814
ID AAB76814 standard; Protein: 119 AA.

AC AAB76814;

DT 07-DEC-1995 (first entry)

DE Porcine BDNF mature protein.

KM Brain derived neurotrophic factor; BDNF; neuron; Alzheimer's disease;
KM trauma; Parkinson's disease.

OS Sus scrofa.

PN US5438121-A.

PD 01-AUG-1995.

PF 30-AUG-1989; 89US-0400591.

PR 25-APR-1991; 91US-0691612.

PR 30-AUG-1989; 89US-0400591.

PR 20-AUG-1990; 90US-0570657.

PA (PLAC) MAX PLANCK GES FORDERUNG WISSENSCHAFTEN.

PA (REG-) REGENERON PHARM INC.

PI Barde Y, Edgar D, Leibel J, Lottspeltch F, Thoenen H;

PI Yancopoulos G;

DR WPI; 1995-274920/36.

XX Claim 2; Column 89; 100pp; English.

XX Mature BDNF proteins isolated from pig brain are given in AAB76813-15.

CC They are used to isolate nucleic acids encoding BDNF and to develop

CC antibodies and other prods. useful in the diagnosis and treatment of

CC neurological disorders.

XX Sequence 119 AA:

Query Match 97.3%; Score 622.5; DB 16; Length 119;
Best Local Similarity 99.2%; Pred. No. 7,8e-61;
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARRGELSYVCDISSEVNTADKKTAVDMSGCTVLEKVPVSKGOLKQYFETKCNP 61

DB 1 HSDPARRGELSYVCDISSEVNTADKKTAVDMSGCTVLEKVPVSKGOLKQYFETKCNP 60

OY 62 MGYTKEGCGIDKRHMNSOCRTTOSYVRLTMDSKKRIGMRIRIDTSCV-TLTIKRGR 119

DB 61 MGYTKEGCGIDKRHMNSOCRTTOSYVRLTMDSKKRIGMRIRIDTSCV-TLTIKRGR 119

RESULT 5

AAB35945
ID AAB35945 standard; Protein: 119 AA.

AC AAB35945;

DT 26-FEB-2001 (first entry)

DE BDNF amino acid sequence.

KM Heparin binding; vascular graft; matrix; cell adhesion; growth factor;

KM wound healing; dermal wound; wound healing; BDNF.

OS Unidentified.

PN WO20064481-A1.

PD 02-NOV-2000.

PF 22-APR-1999; 99WO-1B00800.

PR 22-APR-1999; 99WO-1B00800.

PA (ETH2-) ETH ZURICH & UNIV ZURICH.

PI Sakiyama SE, Hubbard JA;

DR WPI; 2001-024627/03.

XX Matrix for controlled release of growth factor for wound healing, has

XX substrate that attaches heparin binding peptide, protein growth factor

XX that bind heparin with low affinity, and heparin or heparin-like

XX polymer

PS Example 5; Page 21; 48pp; English.

XX This invention relates to a matrix comprising a substrate capable of

XX providing attachment of a heparin binding peptide (HBP), a peptide

XX comprising a binding domain which binds heparin with high affinity,

XX heparin or heparin-like polymer, and a protein growth factor or peptide

XX fragment which has a domain that binds heparin with low affinity.

XX which is capable of supporting cell adhesion. The matrix is used for

XX delivering low heparin binding affinity growth factor proteins or

XX peptides in a controlled manner suitable for wound healing, and in an

XX can be used in an article for treating dermal wounds, and in an

XX implantable sterilized composition capable of supporting cell adhesion.

XX The present sequence represents a growth factor protein. The protein is

XX used in an example illustrating that non-heparin binding growth factors

XX can be released in a controlled manner from heparin-based drug delivery

XX systems based on their low affinity for heparin.

Sequence 119 AA:

Query Match 97.3%; Score 622.5; DB 22; Length 119;
Best Local Similarity 99.2%; Pred. No. 7,8e-61;
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARRGELSYVCDISSEVNTADKKTAVDMSGCTVLEKVPVSKGOLKQYFETKCNP 61

DB 1 HSDPARRGELSYVCDISSEVNTADKKTAVDMSGCTVLEKVPVSKGOLKQYFETKCNP 60

OY 62 MGYTKEGCGIDKRHMNSOCRTTOSYVRLTMDSKKRIGMRIRIDTSCV-TLTIKRGR 119

DB 61 MGYTKEGCGIDKRHMNSOCRTTOSYVRLTMDSKKRIGMRIRIDTSCV-TLTIKRGR 119

D6 61 MGYTEKCGCIGIDKRRHNSOCRTTOSYVALTMDSKRRIGMRFIRIDTSCVCTLTIRKGR 119

RESULT 6

AAW25676
ID AAW25676 standard; protein: 120 AA.

XX
XX AAW25676;

DT 18-NOV-1997 (first entry)

XX Human BDNF recombinantly produced by E. coli.

XX Human; brain derived neurotrophic factor; BDNF; E. coli; epilepsy;

XX neuroplasticity; adult brain; epileptic seizure.

XX Homo sapiens.

XX MO9703689-A1.

XX 06-FEB-1997.

XX 08-JUL-1996; 96MO-US11488.

XX 14-JUL-1995; 95US-0502348.

XX (AMGE-) AMGEN INC.

XX (COLD-) COLD SPRING HARBOR LAB.

XX (UPPA-) UNIT PASTEUR LOUIS.

XX Caronahan JF, Depaulis A, Felte P, Larnet Y, Marescaux C;

XX Nava H;

XX MPI: 1997-13374/12.

XX Treatment of epilepsy in a mammal - by administration of

XX brain-derived neurotrophic factor

XX Claim 5; Page 12; 22pp; English.

XX This sequence represents recombinant human brain derived neurotrophic

XX factor (BDNF) which has been produced in E. coli. BDNF may be used

XX to treat epilepsy in mammals. The BDNF has a protective role in the

XX regulation of neuroplasticity in the adult brain and blocks the

XX development of epileptic seizures. The BDNF is preferably administered

XX in an amount of 0.02-0.25 g/kg/day by intraparenchymal or

XX intraventricular injection.

XX Sequence 120 AA;

XX Query Match 97.3%; Score 622.5; DB 18; Length 120;

XX Best Local Similarity 99.2%; Pred. No. 7.9e-61;

XX Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

XX 2 HSDPARRGELSYVCDISSEVYTAADKRTAVDMSCGTVYLEKVPYSGQLQYETETKCP 61

XX 2 HSDPARRGELSYVCDISSEVYTAADKRTAVDMSCGTVYLEKVPYSGQLQYETETKCP 61

XX 62 MGYTEKCGCIGIDKRRHNSOCRTTOSYVALTMDSKRRIGMRFIRIDTSCVCTLTIRKGR 119

XX 62 MGYTEKCGCIGIDKRRHNSOCRTTOSYVALTMDSKRRIGMRFIRIDTSCVCTLTIRKGR 120

XX DB 62 MGYTEKCGCIGIDKRRHNSOCRTTOSYVALTMDSKRRIGMRFIRIDTSCVCTLTIRKGR 120

XX RESULT 7

XX AAR71614

XX AAR71614 standard; protein: 142 AA.

XX AC AAR71614;

XX XX 27-OCT-1995 (first entry)

XX BDNF.

XX XX

KW Primer: polymerase chain reaction; amplify; PCR;

KW brain-derived neurotrophic factor; BDNF; E. coli; signal sequence;

KW transformation; dorsal root ganglia; chick embryo.

XX Synthetic.

XX JP07023788-A.

XX 27-JAN-1995.

XX 05-JUL-1993; 93JP-0190937.

XX 05-JUL-1993; 93JP-0190937.

XX (HITA) HITACHI LTD.

XX MPI: 1995-100949/14.

XX N-PSDB; NA085598.

XX Vector encoding Brain-derived neurotrophic factor - for the

XX effective production of BDNF by recombinant E. coli

XX Claim 7; Page 2; 9pp; Japanese.

XX This sequence represents brain-derived neurotrophic factor (BDNF). The

XX coding sequence was amplified using the primers given in NA085598-97

XX which were also used to link the amplified sequence to an E.coli

XX signal sequence and further E.coli sequences which control gene

XX expression. The recombinant sequences were used to transform E.coli

XX for the large scale production of BDNF. The biological activity of

XX the isolated BDNF was evaluated using dorsal root ganglia of an 8 day

XX chick embryo.

XX Sequence 142 AA;

XX Query Match 97.3%; Score 622.5; DB 16; Length 142;

XX Best Local Similarity 99.2%; Pred. No. 9.7e-61;

XX Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

XX 2 HSDPARRGELSYVCDISSEVYTAADKRTAVDMSCGTVYLEKVPYSGQLQYETETKCP 61

XX 24 HSDPARRGELSYVCDISSEVYTAADKRTAVDMSCGTVYLEKVPYSGQLQYETETKCP 83

XX 62 MGYTEKCGCIGIDKRRHNSOCRTTOSYVALTMDSKRRIGMRFIRIDTSCVCTLTIRKGR 119

XX 84 MGYTEKCGCIGIDKRRHNSOCRTTOSYVALTMDSKRRIGMRFIRIDTSCVCTLTIRKGR 142

XX DB 84 MGYTEKCGCIGIDKRRHNSOCRTTOSYVALTMDSKRRIGMRFIRIDTSCVCTLTIRKGR 142

XX RESULT 8

XX AAR11364

XX AAR11364 standard; protein: 247 AA.

XX AC AAR11364;

XX XX 31-MAY-1991 (first entry)

XX Human prepro-Brain Derived Neurotrophic Factor.

XX BDNF; Parkinson's disease; Huntington's Chorea; Alzheimer's Disease;

XX neuroblastoma; Parkinson-Plus Syndrome.

XX Homo sapiens.

XX Key

XX Protein

XX Peptide

XX W09103568-A.

XX 21-MAR-1991.

XX Location/Qualifiers

XX 129..247

XX /label= mature human BDNF

XX 1..128

XX /label= pre-pro-sequence

PF 29-AUG-1990; 90MO-US04915.
 XX 20-AUG-1990; 90US-0570557.
 PR 30-AUG-1989; 89US-0400591.
 XX (PLAC) MAX PLANCK GES WISSENSCH.
 PA (REGE-) REGENERON PHARM INC.
 XX Hyman C, Alderson R, Yancopoulos G, Barde YA, Thoenen HE;
 PI Hom A, Lottspeltch F, Lindsay RM;
 DR WPI: 1991-102083/14.
 N-PSDB: AAQ11204.
 XX Brain derived neurotrophic factor and DNA encoding it - for
 PT diagnosis and treatment of neurological disorders, eg
 PR Parkinson's disease and retinal degeneration
 XX Claim 25: Page 154; 229pp; English.
 XX A portion of the coding sequence for mature human BDNF was
 CC amplified by PCR and the sequence determined. The deduced amino
 CC acid sequence for the region of at least amino acids 28 to 111 was
 CC identical to that of porcine BDNF. The BDNF can be used to sustain
 CC the survival of dopaminergic and cholinergic neurons of the CNS, to
 CC suppress the proliferation of astroglial cells, to inhibit the uptake
 CC of GABA into neurons and to upregulate the expression of NGF receptor
 CC on the cell surface.
 CC See also AAQ11203, AAQ11205-6 and AAQ11604.
 XX SQ Sequence 247 AA;
 Query Match 97.3%; Score 622.5; DB 12; Length 247;
 Best Local Similarity 99.2%; Pred. No. 1.9e-60;
 Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 OY 2 HSDPARRGELSYCDISSEWYTAADKKTAVDMSGTIVLEKVPVSKGOLKQYFETKCNP 61
 DB 129 HSDPARRGELSYCDISSEWYTAADKKTAVDMSGTIVLEKVPVSKGOLKQYFETKCNP 188
 OY 62 MGYTEGCGIDKRRHNSOCRTQSYVRALTMDSKKRIGMFRIDTSCV-TLTIRGR 119
 DB 189 MGYTEGCGIDKRRHNSOCRTQSYVRALTMDSKKRIGMFRIDTSCV-TLTIRGR 247
 RESULT 9
 AAR37798
 ID AAR37798 standard; Protein: 247 AA.
 AC AAR37798;
 XX 29-SEP-1993 (first entry)
 DT 29-SEP-1993 (first entry)
 DE Human BDNF.
 XX Chimeric; human; prepro; NGF; brain-derived neurotrophic factor;
 KM BDNF; chimeric; fusion; mouse; nerve growth factor.
 XX Homo sapiens.
 OS Homo sapiens.
 FH Key
 FT Region
 FT 1..128
 FT /note- "Prepro region"
 FT 129..247
 FT Protein
 FT /note- "Mature BDNF"
 XX MO9310150-A.
 XX 27-MAY-1993.
 XX 13-NOV-1992; 92MO-US09792.
 XX 14-NOV-1991; 91US-0792492.

XX (AMGE-) AMGEN.
 PA (REGE-) REGENERON PHARM INC.
 XX Giles D, Hu SS, Ip N, Squinto SP, Yancopoulos GD;
 PI WPI: 1993-182492/22.
 DR N-PSDB: AAQ42570.
 XX Eukaryotic expression of neurotrophins - using prepro region of a
 PT different neurotrophin for more efficient post-translational
 PR processing
 XX Disclosure; Fig 3; 80pp; English.
 XX This sequence represents human brain-derived neurotrophic factor
 CC (BDNF). The protein encoded by this sequence promotes the survival
 CC of dorsal root ganglions. BDNF is a highly basic protein (isoelectric
 CC point, pI 10.1) which has a molecular weight of 12.3 kD. These
 CC characteristics are very similar to the nerve growth factor (NGF).
 CC The cDNA encoding this protein may be used in the construction of a
 CC chimeric nucleic acid molecule to encode a preproBNF/BDNF chimera
 CC (see also AAQ42568-69).
 XX SQ Sequence 247 AA;
 Query Match 97.3%; Score 622.5; DB 14; Length 247;
 Best Local Similarity 99.2%; Pred. No. 1.9e-60;
 Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 OY 2 HSDPARRGELSYCDISSEWYTAADKKTAVDMSGTIVLEKVPVSKGOLKQYFETKCNP 61
 DB 129 HSDPARRGELSYCDISSEWYTAADKKTAVDMSGTIVLEKVPVSKGOLKQYFETKCNP 188
 OY 62 MGYTEGCGIDKRRHNSOCRTQSYVRALTMDSKKRIGMFRIDTSCV-TLTIRGR 119
 DB 189 MGYTEGCGIDKRRHNSOCRTQSYVRALTMDSKKRIGMFRIDTSCV-TLTIRGR 247
 RESULT 10
 AAR44917
 ID AAR44917 standard; Protein: 247 AA.
 AC AAR44917;
 XX 18-OCT-1994 (first entry)
 DT 18-OCT-1994 (first entry)
 DE Human BDNF.
 XX BDNF; brain derived nerve factor; promotor; expression; vector.
 KM BDNF; brain derived nerve factor; promotor; expression; vector.
 XX Homo sapiens.
 OS Homo sapiens.
 XX JP05317049-A.
 XX 03-DEC-1993.
 PD 03-DEC-1993.
 XX 01-JUN-1992; 92JP-0140570.
 PF 01-JUN-1992; 92JP-0140570.
 XX 31-MAY-1991; 91JP-0129666.
 PR 31-MAY-1991; 91JP-0129666.
 XX (TAKE) TAKEDA CHEM IND LTD.
 XX WPI: 1994-011018/02.
 DR N-PSDB: AA054374.
 XX Expression promoter contg. 142 specified bases - is used in
 PT prepn. of diseased model animal and drug screening system
 XX Claim 1; Fig 1; 15pp; Japanese.
 XX The sequence (AA054374) encodes a human brain derived nerve nutrient
 CC factor. This is also transformed into a bacterium using the vector

CC shown in sequence (AA054375). The factor can be used for the
 CC preparation of animal models of diseases and their treatment as
 CC well as establishing a drug screening system.

XX Sequence 247 AA:

Query Match 97.3% Score 622.5; DB 15; Length 247;
 Best Local Similarity 99.2% Pred. No. 1.9e-60;
 Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARRELSTVCSISISMTAAADKTAVDMSGGTIVLEKVPVSKGOLKQFYETKCNP 61
 DB 129 HSDPARRELSTVCSISISMTAAADKTAVDMSGGTIVLEKVPVSKGOLKQFYETKCNP 188
 OY 62 MGYTEGCGIDKRRHNSOCRTTOSYVRLTMDSKKRIGRFRIDTSCV-TLTIRGR 119
 DB 189 MGYTEGCGIDKRRHNSOCRTTOSYVRLTMDSKKRIGRFRIDTSCVTLTIRGR 247

RESULT 11

AA076817
 ID AA076817 standard; Protein: 247 AA.

XX AA076817:
 AC 07-DEC-1995 (first entry)
 XX
 DE Human prepro-BDNF.
 XX
 KW Brain derived neurotrophic factor: BDNF; neuron; Alzheimer's disease;
 KW trauma; Parkinson's disease.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FT Active-site 1..128
 FT /label= prepro-peptide
 XX
 FT US438121-A.

XX 01-AUG-1995.
 PD
 XX 30-AUG-1989; 89US-0400591.

XX 25-APR-1991; 91US-0691612.
 PR 30-AUG-1989; 89US-0400591.
 PR 20-AUG-1990; 90US-0570657.

XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 PA (REG-) REGENERON PHARM INC.

XX Barde Y, Edgar D, Leibrock J, Lottspeich F, Thoenen H;
 PI Yancopoulos G;

XX WPI: 1995-274920/36.
 DR N-PSDB: AA093135.

XX New brain derived neurotrophic factor proteins sustain survival of CNS
 PT dopaminergic and cholinergic neurons - used in the diagnosis and
 PT treatment of neurological disorders, eg. trauma, Alzheimer's disease,
 PT etc.

XX Disclosure: Fig. 4B-H; 100pp; English.

XX An adult human retina cDNA library was screened using a probe
 CC based on pig BDNF to obtain a clone, pBDNF-C-1, that encoded
 CC prepro-BDNF.

XX Sequence 247 AA:

Query Match 97.3% Score 622.5; DB 16; Length 247;
 Best Local Similarity 99.2% Pred. No. 1.9e-60;
 Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARRELSTVCSISISMTAAADKTAVDMSGGTIVLEKVPVSKGOLKQFYETKCNP 61

DB 129 HSDPARRELSTVCSISISMTAAADKTAVDMSGGTIVLEKVPVSKGOLKQFYETKCNP 188

OY 62 MGYTEGCGIDKRRHNSOCRTTOSYVRLTMDSKKRIGRFRIDTSCV-TLTIRGR 119

DB 189 MGYTEGCGIDKRRHNSOCRTTOSYVRLTMDSKKRIGRFRIDTSCVTLTIRGR 247

RESULT 12

AA076238
 ID AA076238 standard; Protein: 247 AA.

XX AA076238:
 AC 16-MAR-1998 (first entry)
 XX
 DE Human preproBDNF.
 XX
 KW Fusion protein: hydrophilic spacer; recombinant; expression system;
 KW carboxypeptidase; preproNGF.
 XX
 OS Homo sapiens.

XX W09728272-A1.
 FN
 XX 07-AUG-1997.

XX 31-JAN-1997; 97MO-US01470.
 PF
 XX 31-JAN-1996; 96US-0595043.

XX (TECH-) TECHNOLOGENE INC.
 PA Sgarlato GD;

XX WPI: 1997-402624/37.
 DR N-PSDB: AAT80163.

XX Recombinant protein expression system for fusion protein production
 PT - useful for high quantity production of authentic recombinant
 PT proteins

XX Example 6; Page 142-143; 194pp; English.

XX A novel recombinant vector has been developed which comprises a
 CC nucleotide sequence encoding a fusion protein. The fusion protein
 CC comprises three domains joined together in order, from N-terminus to
 CC C-terminus, of a first domain comprising a protein of interest, a second
 CC domain comprising a hydrophilic spacer and an affinity domain, each
 CC domain comprising amino acid residues. The present sequence represents
 CC human preproBDNF, used in example 6 of the present invention. The
 CC recombinant vector is used for the production of authentic recombinant
 CC proteins of interest. The method of the invention is useful for the
 CC expression of fusion proteins capable of isolation by affinity
 CC chromatography in pro- or eukaryotic cells. This method allows
 CC for the efficient cleavage and generation of authentic proteins of
 CC interest that do not contain extraneous (i.e. non-naturally occurring)
 CC amino acids.

XX Sequence 247 AA:

Query Match 97.3% Score 622.5; DB 18; Length 247;
 Best Local Similarity 99.2% Pred. No. 1.9e-60;
 Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARRELSTVCSISISMTAAADKTAVDMSGGTIVLEKVPVSKGOLKQFYETKCNP 61

DB 129 HSDPARRELSTVCSISISMTAAADKTAVDMSGGTIVLEKVPVSKGOLKQFYETKCNP 188

OY 62 MGYTEGCGIDKRRHNSOCRTTOSYVRLTMDSKKRIGRFRIDTSCV-TLTIRGR 119

Db 189 MGTYREGCGIDKRMHNSCRRTOSTYVRLTMDSKKRIGMRFIRIDTSCVCTLTIRGR 247

RESULT 13
AAM50846
ID AAM50846 standard; Protein: 247 AA.
XX
XX AAM50846;
XX
XX 01-MAY-2002 (first entry)
XX
XX Human recombinant brain-derived growth factor.
XX
XX Brain-derived growth factor: BDNF; human; neurotrophic factor; NTF;
XX Huntington's disease; Parkinson's disease; Alzheimer's disease;
XX amyotrophic lateral sclerosis; neurodegenerative disease; cancer;
XX neuroprotective; nootropic; anticonvulsant; antiparkinsonian;
XX cytoskeletal; therapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..18
XX /label= Signal_peptide
XX Peptide 19..128
XX /label= Propeptide
XX Protein 129..247
XX /label= Mature_protein
XX Disulfide-bond 141..208
XX Disulfide-bond 186..237
XX Disulfide-bond 196..237
XX Disulfide-bond 196..239
XX Misc-difference 66
XX /note= "may be replaced by Met"
XX
XX W020202071-A2.
XX
XX 10-JAN-2002.
XX
XX 05-JUL-2001: 2001MO-US21472.
XX
XX 05-JUL-2000: 2000US-215778P.
XX
XX (PANG-) PANGENE CORP.
XX
XX Bates AT:
XX
XX WPI: 2002-179638/23.
XX
XX Screening for a neurotrophic factor mimetic, useful for treating, e.g.,
XX cancer and Alzheimer's, comprises combining a candidate mimetic with a
XX fragment of a tyrosine kinase protein -
XX
XX Disclosure: Fig 6: 107pp: English.
XX
XX The present sequence is that of human recombinant brain-derived
XX growth factor (BDNF), a neurotrophic factor (NTF) that binds to TrkB
XX receptor tyrosine kinase. The invention concerns Trks and their
XX ligands that modulate cell growth, differentiation and survival.
XX Trk proteins are known to mediate the activities of neurotrophins
XX and are also known proto-oncogenes. Methods are claimed for screening
XX for small molecule NTF mimetics, such as the cyclic peptide given
XX in AAM50844, capable of binding to a Trk protein or of modulating
XX the binding of a neurotrophin to a Trk protein. Also claimed are
XX medicaments comprising a small molecule NTF mimetic and their use
XX in claimed methods for treatment of cancer or a neurodegenerative
XX disease selected from Huntington's disease, Parkinson's disease,
XX Alzheimer's disease and amyotrophic lateral sclerosis.
XX
XX Sequence 247 AA:
XX
Query Match 97.3%; Score 622.5; DB 23; Length 247;
Best Local Similarity 99.2%; Pred. No. 1,9e-60;

Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARRGELSYCDSISPMYTAADKTAADMSSGTYVLEKRVNSGOLKQFYETKCP 61
DB 129 HSDPARRGELSYCDSISPMYTAADKTAADMSSGTYVLEKRVNSGOLKQFYETKCP 108
OY 62 MGTYREGCGIDKRMHNSCRRTOSTYVRLTMDSKKRIGMRFIRIDTSCV-TLTIRGR 119
DB 189 MGTYREGCGIDKRMHNSCRRTOSTYVRLTMDSKKRIGMRFIRIDTSCVCTLTIRGR 247

RESULT 14
AAR11365
ID AAR11365 standard; Protein: 249 AA.
XX
XX AAR11365;
XX
XX 31-MAY-1991 (first entry)
XX
XX Rat prepro-Brain Derived Neurotrophic Factor.
XX
XX BDNF; Parkinson's disease; Huntington's Chorea; Alzheimer's Disease;
XX neuroblastoma; Parkinson-Plus Syndrome.
XX
XX Rattus rattus.
XX
XX Key Location/Qualifiers
XX Protein 131..249
XX /label= mature rat BDNF
XX Peptide 1..130
XX /label= pre-pro-sequence
XX
XX W09103568-A.
XX
XX 21-MAR-1991.
XX
XX 29-AUG-1990: 90MO-US04915.
XX
XX 20-AUG-1990: 90US-0570657.
XX 30-AUG-1989: 89US-0400591.
XX
XX (PLAC) MAX PLANCK GES WISSENSCH.
XX (REG-) REGENERON PHARM INC.
XX
XX Hyman C, Alderson R, Yancopoulos G, Barde YA, Thoenen HFE;
XX Hohn A, Lottspeich F, Lindsay RM;
XX
XX WPI: 1991-102083/14.
XX N-PSDB: AAQ11205.
XX
XX Brain derived neurotrophic factor and DNA encoding it - for
XX diagnosis and treatment of neurological disorders, eg
XX Parkinson's disease and retinal degeneration
XX
XX Claim 30; Page 155; 229pp: English.
XX
XX A portion of the coding sequence for mature rat BDNF was
XX amplified by PCR and the sequence determined. The sequence contains
XX a number of conservative changes from the porcine BDNF gene
XX although the deduced amino acid sequence for the region of at least
XX amino acids 28 to 111 was identical to that of porcine BDNF.
XX The BDNF can be used to sustain the survival of dopaminergic and
XX cholinergic neurons of the CNS, to suppress the proliferation of
XX astroglial cells, to inhibit the uptake of GABA into neurons and to
XX upregulate the expression of NGF receptor on the cell surface.
XX See also AAQ11205-4, AAQ11206 and AAQ11604.
XX
XX Sequence 249 AA:
XX
Query Match 97.3%; Score 622.5; DB 12; Length 249;
Best Local Similarity 99.2%; Pred. No. 2e-60;
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARGELSVCDISEMYTADKKTAVDMSCGTVTLEKVPVSKGOLKQYFETKCNP 61
DB 131 HSDPARRELSVCDISEMYTADKKTAVDMSCGTVTLEKVPVSKGOLKQYFETKCNP 190
OY 62 MGYTKEGCGRIDKRRHNSOCRTTOSYVRALTNDSKKRIGRFRIRIDTSCVCTLTIRGR 119
DB 191 MGYTKEGCGRIDKRRHNSOCRTTOSYVRALTNDSKKRIGRFRIRIDTSCVCTLTIRGR 249

RESULT 15

AB857117
ID AB857117 standard; Protein: 249 AA.

XX
AC AB857117;

XX
DT 07-MAR-2002 (first entry)

XX
DE Mouse ischemic condition related protein sequence SEQ ID NO:266.

XX
KW Mouse; ischemia; compressive ischemia; occlusive ischemia;
XX vasospastic ischemia; ischemic condition; ischemic disease.

XX
OS Mus musculus.

XX
PN W0200188188-A2.

XX
PD 22-NOV-2001.

XX
PF 18-MAY-2001; 2001MO-JP04192.

XX
PR 18-MAY-2000; 2000JP-0145977.

XX
PA (UYN1-) UNIV NINON SCHOOL JURIDICAL PERSON.

XX
PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;

XX
DR MPI: 2002-034733/04.

XX
DR N-PSDB: AB199369.

XX
PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
XX expression levels of particular genes defined in the specification or
XX by determining the expression profile of a gene group comprising these
XX genes -

XX
PS Claim 2: Page 748-749; 2690pp: English.

XX
CC The present invention describes a method for examining ischemic
XX conditions, comprising measuring the expression levels of particular
XX genes (1) in a test sample or determining the expression profile of a
XX gene group in the sample comprising genes selected from (1). The method
XX is useful for examining the ischemic condition (e.g. compressive
XX ischemia, occlusive ischemia or vasospastic ischemia) by measuring
XX expression levels of particular genes (AB199202 to AB199912, encoding
XX the protein sequences in AB857020 to AB857374) or by determining the
XX expression profile of a gene group comprising these genes. The
XX expression levels or expression profiles produced by these genes are
XX used as an indicator when screening for ischemic condition-improving
XX drugs or therapeutics for ischemic diseases. AB199913 and AB199914
XX represent PCR primers for a mouse ischemic disease related sequence,
XX which are used in the exemplification of the present invention.

XX
SO Sequence 249 AA;

Query Match 97.3%; Score 622.5; DB 23; Length 249;
Best Local Similarity 99.2%; Pred. No. 2e-60; 0; Indels 1; Gaps 1;

Matches 118; Conservative 0; Mismatches 0;

OY 2 HSDPARGELSVCDISEMYTADKKTAVDMSCGTVTLEKVPVSKGOLKQYFETKCNP 61
DB 131 HSDPARRELSVCDISEMYTADKKTAVDMSCGTVTLEKVPVSKGOLKQYFETKCNP 190
OY 62 MGYTKEGCGRIDKRRHNSOCRTTOSYVRALTNDSKKRIGRFRIRIDTSCVCTLTIRGR 119
DB 191 MGYTKEGCGRIDKRRHNSOCRTTOSYVRALTNDSKKRIGRFRIRIDTSCVCTLTIRGR 249

DB 191 MGYTKEGCGRIDKRRHNSOCRTTOSYVRALTNDSKKRIGRFRIRIDTSCVCTLTIRGR 249

Search completed: December 2, 2002, 15:08:39
Job time : 24.7163 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 2, 2002, 15:05:43 ; Search time 9.48652 Seconds
(without alignments)
1205.921 Million cell updates/sec

Title: US-10-072-681-4

Sequence: 1 PHSDPARRGELSYVCSIDSEM.....GWRFRIDTSCVTITIKRGR 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: PIR_73:.*
2: PIR1:.*
3: PIR2:.*
4: PIR3:.*
5: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	622.5	97.3	247	2 A40304	brain-derived neur
2	622.5	97.3	249	2 S12555	brain-derived neur
3	622.5	97.3	249	2 B40304	brain-derived neur
4	622.5	97.3	252	2 A30361	brain-derived neur
5	613.5	95.9	248	2 UC6183	brain-derived neur
6	594	92.8	114	2 I84765	brain-derived neur
7	570.5	89.1	269	2 I51708	brain-derived neur
8	564	88.1	114	2 I50606	brain-derived neur
9	559	87.3	114	2 I51599	brain-derived neur
10	375.5	58.7	236	2 JH0400	neurotrophin-4 pre
11	344.5	53.8	257	2 C40304	neurotrophin-3 pre
12	344.5	53.8	257	2 S09155	neurotrophin-3 pre
13	344.5	53.8	258	2 A35781	neurotrophin-3 pre
14	344.5	53.8	258	2 S09155	neurotrophin-3 pre
15	336.5	52.6	209	2 B42687	hippocampus-derive
16	332.5	52.0	210	2 A42687	neurotrophin-4 pre
17	317	49.5	229	2 I46614	neurotrophin-4 pre
18	317	49.5	229	2 I46614	neurotrophin-4 pre
19	313	48.9	243	2 A26311	nerve growth facto
20	311.5	48.7	125	2 A26312	nerve growth facto
21	310	48.4	303	1 NGRHUB	nerve growth facto
22	308.5	48.2	235	2 S14881	nerve growth facto
23	308.5	48.2	235	2 S14881	nerve growth facto
24	308.5	48.2	235	2 S14881	nerve growth facto
25	306.5	47.9	307	1 NGMSMG	nerve growth facto
26	301.5	47.1	241	2 J10097	nerve growth facto
27	300.5	47.0	243	2 S28161	nerve growth facto
28	298	46.6	116	1 NGMXXI	nerve growth facto
29	295.5	46.2	116	2 A58566	nerve growth facto

30	295.5	46.2	246	2 A59218	nerve growth facto
31	254	39.7	286	2 S50855	neurotrophin-6 - 8
32	253.5	39.6	194	2 I51709	nerve growth facto
33	74	11.6	796	2 H82406	probable lipase VC
34	69.5	10.9	184	2 G83591	hypothetical prote
35	69	10.8	476	2 T79463	hypothetical prote
36	69	10.8	481	2 H75198	hypothetical prote
37	69	10.8	1006	2 T13331	probable tail prot
38	68	10.6	195	2 S77401	hypothetical prote
39	68	10.6	245	1 PSHUAM	14-3-3 protein zet
40	68	10.6	245	2 A47389	14-3-3 protein zet
41	68	10.6	245	2 S65013	14-3-3 protein zet
42	68	10.6	294	2 T34189	hypothetical prote
43	68	10.6	347	2 S60428	hypothetical prote
44	68	10.6	479	2 A97027	hydrolyase of alpha
45	67.5	10.5	1039	2 C87083	C-term 19ey1-cRNA

ALIGNMENTS

RESULT 1

A40304
brain-derived neurotrophic factor precursor - human
C:Species: Homo sapiens (man)
C:Date: 03-Apr-1992 #sequence, revision 30-Sep-1993 #text change 21-Jul-2000
C:Accession: B36208; A60536; A40304; A37218; A61115; I38072
R:Jones, R.R.; Reichardt, L.F.
Proc. Natl. Acad. Sci. U.S.A. 87, 8060-8064, 1990
A:Title: Molecular cloning of a human gene that is a member of the nerve growth facto
A:Reference number: A36208; MUID:91045537; PMID:2236018
A:Accession: B36208
A:Molecule type: DNA
A:Residues: 1-247 <CON>
A:Cross-references: GB:M3762; MID:q179402; PIDN:AAA51820.1; PID:q179403
R:Panopoulos, G.D.; Malsompliere, P.C.; IP, N.Y.; Aldrich, T.H.; Belluscio, L.; Boul
Cold Spring Harb. Symp. Quant. Biol. 55, 371-379, 1990
A:Title: Neurotrophic factors, their receptors, and the signal transduction pathways
A:Reference number: A60536; MUID:9211157; PMID:1966766
A:Accession: A60536
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-65, 'M', 67-247 <YAN>
R:Malsompliere, P.C.; Le Beau, M.N.; Espinosa III, R.; IP, N.Y.; Belluscio, L.; de la
Genomics 10, 558-568, 1991
A:Title: Human and rat brain-derived neurotrophic factor and neurotrophin-3: gene str
A:Reference number: A40304; MUID:91365361; PMID:189806
A:Accession: A40304
A:Molecule type: mRNA
A:Residues: 1-247 <MAN>
A:Cross-references: GB:M61176; MID:q179404; PIDN:AAA69805.1; PID:9896463
M:NOTE: the sequence in Genbank entry HUMBNFB, release 106.0, (PID:9896463) begins c
R:Ramamoji, H.; Gurney, M.E.
J. Neurosci. 10, 3469-3478, 1990
A:Title: Human platelets contain brain-derived neurotrophic factor.
A:Reference number: A37218; MUID:91038253; PMID:2230938
A:Accession: A37218
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 138-236 <YAN>
R:Rosenthal, A.; Goeddel, D.V.; Nguyen, T.; Martin, E.; Burton, L.E.; Shih, A.; Laram
Endocrinology 129, 1289-1294, 1991
A:Title: Primary structure and biological activity of human brain-derived neurotroph
A:Reference number: A61115; MUID:91339743; PMID:1874171
A:Accession: A61115
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-65, 'M', 67-247 <ROS>
R:Shinmura, A.; Ono, Y.; Kaisho, Y.; Igarashi, K.
Biochem. Biophys. Res. Commun. 187, 325-332, 1992
A:Title: Characterization of the 5'-flanking region of the human brain-derived neuro
A:Reference number: I38072; MUID:92118032; PMID:1339267
A:Accession: I38072

A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-247 <SH1>
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 03-Apr-1992 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
 A:Cross-references: EMBL:X60201; NID:g9328269; PIDN:CAA4761.1; PID:g496626
 A:Notes: the authors do not discuss this mRNA sequence in this reference; attribution 18
 C:Genetics:
 A:Gene: GDB:BNF
 A:Cross-references: GDB:125916; OMIM:113505
 A:Map position: 11p13-11p13
 A:Superfamily: nerve growth factor beta chain
 C:Keywords: dimer; glycoprotein
 F:1-6/Domain: signal sequence #status predicted <SIG>
 F:17-128/Domain: propeptide #status predicted <PRO>
 F:129-247/Product: brain-derived neurotrophic factor #status predicted <MAT>
 F:121/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 97.3% Score 622.5; DB 2; Length 249;
 Best Local Similarity 99.2% Pred. No. 1,1e-56;
 Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARRGELSYCDISSEWYTAADKTAVDMSGTYVLEKYPVSKGOLKQFYETKCNP 61
 DB 129 HSDPARRGELSYCDISSEWYTAADKTAVDMSGTYVLEKYPVSKGOLKQFYETKCNP 188
 OY 62 MGYTEGCGIDKRRHNSOCRTTOSYVRALTMDSKRRIGRFIRIDTSCV-TLTIKRR 119
 DB 189 MGYTEGCGIDKRRHNSOCRTTOSYVRALTMDSKRRIGRFIRIDTSCVTLTIKRR 247

RESULT 2

S12555 brain-derived neurotrophic factor - mouse

N:Alternate names: BDNF protein
 C:Species: Mus musculus (house mouse)
 C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
 C:Accession: S12555; S51180; S51181
 R:Hofer, M.; Pegliusi, S. R.; Kohn, A.; Lebrock, J.; Barde, Y. A.
 EMBD J. 9, 2459-2464, 1990
 A:Title: Regional distribution of brain-derived neurotrophic factor mRNA in the adult mouse
 A:Reference number: S12555; MUID:90316101; PMID:2369858
 A:Accession: S12555
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-249 <HOF>
 A:Cross-references: GB:X55573; NID:g287898; PIDN:CAA39159.1; PID:g287899
 R:Kolbeck, R.; Jungbluth, S.; Barde, Y. A.
 Eur. J. Biochem. 225, 995-1003, 1994
 A:Title: Characterisation of neurotrophin dimers and monomers.
 A:Reference number: S51179; MUID:95045576; PMID:7957235
 A:Accession: S51180
 A:Status: preliminary
 A:Molecule type: Protein
 A:Residues: 131-135 <KOL>
 A:Accession: S51181
 A:Status: preliminary
 A:Molecule type: Protein
 A:Residues: 117-121 <KO2>
 C:Superfamily: nerve growth factor beta chain

Query Match 97.3% Score 622.5; DB 2; Length 249;
 Best Local Similarity 99.2% Pred. No. 1,1e-56;
 Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARRGELSYCDISSEWYTAADKTAVDMSGTYVLEKYPVSKGOLKQFYETKCNP 61
 DB 131 HSDPARRGELSYCDISSEWYTAADKTAVDMSGTYVLEKYPVSKGOLKQFYETKCNP 190
 OY 62 MGYTEGCGIDKRRHNSOCRTTOSYVRALTMDSKRRIGRFIRIDTSCV-TLTIKRR 119
 DB 191 MGYTEGCGIDKRRHNSOCRTTOSYVRALTMDSKRRIGRFIRIDTSCVTLTIKRR 249

RESULT 3

B40304 brain-derived neurotrophic factor precursor - rat

C:Species: Rattus norvegicus (Norway rat)
 C>Date: 03-Apr-1992 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
 A:Cross-references: EMBL:X67108; NID:g55820; PIDN:CAA47481.1; PID:g55821
 A:Accession: S24955
 A:Molecule type: mRNA
 A:Residues: 1-249 <MAT>
 A:Status: not compared with conceptual translation
 A:Accession: B60536
 A:Map position: 6p21
 A:Superfamily: nerve growth factor beta chain
 C:Keywords: dimer; glycoprotein
 F:1-6/Domain: signal sequence #status predicted <SIG>
 F:17-128/Domain: propeptide #status predicted <PRO>
 F:129-247/Product: brain-derived neurotrophic factor and neurotrophin-3; gene str
 F:121/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 97.3% Score 622.5; DB 2; Length 249;
 Best Local Similarity 99.2% Pred. No. 1,1e-56;
 Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARRGELSYCDISSEWYTAADKTAVDMSGTYVLEKYPVSKGOLKQFYETKCNP 61
 DB 131 HSDPARRGELSYCDISSEWYTAADKTAVDMSGTYVLEKYPVSKGOLKQFYETKCNP 190
 OY 62 MGYTEGCGIDKRRHNSOCRTTOSYVRALTMDSKRRIGRFIRIDTSCV-TLTIKRR 119
 DB 191 MGYTEGCGIDKRRHNSOCRTTOSYVRALTMDSKRRIGRFIRIDTSCVTLTIKRR 249

RESULT 4

A30361 brain-derived neurotrophic factor precursor - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 16-Jul-1999
 A:Cross-references: EMBL:X67108; NID:g55820; PIDN:CAA47481.1; PID:g55821
 A:Accession: S24955
 A:Molecule type: mRNA
 A:Residues: 1-249 <MAT>
 A:Status: not compared with conceptual translation
 A:Accession: B60536
 A:Map position: 6p21
 A:Superfamily: nerve growth factor beta chain
 C:Keywords: dimer; glycoprotein
 F:1-6/Domain: signal sequence #status predicted <SIG>
 F:17-128/Domain: propeptide #status predicted <PRO>
 F:129-247/Product: brain-derived neurotrophic factor and neurotrophin-3; gene str
 F:121/Binding site: carbohydrate (Asn) (covalent) #status experimental

A:Accession: A30361
A:Molecule type: mRNA
A:Residues: 1-252 <LEI>
A:Cross-references: GB:X16713; NID:q1903; PIDN:CAA34685.1; PID:q1904
C:Superfamily: nerve growth factor beta chain
C:Keywords: glycoprotein; growth factor
F:126/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 97.3%; Score 622.5; DB 2; Length 252;
Best Local Similarity 99.2%; Pred. No. 1.1e-56;
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 HSDPARRGELSYCDISSEMYTAAADKTAADMSGGTVVLEKVPVSKGOLKQYFETKCNP 61
DB 134 HSDPARRGELSYCDISSEMYTAAADKTAADMSGGTVVLEKVPVSKGOLKQYFETKCNP 193
62 MGYTEGCGRIDKRHMNSOCRTTOSYVRLTMDSKKRIGRFIRIDTSCVTLTIKGR 119
DB 194 MGYTEGCGRIDKRHMNSOCRTTOSYVRLTMDSKKRIGRFIRIDTSCVTLTIKGR 252

RESULT 5
JC6183
brain-derived neurotrophic factor precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 20-Jun-2000
C:Accession: JC6183
R:Ratb, S.F.; Kohn, K.; Lachmund, A.; Unsicker, K.; Suter-Crazzolara, C.
Gene 185; 95-98, 1997
A:Title: The gene encoding bovine brain-derived neurotrophic factor (BDNF).
A:Reference number: JC6183; MUID:97186702; PMID:9034318
A:Accession: JC6183
A:Molecule type: mRNA
A:Residues: 1-248 <ARA>
A:Cross-references: EMBL:X97914; NID:q1668709; PIDN:CAA66488.1; PID:q1668710
C:Experimental source: adrenal glands
C:Comment: This factor plays the essential roles in the regulation of neuron survival and dopaminergic, glutamatergic, and cholinergic neurons, and it is effective in the treatment of superfamily: nerve growth factor beta chain
C:Keywords: neurotrophic factor
F:1-16/Domain: signal sequence #status predicted <SIG>
F:1-248/Product: brain-derived neurotrophic factor #status predicted <MNT>
F:198-211/Region: nerve growth factor signature

Query Match 95.9%; Score 613.5; DB 2; Length 248;
Best Local Similarity 97.3%; Pred. No. 9.1e-56;
Matches 116; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 2 HSDPARRGELSYCDISSEMYTAAADKTAADMSGGTVVLEKVPVSKGOLKQYFETKCNP 61
DB 130 HSDPARRGELSYCDISSEMYTAAADKTAADMSGGTVVLEKVPVSKGOLKQYFETKCNP 169
62 MGYTEGCGRIDKRHMNSOCRTTOSYVRLTMDSKKRIGRFIRIDTSCVTLTIKGR 119
DB 190 MGYTEGCGRIDKRHMNSOCRTTOSYVRLTMDSKKRIGRFIRIDTSCVTLTIKGR 248

RESULT 6
184765
brain-derived neurotrophic factor - rhesus macaque (fragment)
C:Species: Macaca mulatta (rhesus macaque)
C:Date: 04-Sep-1997 #sequence_revision 13-Mar-1998 #text_change 16-Jul-1999
C:Accession: 184765
R:Jackson, P.J.; Towne, M.D.; Huntsman, M.M.
FEBS Lett. 285; 260-264, 1991
A:Title: Comparison of mammalian, chicken and Xenopus brain-derived neurotrophic factor
A:Reference number: 150606; MUID:91309745; PMID:1906813
A:Accession: 184765
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-114 <ISA>
A:Cross-references: EMBL:X61475; NID:q288317; PIDN:CAA43703.1; PID:q288318
C:Superfamily: nerve growth factor beta chain

C:Keywords: brain; growth factor

Query Match 92.8%; Score 594; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 4.1e-54;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HSDPARRGELSYCDISSEMYTAAADKTAADMSGGTVVLEKVPVSKGOLKQYFETKCNP 61
DB 2 HSDPARRGELSYCDISSEMYTAAADKTAADMSGGTVVLEKVPVSKGOLKQYFETKCNP 61
62 MGYTEGCGRIDKRHMNSOCRTTOSYVRLTMDSKKRIGRFIRIDTSCV 111
DB 62 MGYTEGCGRIDKRHMNSOCRTTOSYVRLTMDSKKRIGRFIRIDTSCV 111

RESULT 7
151708
brain-derived neurotrophic factor precursor - southern platyfish
C:Species: Xiphophorus maculatus (southern platyfish)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C:Accession: 151708; S26673
R:Gotz, R.; Raulf, F.; Schartl, M.
J. Neurochem. 59; 432-442, 1992
A:Title: Brain-derived neurotrophic factor is more highly conserved in structure and
A:Reference number: 151708; MUID:92333301; PMID:1629719
A:Accession: 151708
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-269 <GOT>
A:Cross-references: EMBL:X59942; NID:q65275; PIDN:CAA2567.1; PID:q65276
C:Genetics:
A:Gene: BDNF
C:Superfamily: nerve growth factor beta chain
C:Keywords: glycoprotein
F:1-18/Domain: signal sequence #status predicted <SIG>
F:1-150/Domain: propeptide #status predicted <PRO>
F:151-269/Product: brain-derived neurotrophic factor #status predicted <MNT>
F:143/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:143-230,208-259,218-261/Disulfide bonds: #status predicted

Query Match 89.1%; Score 570.5; DB 2; Length 269;
Best Local Similarity 89.1%; Pred. No. 2.7e-51;
Matches 106; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

QY 2 HSDPARRGELSYCDISSEMYTAAADKTAADMSGGTVVLEKVPVSKGOLKQYFETKCNP 61
DB 151 HSDPARRGELSYCDISSEMYTAAADKTAADMSGGTVVLEKVPVSKGOLKQYFETKCNP 210
62 MGYTEGCGRIDKRHMNSOCRTTOSYVRLTMDSKKRIGRFIRIDTSCVTLTIKGR 119
DB 211 MGYTEGCGRIDKRHMNSOCRTTOSYVRLTMDSKKRIGRFIRIDTSCVTLTIKGR 269

RESULT 8
150606
brain-derived neurotrophic factor - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C:Accession: 150606
R:Jackson, P.J.; Towne, M.D.; Huntsman, M.M.
FEBS Lett. 285; 260-264, 1991
A:Title: Comparison of mammalian, chicken and Xenopus brain-derived neurotrophic factor
A:Reference number: 150606; MUID:91309745; PMID:1906813
A:Accession: 150606
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-114 <ISA>
A:Cross-references: EMBL:X61476; NID:q288305; PIDN:CAA43704.1; PID:q288306
C:Superfamily: nerve growth factor beta chain

Query Match 88.1%; Score 564; DB 2; Length 114;
Best Local Similarity 93.6%; Pred. No. 5.1e-51;
Matches 103; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 2 HSDPARBELSVCDISEMYTAAADKTAVDMSGCTVLEKVPVSGQLKQYFETKCNP 61
DB 2 HSDPARBELSVCDISEMYTAAADKTAVDMSGCTVLEKVPVSGQLKQYFETKCNP 61
OY 62 MGYTEGCGRIDKRMHNSCCTTOSYVRLATMDSKRIGRFRIRIDTSCV 111
DB 62 MGYTEGCGRIDKRMHNSCCTTOSYVRLATMDSKRIGRFRIRIDTSCV 111

RESULT 9

151599
brain-derived neurotrophic factor - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C>Date: 13-Sep-1996 Sequence_revision 13-Sep-1996 #ext_change 16-Jul-1999
C:Accession: 151599
R:Jackson, P.J.; Townet, M.D.; Huntman, M.M.
FEBS Lett. 285, 260-264, 1991
A:Title: Comparison of mammalian, chicken and xenopus brain-derived neurotrophic factor
A:Reference number: 150606; MUID:91309745; PMID:1306813
A:Accession: 151599
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-114 <ISA>
A:Cross-references: EMBL:X61477; NID:9288363; PIDN:CAA43705.1; PID:9288364
C:Superfamily: nerve growth factor beta chain

Query Match

Best Local Similarity 87.3%; Score 559; DB 2; Length 114;
Matches 102; Conservative 92.7%; Pred. No. 1.7e-50;
Mismatches 3; Indels 0; Gaps 0;

OY 2 HSDPARBELSVCDISEMYTAAADKTAVDMSGCTVLEKVPVSGQLKQYFETKCNP 61
DB 2 HSDPARBELSVCDISEMYTAAADKTAVDMSGCTVLEKVPVSGQLKQYFETKCNP 61
OY 62 MGYTEGCGRIDKRMHNSCCTTOSYVRLATMDSKRIGRFRIRIDTSCV 111
DB 62 MGYTEGCGRIDKRMHNSCCTTOSYVRLATMDSKRIGRFRIRIDTSCV 111

RESULT 10

JH0400
neurotrophin-4 precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #ext_change 16-Jul-1999
C:Accession: JH0400
R:Haliboeck, F.; Ibanez, C.F.; Persson, H.
Neuron 6, 845-858, 1991
A:Title: Evolutionary studies of the nerve growth factor family reveal a novel member at
A:Reference number: JH0400; MUID:9122573; PMID:2025430
A:Accession: JH0400
A:Molecule type: DNA
A:Residues: 1-236 <NAL>
A:Cross-references: GB:230090; NID:9455533; PIDN:CAA82906.1; PID:9455534
C:Comment: This protein belongs to the nerve growth factor family.
C:Superfamily: nerve growth factor beta chain
C:Keywords: glycoprotein
F:1-18/Domain: signal sequence #status predicted <SIG>
F:119-113/Domain: propeptide #status predicted <PRO>
F:114-236/Product: neurotrophin-4 #status predicted <MAT>
F:106/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 58.7%; Score 375.5; DB 2; Length 236;
Best Local Similarity 60.9%; Pred. No. 3.2e-31;
Matches 70; Conservative 18; Mismatches 24; Indels 3; Gaps 2;

OY 6 ARRGELSVCDISEMYTAAADKTAVDMSGCTVLEKVPVSGQLKQYFETKCNP 65
DB 123 SRGELSVCDISEMYTAAADKTAVDMSGCTVLEKVPVSGQLKQYFETKCNP 180
OY 66 KEGCGIDKRMHNSCCTTOSYVRLATMDSKRIGRFRIRIDTSCV-TLIRGR 119
DB 181 TRGCGVDKRMHNSCCTTOSYVRLATMDSKRIGRFRIRIDTSCV-TLIRGR 235

RESULT 11

C40304
neurotrophin-3 precursor - human
N:Alternate names: nerve growth factor 2; NCF-2
C:Species: Homo sapiens (man)
C>Date: 03-Apr-1992 #sequence_revision 30-Sep-1993 #ext_change 16-Jul-1999
C:Accession: A36208; JH0141; C40304; S10719; C60536
R:Jones, K.R.; Reichardt, L.F.
Proc. Natl. Acad. Sci. U.S.A. 87, 8060-8064, 1990
A:Title: Molecular cloning of a human gene that is a member of the nerve growth factor
A:Reference number: A36208; MUID:9104537; PMID:2256018
A:Accession: A36208
A:Molecule type: DNA
A:Residues: 1-257 <JON>
A:Cross-references: GB:M37763; NID:9189300; PIDN:AAA5953.1; PID:9189301
R:Rosenthal, A.; Goeddel, D.V.; Nguyen, T.; Lewis, M.; Shih, A.; Laramée, G.R.; Nikol
Neuron 4, 767-773, 1990
A:Title: Primary structure and biological activity of a novel human neurotrophic fact
A:Reference number: JH0141; MUID:90262727; PMID:2344409
A:Accession: JH0141
A:Molecule type: DNA
A:Residues: 1-257 <ROS>
R:Maisonpierre, P.C.; Le Beau, M.M.; Esplinoza III, R.; Ip, N.Y.; Belluscio, L.; de la
Genomics 10, 558-568, 1991
A:Title: Human and rat brain-derived neurotrophic factor and neurotrophin-3: gene str
A:Reference number: A40304; MUID:91365361; PMID:1889806
A:Accession: C40304
A:Molecule type: DNA
A:Residues: 1-257 <NAI>
A:Cross-references: GB:M61180; NID:9189302; PIDN:AAA63231.1; PID:9189303
R:Kishino, Y.; Yoshimura, K.; Nakahama, K.
FEBS Lett. 266, 187-191, 1990
A:Title: Cloning and expression of a cDNA encoding a novel human neurotrophic factor.
A:Reference number: S10719; MUID:90306351; PMID:2365067
A:Accession: S10719
A:Molecule type: mRNA
A:Residues: 1-257 <NAI>
A:Cross-references: GB:X53655; NID:9287794; PIDN:CAA37703.1; PID:9287795
R:Yancopoulos, G.D.; Maisonpierre, P.C.; Ip, N.Y.; Aldrich, T.H.; Belluscio, L.; Boul
Cold Spring Harb. Symp. Quant. Biol. 55, 371-379, 1990
A:Title: Neurotrophic factors, their receptors, and the signal transduction pathways
A:Reference number: A60536; MUID:92111157; PMID:1966766
A:Accession: C60536
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-73, 'Q', '75-77', 'R', '79-108', 'T', '110-257' <YAN>
C:Genetics:
A:Gene: GDB:NFP3
A:Cross-references: GDB:125917; OMIM:162660
A:Map position: 12p13-12p13
C:Superfamily: nerve growth factor beta chain
C:Keywords: glycoprotein
F:1-18/Domain: signal sequence #status predicted <SIG>
F:119-138/Domain: propeptide #status predicted <PRO>
F:139-257/Product: neurotrophin-3 #status predicted <MAT>
F:131/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 53.8%; Score 344.5; DB 2; Length 257;
Best Local Similarity 57.4%; Pred. No. 5.5e-28;
Matches 66; Conservative 17; Mismatches 29; Indels 3; Gaps 2;

OY 6 ARRGELSVCDISEMYTAAADKTAVDMSGCTVLEKVPVSGQLKQYFETKCNP 65
DB 144 SRGELSVCDISEMYTAAADKTAVDMSGCTVLEKVPVSGQLKQYFETKCNP 201
OY 66 KEGCGIDKRMHNSCCTTOSYVRLATMDSKRIGRFRIRIDTSCV-TLIRGR 119
DB 202 KEGCGIDKRMHNSCCTTOSYVRLATMDSKRIGRFRIRIDTSCV-TLIRGR 256

RESULT 12

150400

neurotrophin-3 precursor - chicken

C:Species: Gallus gallus (chicken)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999

C:Accession: 150400; S42227

R:Malsonpierre, P.C.; Belluscio, L.; Conover, J.C.; Yancopoulos, G.D.

DNA Seq. 3, 49-54, 1992

A:Title: Gene sequences of chicken BDNF and NT-3.

A:Reference number: 150400; MUID:93091238; PMID:1457809

A:Accession: 150400

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-257 <NAI>

A:Cross-references: GB:M83378; NID:9212464; PIDN:AAA68880.1; PID:9212465

R:Hallboeck, F.; Ibanez, C.F.; Ebdendal, T.; Persson, H.

Eur. J. Neurosci. 5, 1-14, 1993

A:Title: Cellular localization of brain-derived neurotrophic factor and neurotrophin-3

A:Reference number: S42227; MUID:94084226; PMID:8074744

A:Accession: S42227

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 32-257 <NAI>

A:Cross-references: EMBL:Z30092; NID:9455531; PIDN:CAA82908.1; PID:927570

A:Genetics:

A:Gene: NT-3

C:Superfamily: nerve growth factor beta chain

Query Match

53.8%; Score 344.5; DB 2; Length 257;

Best Local Similarity 57.4%; Pred. No. 5.5e-28;

Matches 66; Conservative 17; Mismatches 29; Indels 3; Gaps 2;

Oy 6 ARGELSYVCDISSEVMTAAADKKTAVDMSCGTVYLVKVPVSKQLQYETETKCPMKT 65

Db 144 SHRGYSVCDSESLMT--DKSSAIDIRGHQVYLVGEITGKSPVQYETETKCEARPV 201

Oy 66 KECRCIDKRHMNSCARTTOSYVRLATMDSKRRIGRFRIDTSCV-TLTTRGR 119

Db 202 KNGCRIDDKHMNSCARTTOSYVRLATMDSKRRIGRFRIDTSCVCAISRTIGR 256

RESULT 13

S09155

neurotrophin-3 precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999

C:Accession: S09155; S51179

R:Hom, A.; Leibrock, J.; Bailey, K.; Barde, Y.A.

Nature 344, 339-341, 1990

A:Title: Identification and characterization of a novel member of the nerve growth factor

A:Reference number: S09155; MUID:9019085; PMID:2314473

A:Accession: S09155

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-258 <HCH>

A:Cross-references: GB:M53357; NID:953451; PIDN:CAA37348.1; PID:953452

R:Kolbeck, R.; Jungbluth, S.; Barde, Y.A.

Eur. J. Biochem. 225, 995-1003, 1994

A:Title: Characterization of neurotrophin dimers and monomers.

A:Reference number: S51179; MUID:95045576; PMID:7957235

A:Accession: S51179

A:Status: preliminary

A:Molecule type: protein

A:Residues: 140-152 <KOL>

C:Superfamily: nerve growth factor beta chain

C:Keywords: glycoprotein

F.1-18/Domain: signal sequence #status predicted <STIG>

F.140-258/Product: neurotrophin-3 #status predicted <NAI>

F.133/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

53.8%; Score 344.5; DB 2; Length 258;

Best Local Similarity 57.4%; Pred. No. 5.5e-28;

Matches 66; Conservative 17; Mismatches 29; Indels 3; Gaps 2;

Oy 6 ARGELSYVCDISSEVMTAAADKKTAVDMSCGTVYLVKVPVSKQLQYETETKCPMKT 65

Db 145 SHRGYSVCDSESLMT--DKSSAIDIRGHQVYLVGEITGKSPVQYETETKCEARPV 202

Oy 66 KECRCIDKRHMNSCARTTOSYVRLATMDSKRRIGRFRIDTSCV-TLTTRGR 119

Db 203 KNGCRIDDKHMNSCARTTOSYVRLATMDSKRRIGRFRIDTSCVCAISRTIGR 257

RESULT 14

A35781

hippocampus-derived neurotrophic factor precursor - rat

N:Alternate names: neurotrophin-3 precursor

C:Species: Rattus norvegicus (Norway rat)

C:Date: 05-Oct-1990 #sequence_revision 05-Oct-1990 #text_change 16-Jul-1999

C:Accession: A35781; A40094

R:Ernfors, P.; Ibanez, C.F.; Ebdendal, T.; Olsson, L.; Persson, H.

Proc. Natl. Acad. Sci. U.S.A. 87, 5454-5458, 1990

A:Title: Molecular cloning and neurotrophic activities of a protein with structural s

A:Reference number: A35781; MUID:90319130; PMID:2164684

A:Accession: A35781

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-282 <ERN>

A:Cross-references: GB:M44643

R:Malsonpierre, P.C.; Belluscio, L.; Squinto, S.; Ip, N.Y.; Furch, M.E.; Lindsay, R.M

Science 247, 1446-1451, 1990

A:Title: Neurotrophin-3: a neurotrophic factor related to NGF and BDNF.

A:Reference number: A40094; MUID:90208301; PMID:2321006

A:Accession: A40094

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 25-282 <NAI>

A:Cross-references: GB:M33968; NID:9205771; PIDN:AAA11727.1; PID:9205772

C:Superfamily: nerve growth factor beta chain

Query Match

53.8%; Score 344.5; DB 2; Length 282;

Best Local Similarity 57.4%; Pred. No. 6e-28;

Matches 66; Conservative 17; Mismatches 29; Indels 3; Gaps 2;

Oy 6 ARGELSYVCDISSEVMTAAADKKTAVDMSCGTVYLVKVPVSKQLQYETETKCPMKT 65

Db 169 SHRGYSVCDSESLMT--DKSSAIDIRGHQVYLVGEITGKSPVQYETETKCEARPV 226

Oy 66 KECRCIDKRHMNSCARTTOSYVRLATMDSKRRIGRFRIDTSCV-TLTTRGR 119

Db 227 KNGCRIDDKHMNSCARTTOSYVRLATMDSKRRIGRFRIDTSCVCAISRTIGR 281

RESULT 15

B42687

neurotrophin-4 precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999

C:Accession: B42687; JH0504; JH0505

R:Rip, N.Y.; Ibanez, C.F.; Nye, S.H.; McGiln, J.; Jones, P.F.; Gies, D.R.; Belluscio,

Proc. Natl. Acad. Sci. U.S.A. 89, 3060-3064, 1992

A:Title: Mammalian neurotrophin-4: structure, chromosomal localization, tissue distri

A:Reference number: B42687; MUID:92212967; PMID:1313578

A:Accession: B42687

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-209 <TPA>

A:Cross-references: GB:M6742; NID:9205775; PIDN:AAA11728.1; PID:9205776

R:Berkeley, L.R.; Wnirow, J.W.; Kaplan, D.R.; Nikolic, K.; Goeddel, D.V.; Rosenth

Neuron 7, 857-866, 1991

A:Title: Neurotrophin-5: a novel neurotrophic factor that activates trk and trkB.

A:Reference number: JH0503; MUID:92075279; PMID:1742028

A:Accession: JH0504

A:Molecule type: DNA

A:Residues: 1-209 <BER>

A:Accession: JH0505

A:Molecule type: mRNA

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 2, 2002, 15:05:43 ; Search time 4.88277 Seconds

(without alignments)
1010.837 Million cell updates/sec

Title: US-10-072-681-4

Perfect score: 640

Sequence: 1 PHSDPARGELSYVCSISEM.....GMRFRIDTSCVTLTKRGR 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	622.5	97.3	247	1	BDNF_HUMAN
2	622.5	97.3	247	1	BDNF_PROLO
3	622.5	97.3	247	1	BDNF_URSML
4	622.5	97.3	249	1	BDNF_MOUSE
5	622.5	97.3	249	1	BDNF_MOUSE
6	622.5	97.3	252	1	BDNF_RAT
7	621.5	97.1	255	1	BDNF_CAVPO
8	618.5	96.6	247	1	BDNF_FELCA
9	618.5	96.6	247	1	BDNF_URSAR
10	613.5	95.9	248	1	BDNF_BOVIN
11	594	92.8	114	1	BDNF_MACMU
12	592.5	92.6	246	1	BDNF_CHICK
13	570.5	90.5	270	1	BDNF_CITCA
14	570.5	89.1	269	1	BDNF_XIPMA
15	559	87.3	114	1	BDNF_XENLA
16	375.5	58.7	236	1	NT4_XENLA
17	344.5	53.8	257	1	NT3_CHICK
18	344.5	53.8	257	1	NT3_CHICK
19	344.5	53.8	258	1	NT3_HUMAN
20	344.5	53.8	258	1	NT3_MOUSE
21	347.5	53.8	260	1	NT3_RAT
22	339.5	53.0	257	1	NT3_XENLA
23	336.5	52.6	209	1	NT3_FELCA
24	336.5	52.0	210	1	NT5_RAT
25	317	49.5	229	1	NGF_HUMAN
26	317	49.5	243	1	NGF_PIG
27	311.5	48.7	241	1	NGF_CHICK
28	310	48.4	231	1	NGF_BOVIN
29	310	48.4	241	1	NGF_HUMAN
30	308.5	48.2	231	1	NGF_PRANA
31	308.5	48.2	241	1	NGF_XENLA
32	308.5	48.2	241	1	NGF_MOUSE
33	306.5	47.9	241	1	NGF_RAT
					NGF_CAVPO

34	301.5	47.1	243	1	NGF_BUNMU
35	300.5	47.0	117	1	NGF_DABRR
36	295	46.1	116	1	NGF_NAJNA
37	292.5	45.7	116	1	NGF_NAJAT
38	253.5	39.6	194	1	NGF_XIPMA
39	245	38.3	140	1	NT7_CYPCA
40	245	38.3	233	1	NT7_BRARE
41	222	34.7	186	1	NT66_HUMAN
42	221	34.5	257	1	NT6A_HUMAN
43	215	33.6	257	1	BDNF_HUMAN
44	214	33.4	43	1	BDNF_RAVCL
45	209	32.7	43	1	BDNF_VIPRE

ALIGNMENTS

RESULT 1
BDNF_HUMAN
ID BDNF_HUMAN STANDARD: PRT: 247 AA.
AC P23560; 090C24; 09BY7;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Brain-derived neurotrophic factor precursor (BDNF).
GN BDNF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-91045937; PubMed-2236018;
RA Jones K.R., Reichardt L.F.,
RT "Molecular cloning of a human gene that is a member of the nerve
RT growth factor family.",
RT Proc. Natl. Acad. Sci. U.S.A. 87:8060-8064(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-91365361; PubMed-1889806;
RA Maisonneuve P.C., Le Beau M.M., Espinosa R. III, Ip N.Y.,
RA Belluscio L., de la Monte S.M., Squinto S., Furch M.E.,
RT Yancopoulos G.D.,
RT Human and rat brain-derived neurotrophic factor and neurotrophin-3:
RT gene structures, distributions, and chromosomal localizations.",
RL Genomics 10:558-568(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-92118032; PubMed-1339267;
RA Shitara A., Ono Y., Katsuo Y., Igarashi K.,
RT "Characterization of the 5'-flanking region of the human
RT brain-derived neurotrophic factor gene.",
RL Biochem. Biophys. Res. Commun. 182:325-334(1992).
RN [4]
RP SEQUENCE FROM N.A.
RX Cheng Y., Gu J.,
RT Submitted (May-1995) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX Wu J., Zhang B., Zhou Y., Peng X., Yuan J., Qiang B.,
RT Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 185-227 FROM N.A.
RX TISSUE-Leukocyte;
RA MEDLINE-9122573; PubMed-2025430;
RA Hallboeck F., Ibanez C.F., Persson H.,
RT "Evolutionary studies of the nerve growth factor family reveal a
RT novel member abundantly expressed in Xenopus ovary.",
RL Neuron 6:845-858(1991).
RN [7]
RP SEQUENCE OF 129-144.
RX TISSUE-Serum;
RA MEDLINE-96136633; PubMed-8527932;

RA Rosenfeld L.D., Zeng L., Hanlu M., Talvenhelmo J., Radka S.F.,
 RA Bennett L., Miller J.A., Welcher A.A.;
 RT "Purification and identification of brain-derived neurotrophic factor
 RT from human serum.";
 RL Protein Expr. Purif. 6:465-471(1995).
 (8)
 RN SEQUENCE OF 12-197 FROM N.A.
 RX MEDLINE-21082082; PubMed-11214319;
 RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
 RA O'Brien S.J.;
 RT "Molecular phylogenetics and the origins of placental mammals.";
 RL Nature 409:614-618(2001).
 (9)
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RP MEDLINE-95217877; PubMed-7703225;
 RX Radziejewski C., Stuart D.I., Jones E.Y.;
 RA "Structure of the brain-derived neurotrophic factor/neurotrophin 3
 RT heterodimer.";
 RL Biochemistry 34:4139-4146(1995).
 (10)
 RP CHARACTERIZATION AND MUTAGENESIS OF ARG-54.
 RX MEDLINE-21201090; PubMed-11152678;
 RA Nowla S.J., Farhadi H.F., Pareek S., Atwal J.K., Morris S.J.,
 RA Seidah N.G., Murphy R.A.;
 RT "Biosynthesis and post-translational processing of the precursor to
 RT brain-derived neurotrophic factor.";
 RL J. Biol. Chem. 276:12660-12666(2001).
 CC -1- FUNCTION: PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS THAT ARE
 CC ALL LOCATED EITHER IN THE CENTRAL NERVOUS SYSTEM OR DIRECTLY
 CC CONNECTED TO IT.
 CC SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: The propeptide is N-glycosylated and glycosylated.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
 CC -----
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 DR EMBL: M37762; AAA51820.1; -
 DR EMBL: M61176; AAA69805.2; -
 DR EMBL: X60201; CAA42761.1; -
 DR EMBL: AF400438; AAK92487.1; -
 DR EMBL: M61181; AAA66140.1; -
 DR EMBL: X51251; CAA62632.1; -
 DR EMBL: AY011481; AAG47514.1; -
 DR PIR: B36208; B36208.
 DR PIR: A40304; A40304.
 DR PDB: 1BND; 04-APR-96.
 DR PDB: 1B8M; 09-FEB-99.
 DR GeneW: HGNC:1033; BDNF.
 DR MIM: 113503; -
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF; 2.
 DR PRINTS: PR00268; NGF.
 DR PRODOM: PD002052; NGF; 1.
 DR SMART: SM00140; NGF; 1.
 DR PROSITE: PS00248; NGF-1; 1.
 DR PROSITE: PS0270; NGF-2; 1.
 DR Growth factor: Signal; Glycoprotein; Polymorphism; 3D-structure.
 KW SIGNAL; 1; 18
 FT SIGNAL 1 18
 FT PROPEP 19 128
 FT CHAIN 129 247
 FT DISULFID 141 208
 FT DISULFID 186 237
 FT DISULFID 196 239
 FT CARBOHYD 121 121
 FT SITE 57 58
 FT VARIANT 66 66
 V -> M.
 /FTID-VAR_004626.

FT VARIANT 75 75 0 -> H (IN DBSNP:1048218).
 FT VARIANT 125 125 /FTID-VAR_011797.
 FT VARIANT 127 127 R -> N (IN DBSNP:1048220).
 FT VARIANT 127 127 /FTID-VAR_011798.
 FT VARIANT 127 127 R -> L (IN DBSNP:1048221).
 FT VARIANT 127 127 /FTID-VAR_011799.
 FT MUTAGEN 54 54 R -> A; ABOLISHES PROCESSING BY SLP.
 SQ SEQUENCE 247 AA: 27818 MW: 0860488254722A99 CRC64;
 Query Match 97.3%; Score 632.5; DB 1; Length 247;
 Best local similarity 99.2%; Pred. No. 1e-58;
 Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 2 HSDPARGELSDSISEMTAAADKRTAVDMSGGVTYLEKYPVSKOLKQYFETKCNP 61
 DB 129 HSDPARGELSDSISEMTAAADKRTAVDMSGGVTYLEKYPVSKOLKQYFETKCNP 188
 QY 62 MGYTREGCGIDRRHNSCORTTOSYVRLTMDSKRIGMFRIDISCV-TLITKGR 119
 DB 189 MGYTREGCGIDRRHNSCORTTOSYVRLTMDSKRIGMFRIDISCVCTLTIKGR 247
 RESULT 2
 BDNF_PROTO STANDARD: PRT: 247 AA.
 ID BDNF_PROTO 018735;
 AC 018735;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Brain-derived neurotrophic factor precursor (BDNF).
 GN BDNF.
 OS Procyon lotor (Raccoon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Procyonidae; Procyon.
 OX MBL_TaxID=9634;
 RX [1]
 RN LIn F.;
 RA Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RL -1- FUNCTION: PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS THAT ARE
 CC ALL LOCATED EITHER IN THE CENTRAL NERVOUS SYSTEM OR DIRECTLY
 CC CONNECTED TO IT (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
 CC -----
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 CC -----
 DR EMBL: AF003188; AAB71654.1; -
 DR HSSP: P23560; 1B8M.
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF; 1.
 DR PRINTS: PR00268; NGF.
 DR PRODOM: PD002052; NGF; 1.
 DR SMART: SM00140; NGF; 1.
 DR PROSITE: PS00248; NGF-1; 1.
 DR PROSITE: PS0270; NGF-2; 1.
 DR Growth factor: Signal; 1; 18
 FT SIGNAL 1 18
 FT PROPEP 19 128
 FT CHAIN 129 247
 FT SITE 57 58
 FT DISULFID 141 208
 FT DISULFID 186 237
 FT DISULFID 196 239
 FT CARBOHYD 121 121
 SQ SEQUENCE 247 AA: 27834 MW: 5FC377E4FE1F52A0 CRC64;
 POTENTIAL.
 BY SIMILARITY.
 BRAIN-DERIVED NEUROTROPHIC FACTOR.
 CLEAVAGE (BY SLP) (BY SIMILARITY).
 BY SIMILARITY.
 BY SIMILARITY.
 N-LINKED (GLCNAc...) (POTENTIAL).
 CLEAVAGE (BY SLP).
 V -> M.
 /FTID-VAR_004626.

Query Match 97.3% Score 622.5; DB 1; Length 247;
 Best Local Similarity 99.2% Pred. No. 1e-58;
 Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

DB 2 HSDPARRGELSYCDISISEVNTAADKKTAVDMSGGTVLEKVPVSKQLQYFETKCNP 61
 129 HSDPARRGELSYCDISISEVNTAADKKTAVDMSGGTVLEKVPVSKQLQYFETKCNP 188

DB 62 MGYTEGCGIDKRRHNSOCRTTOSYVRALTMDSKKRIGRFIRIDTSCV-TLTIKGR 119
 189 MGYTEGCGIDKRRHNSOCRTTOSYVRALTMDSKKRIGRFIRIDTSCV-TLTIKGR 247

RESULT 3
 ID BDNF_URSML STANDARD; PRT; 247 AA.
 AC 018753;
 DT 15-JUN-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-1998 (Rel. 36, Last annotation update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Brain-derived neurotrophic factor precursor (BDNF).
 GN BDNF.
 OS Ursus malayanus (Malayan sun bear) (Heliarctos malayanus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Heliarctos.
 ON NCBI_TaxID=9634;
 RN [1]
 RP SEQUENCE FROM N.A.
 RL Lin F.
 RA Submitted (May-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS THAT ARE
 CC ALL LOCATED EITHER IN THE CENTRAL NERVOUS SYSTEM OR DIRECTLY
 CC CONNECTED TO IT (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF002240; AAB71653.1; -
 DR HSSP: P23560; 188M.
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF; 1.
 DR PRINTS: PR00268; NGF.
 DR PRODOM: PD002052; NGF; 1.
 DR SMART: SM00140; NGF; 1.
 DR PROSITE: PS00248; NGF; 1.
 DR PROSITE: PS50270; NGF; 2; 1.
 DR Growth factor: Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 128
 FT CHAIN 129 247
 FT SITE 57 58
 FT DISULFID 141 208
 FT DISULFID 186 237
 FT DISULFID 196 239
 FT CARBOHYD 121 121
 SO SEQUENCE 247 AA; 27807 MW; FA1B3DFC4704D883 CRC64;

Query Match 97.3% Score 622.5; DB 1; Length 247;
 Best Local Similarity 99.2% Pred. No. 1e-58;
 Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

DB 2 HSDPARRGELSYCDISISEVNTAADKKTAVDMSGGTVLEKVPVSKQLQYFETKCNP 61
 129 HSDPARRGELSYCDISISEVNTAADKKTAVDMSGGTVLEKVPVSKQLQYFETKCNP 188

DB 62 MGYTEGCGIDKRRHNSOCRTTOSYVRALTMDSKKRIGRFIRIDTSCV-TLTIKGR 119
 191 MGYTEGCGIDKRRHNSOCRTTOSYVRALTMDSKKRIGRFIRIDTSCV-TLTIKGR 249

DB 189 MGYTEGCGIDKRRHNSOCRTTOSYVRALTMDSKKRIGRFIRIDTSCV-TLTIKGR 247

RESULT 4
 ID BDNF_MOUSE STANDARD; PRT; 249 AA.
 AC P21237;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Brain-derived neurotrophic factor precursor (BDNF).
 GN BDNF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-90316101; PubMed-2369898;
 RA Hofer M., Pagliusi S.R., Hohn A., LeDrook J., Barde Y.-A.;
 RT Regional distribution of brain-derived neurotrophic factor mRNA in
 RT the adult mouse brain.
 RL EMBO J. 9:2459-2464(1990).
 CC -1- FUNCTION: PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS THAT ARE
 CC ALL LOCATED EITHER IN THE CENTRAL NERVOUS SYSTEM OR DIRECTLY
 CC CONNECTED TO IT.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
 CC -----
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 CC -----
 DR EMBL: X55373; CAA39159.1; -
 DR PIR: S12555; S12555.
 DR HSSP: P23560; 188M.
 DR MGD: MGI:88145; Bdnf.
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF; 1.
 DR PRINTS: PR00268; NGF.
 DR PRODOM: PD002052; NGF; 1.
 DR SMART: SM00140; NGF; 1.
 DR PROSITE: PS00248; NGF; 1.
 DR PROSITE: PS50270; NGF; 2; 1.
 DR Growth factor: Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 130
 FT CHAIN 131 249
 FT SITE 57 58
 FT DISULFID 143 210
 FT DISULFID 188 239
 FT DISULFID 198 241
 FT CARBOHYD 123 123
 SO SEQUENCE 249 AA; 28123 MW; 90CE1F16B8235C97 CRC64;

Query Match 97.3% Score 622.5; DB 1; Length 249;
 Best Local Similarity 99.2% Pred. No. 1e-58;
 Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

DB 2 HSDPARRGELSYCDISISEVNTAADKKTAVDMSGGTVLEKVPVSKQLQYFETKCNP 61
 131 HSDPARRGELSYCDISISEVNTAADKKTAVDMSGGTVLEKVPVSKQLQYFETKCNP 190

DB 62 MGYTEGCGIDKRRHNSOCRTTOSYVRALTMDSKKRIGRFIRIDTSCV-TLTIKGR 119
 191 MGYTEGCGIDKRRHNSOCRTTOSYVRALTMDSKKRIGRFIRIDTSCV-TLTIKGR 249

```

RESULT 5
ID BDNF_RAT STANDARD: PRT: 249 AA.
AC P23163:
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Brain-derived neurotrophic factor precursor (BDNF).
GN BDNF.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OK NCBI_TaxID=10116;
RN 11
RP MEDLINE-91365361; PubMed-1889806;
RX Malsinier P.C., le Beau M.M., Epplnose R. III, Ip N.Y.,
RX Belluscio L., de la Monte S.M., Squinto S., Furth M.E.,
RX Yancopoulos G.D.;
RA "Human and rat brain-derived neurotrophic factor and neurotrophin-3:
RT gene structures, distributions, and chromosomal localizations.";
RL Genomics 10:558-568(1991).
RN 12
RP SEQUENCE FROM N.A.
RA Ohara O.;
RL Submitted (XX-1992) to the EMBL/GenBank/DBJ databases.
RN 13
RP SEQUENCE FROM N.A.
RX MEDLINE-9211157; PubMed-1966766;
RX Yancopoulos G.D., Malsinier P.C., Ip N.Y., Aldrich T.H.,
RX Belluscio L., Boulton T.G., Cobb M.H., Squinto S.P., Furth M.E.;
RT "Neurotrophic factors, their receptors, and the signal transduction
RT pathways they activate.";
RL Cold Spring Harb. Symp. Quant. Biol. 55:371-379(1990).
RN 14
RP SEQUENCE OF 8-249 FROM N.A.
RX MEDLINE-93213504; PubMed-8461137;
RX Timmusk T., Palm K., Metsis M., Reintam T., Palme V., Saarma N.,
RA Persson H.;
RT "Multiple promoters direct tissue-specific expression of the rat BDNF
RT gene.";
RL Neuron 10:475-489(1993).
RN 15
RP SEQUENCE OF 187-229 FROM N.A.
RX STRAIN-Sprague-Dawley; TISSUE-Liver;
RX MEDLINE-9122573; PubMed-2025430;
RX Hallböök F., Ibanez C.F., Persson H.;
RA "Evolutionary studies of the nerve growth factor family reveal a
RT novel member abundantly expressed in Xenopus ovary.";
RL Neuron 6:845-858(1991).
CC -1- FUNCTION: PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS THAT ARE
CC ALL LOCATED EITHER IN THE CENTRAL NERVOUS SYSTEM OR DIRECTLY
CC CONNECTED TO IT.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC
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DR PRINTS: PR00268; NGF.
DR Prodom: PD002052; NGF; 1.
DR SMART: SM00140; NGF; 1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS0270; NGF_2; 1.
KM Growth factor; Signal.
FT SIGNAL 1 18
FT PROPEP 19 130
FT CHAIN 131 249
FT SITE 57 58
FT DISULFID 143 210
FT DISULFID 168 239
FT DISULFID 198 241
FT CARBOHYD 123 123
FT SEQUENCE 249 AA; 28109 MW; F9CAA5DEF9A78B7 CRC64;

Query Match 97.3%; Score 62.5; DB 1; Length 249;
Best Local Similarity 99.2%; Pred. No. 1e-58; 0; Indels 1; Gaps 1;
Matches 118; Conservative 0; Mismatches 0;

QY 2 HSDPARGELSYDSEISSEWTAADKRTAVDMSGTVLEVPVSKGOLKQYFETKCNP 61
DB 131 HSDPARGELSYDSEISSEWTAADKRTAVDMSGTVLEVPVSKGOLKQYFETKCNP 130
QY 62 MGTKKCGRIDRHNNSCORTTOSYVRLTMDSKRIGRIFRIDTSCV-TLTIKGR 119
DB 191 MGTKKCGRIDRHNNSCORTTOSYVRLTMDSKRIGRIFRIDTSCV-TLTIKGR 249

RESULT 6
ID BDNF_PIG STANDARD: PRT: 252 AA.
AC P14082:
DT 01-JUN-1990 (Rel. 13, Last sequence update)
DT 01-JUN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Brain-derived neurotrophic factor precursor (BDNF).
GN BDNF.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OK NCBI_TaxID=9623;
RN 11
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RX MEDLINE-9384866; PubMed-2779653;
RX Leibrock J., Lottspeich F., Hohn A., Hofer M., Hengeler B.,
RX Maslakowski P., Thoenen H., Barde Y.-A.;
RA "Molecular cloning and expression of brain-derived neurotrophic
RT factor.";
RL Nature 341:149-152(1989).
CC -1- FUNCTION: PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS THAT ARE
CC ALL LOCATED EITHER IN THE CENTRAL NERVOUS SYSTEM OR DIRECTLY
CC CONNECTED TO IT.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: BRAIN AND CENTRAL NERVOUS SYSTEM.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC
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DR PROSITE: PS00248; NCF_1; 1.
 DR PROSITE: PS00270; NCF_2; 1.
 KW Growth factor; Signal.
 FT SIGNAL 1 18
 FT PROPEP 13 133
 FT CHAIN 134 252
 FT SITE 57 58
 FT DISULFID 146 213
 FT DISULFID 191 242
 FT DISULFID 201 244
 FT CARBOHYD 126 126
 SO SEQUENCE 253 AA; 28287 MW; 5DAB45E73BE0B7E CRC64;

Query Match 97.3%; Score 622.5; DB 1; Length 252;
 Best Local Similarity 99.2%; Pred. No. 1e-58;
 Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARGELSVCDISEWVTADKRTAVDSGCTVLEKVPVSKGLQYFETKCNP 61
 DB 134 HSDPARGELSVCDISEWVTADKRTAVDSGCTVLEKVPVSKGLQYFETKCNP 193
 OY 62 MGYTEGCGIDKRMHNSOCTRTOSYVRALTMDSKKRIGWRIRIDTSCV-TLTIKGR 119
 DB 194 MGYTEGCGIDKRMHNSOCTRTOSYVRALTMDSKKRIGWRIRIDTSCVTLTIKGR 252

RESULT 7

ID BDNF_CAVPO STANDARD: PRT: 255 AA.
 AC 070183;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Brain-derived neurotrophic factor precursor (BDNF).
 GN BDNF.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Cavidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Hartley white; TISSUE-Liver;
 RA Inoue M., Nakayama C., Noguchi H.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.

-1- FUNCTION: PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS THAT ARE

ALL LOCATED EITHER IN THE CENTRAL NERVOUS SYSTEM OR DIRECTLY
 CONNECTED TO IT (BY SIMILARITY).

-1- SUBCELLULAR LOCATION: Secreted.

-1- SIMILARITY: BELONGS TO THE NCF-BETA FAMILY.

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 or send an email to license@isb-sib.ch).

CC EMBL: AB012097; BAA25116.1; -
 DR HSSP: P23560; 1BBM.
 DR InterPro: IPR002072; NCF.
 DR Pfam: PF00243; NCF; 1.
 DR PRINTS: PR00268; NCF.
 DR PRODOM: PD002052; NCF; 1.
 DR SMART: SM00140; NCF; 1.
 DR PROSITE: PS00248; NCF_1; 1.
 DR PROSITE: PS00270; NCF_2; 1.
 KW Growth factor; Signal.
 FT SIGNAL 1 18
 FT PROPEP 13 136
 FT CHAIN 137 255
 FT SITE 57 58
 FT DISULFID 149 216

POTENTIAL.
 BY SIMILARITY.
 BRAIN-DERIVED NEUROTROPHIC FACTOR.
 CLEAVAGE (BY SLIP) (BY SIMILARITY).
 BY SIMILARITY.

FT DISULFID 194 245
 FT DISULFID 204 247
 FT CARBOHYD 129 129
 SO SEQUENCE 255 AA; 28308 MW; BA05BA3EBB8FA04 CRC64;

Query Match 97.1%; Score 621.5; DB 1; Length 255;
 Best Local Similarity 98.3%; Pred. No. 1.3e-58;
 Matches 117; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARGELSVCDISEWVTADKRTAVDSGCTVLEKVPVSKGLQYFETKCNP 61
 DB 137 HSDPARGELSVCDISEWVTADKRTAVDSGCTVLEKVPVSKGLQYFETKCNP 196
 OY 62 MGYTEGCGIDKRMHNSOCTRTOSYVRALTMDSKKRIGWRIRIDTSCV-TLTIKGR 119
 DB 197 MGYTEGCGIDKRMHNSOCTRTOSYVRALTMDSKKRIGWRIRIDTSCVTLTIKGR 255

RESULT 8

ID BDNF_FELCA STANDARD: PRT: 247 AA.
 AC 097573;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Brain-derived neurotrophic factor precursor (BDNF).
 GN BDNF.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20211727; PubMed=10745216;
 RA Lein E.S., Hohn A., Shatz C.J.;
 RT "Dynamic regulation of BDNF and NT-3 expression during visual system
 development.";
 J. Comp. Neurol. 420:1-18(2000).

-1- FUNCTION: PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS THAT ARE

ALL LOCATED EITHER IN THE CENTRAL NERVOUS SYSTEM OR DIRECTLY
 CONNECTED TO IT (BY SIMILARITY).

-1- SUBCELLULAR LOCATION: Secreted.

-1- SIMILARITY: BELONGS TO THE NCF-BETA FAMILY.

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CC EMBL: AF192537; AAF03423.1; -
 DR HSSP: P23560; 1BBM.
 DR InterPro: IPR002072; NCF.
 DR Pfam: PF00243; NCF; 1.
 DR PRINTS: PR00268; NCF.
 DR PRODOM: PD002052; NCF; 1.
 DR SMART: SM00140; NCF; 1.
 DR PROSITE: PS00248; NCF_1; 1.
 DR PROSITE: PS00270; NCF_2; 1.
 KW Growth factor; Signal.
 FT SIGNAL 1 18
 FT PROPEP 13 128
 FT CHAIN 129 247
 FT DISULFID 141 208
 FT DISULFID 186 237
 FT DISULFID 196 239
 FT CARBOHYD 121 121
 SO SEQUENCE 247 AA; 27802 MW; 864BA1BD26E0A0F3 CRC64;

Query Match 96.6%; Score 618.5; DB 1; Length 247;
 Best Local Similarity 98.3%; Pred. No. 2.7e-58;

Matches 117: Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 2 HSDPARGEISVCSISSEMTADKRTAVDMGSGTIVLEKVPVSKGOLKOFETKCNP 61
 DB 129 HSDPARGEISVCSISSEMTADKRTAVDMGSGTIVLEKVPVSKGOLKOFETKCNP 188
 OY 62 MGYTEGCGRIDKRMHNSOCTTOSYVRLATMDSKRRIGMRFIRIDTSCV-TLTIKGR 119
 DB 189 MGYTEGCGRIDKRMHNSOCTTOSYVRLATMDSKRRIGMRFIRIDTSCVTLTIKGR 247

RESULT 9

BDNF_URSAR STANDARD: PRT: 247 AA.

AC 018752;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Brain-derived neurotrophic factor precursor (BDNF).
 GN BDNF.

OS Ursus arctos (Brown bear) (Grizzly bear).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
 ON NCBI_TaxID=9644;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Lin F.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS THAT ARE
 CC ALL LOCATED EITHER IN THE CENTRAL NERVOUS SYSTEM OR DIRECTLY
 CC CONNECTED TO IT (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.

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CC -----
 CC EMBL: AF002239; AAB71652.1; --
 CC HSSP: P23560; 188M.
 CC InterPro: IPR002072; NGF.
 CC Pfam: PF00243; NGF. 1.
 CC PRINTS: PR00268; NGF. 1.
 CC PRODOM: PD002052; NGF. 1.
 CC SMART: SM00140; NGF. 1.
 CC PROSITE: PS00248; NGF_1; 1.
 CC PROSITE: PS50270; NGF_2; 1.
 CC Growth factor; Signal.
 KW Growth factor; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 128
 FT CHAIN 129 247
 FT SITE 57 58
 FT DISULFID 141 208
 FT DISULFID 186 237
 FT CARBOHYD 121 121
 SQ SEQUENCE 247 AA; 27837 MW; EF1B3256F70AD883 CMC64;
 Query Match 96.6%; Score 618.5; DB 1; Length 247;
 Best Local Similarity 98.3%; Pred. No. 2.7e-58;
 Matches 117: Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 2 HSDPARGEISVCSISSEMTADKRTAVDMGSGTIVLEKVPVSKGOLKOFETKCNP 61
 DB 129 HSDPARGEISVCSISSEMTADKRTAVDMGSGTIVLEKVPVSKGOLKOFETKCNP 188
 OY 62 MGYTEGCGRIDKRMHNSOCTTOSYVRLATMDSKRRIGMRFIRIDTSCV-TLTIKGR 119
 DB 189 MGYTEGCGRIDKRMHNSOCTTOSYVRLATMDSKRRIGMRFIRIDTSCVTLTIKGR 247

RESULT 10
 BDNF_BOVIN STANDARD: PRT: 248 AA.
 ID BDNF_BOVIN
 AC 095106;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Brain-derived neurotrophic factor precursor (BDNF) (Fragment).
 GN BDNF.

OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 ON NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.

RA MEDLINE-97186702; PubMed-9034318;
 RA Arab S.F., Krohn K., Lachmund A., Unsicker K., Suter-Crazzolara C.,
 RT "The gene encoding bovine brain-derived neurotrophic factor (BDNF)."
 RL Gene 185:95-98(1997).
 CC -1- FUNCTION: PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS THAT ARE
 CC ALL LOCATED EITHER IN THE CENTRAL NERVOUS SYSTEM OR DIRECTLY
 CC CONNECTED TO IT (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.

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CC -----
 CC EMBL: X97914; CA66488.1; --
 CC HSSP: P23560; 188M.
 CC InterPro: IPR002072; NGF.
 CC Pfam: PF00243; NGF. 1.
 CC PRODOM: PD002052; NGF. 1.
 CC SMART: SM00140; NGF. 1.
 CC PROSITE: PS00248; NGF_1; 1.
 CC PROSITE: PS50270; NGF_2; 1.
 CC Growth factor; Signal.
 KW Growth factor; Signal.
 FT SIGNAL 1 16
 FT PROPEP 17 129
 FT CHAIN 130 248
 FT SITE 55 56
 FT DISULFID 142 208
 FT DISULFID 187 238
 FT DISULFID 197 240
 SQ SEQUENCE 248 AA; 28012 MW; 27EB97E233F777C7 CMC64;
 Query Match 95.9%; Score 613.5; DB 1; Length 248;
 Best Local Similarity 97.5%; Pred. No. 9.1e-58;
 Matches 116: Conservative 1; Mismatches 1; Indels 1; Gaps 1;

OY 2 HSDPARGEISVCSISSEMTADKRTAVDMGSGTIVLEKVPVSKGOLKOFETKCNP 61
 DB 130 HSDPARGEISVCSISSEMTADKRTAVDMGSGTIVLEKVPVSKGOLKOFETKCNP 189
 OY 62 MGYTEGCGRIDKRMHNSOCTTOSYVRLATMDSKRRIGMRFIRIDTSCV-TLTIKGR 119
 DB 190 MGYTEGCGRIDKRMHNSOCTTOSYVRLATMDSKRRIGMRFIRIDTSCVTLTIKGR 248
 RESULT 11
 BDNF_MACMU STANDARD: PRT: 114 AA.
 ID BDNF_MACMU
 AC 006225;
 DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-1998 (Rel. 36, Last annotation update)
 DE Brain-derived neurotrophic factor (BDNF) (fragment).
 GN BDNF.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 NC NCBI_TaxID=9544;
 RN [1]
 RP MEDLINE-91309745; PubMed-1906813;
 RA Jackson P.J., Townner M.D., Huntsman M.M.;
 RT "Comparison of mammalian, chicken and Xenopus brain-derived
 RT neurotrophic factor coding sequences.";
 RL FEBS Lett. 285:260-264(1991).
 CC -1- FUNCTION: PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS THAT ARE
 CC ALL LOCATED EITHER IN THE CENTRAL NERVOUS SYSTEM OR DIRECTLY
 CC CONNECTED TO IT.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X61475; CAA43703.1; -;
 DR HSSP; P23560; 1BBM.
 DR InterPro: IPR002072; NCF.
 DR Pfam: PF00243; NCF_1.
 DR ProDom: PD002052; NCF_1.
 DR SMART; SM00140; NCF_1.
 DR PROSITE; PS00248; NCF_1; 1.
 DR PROSITE; PS50270; NCF_2; 1.
 DR Growth factor.
 FT NON_TER 1 1 BY SIMILARITY.
 FT DISULFID 14 81 BY SIMILARITY.
 FT DISULFID 59 110 BY SIMILARITY.
 FT DISULFID 69 112 BY SIMILARITY.
 FT NON_TER 114 114 BY SIMILARITY.
 SO SEQUENCE 114 AA; 12956 MW; D5F1BEDD8F4B925 CRC64;
 Query Match 92.8%; Score 594; DB 1; Length 114;
 Best Local Similarity 100.0%; Pred. No. 4.5e-56;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 HSDPARRGELSYCDISISEMTAAADKRTAVMSGCTVYLEKVPVSGQLOKQFYETKCNP 61
 DB 2 HSDPARRGELSYCDISISEMTAAADKRTAVMSGCTVYLEKVPVSGQLOKQFYETKCNP 61
 QY 62 MGYTKEGCGIDKRRHNSOCRTOSYVVALTMDSKRRIGRFRIDTSCV 111
 DB 62 MGYTKEGCGIDKRRHNSOCRTOSYVVALTMDSKRRIGRFRIDTSCV 111
 RESULT 12
 BDNF_CHICK STANDARD: PRT: 246 AA.
 AC P235423;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Brain-derived neurotrophic factor precursor (BDNF).
 GN BDNF.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NC NCBI_TaxID=9031;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Leghorn; TISSUE=Liver;
 RX MEDLINE-913091238; PubMed-1457809;
 RA Maisonneuve P., Belluscio L., Conover J.C., Yancopoulos G.D.;
 RT "Gene sequences of chicken BDNF and NT-3.";
 RL DNA Seq. 3:49-54(1992).
 RN [2]
 RP SEQUENCE OF 127-240 FROM N.A.
 RX MEDLINE-91309745; PubMed-1906813;
 RA Jackson P.J., Townner M.D., Huntsman M.M.;
 RT "Comparison of mammalian, chicken and Xenopus brain-derived
 RT neurotrophic factor coding sequences.";
 RL FEBS Lett. 285:260-264(1991).
 RN [3]
 RP SEQUENCE OF 184-226 FROM N.A.
 RX MEDLINE-91222573; PubMed-2025430;
 RA Hallboeek F., Ibanez C.F., Persson H.;
 RT "Evolutionary studies of the nerve growth factor family reveal a novel
 RT member abundantly expressed in Xenopus ovary.";
 RL Neuron 6:845-858(1991).
 CC -1- FUNCTION: PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS THAT ARE
 CC ALL LOCATED EITHER IN THE CENTRAL NERVOUS SYSTEM OR DIRECTLY
 CC CONNECTED TO IT.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
 CC -----
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 CC -----
 DR EMBL; M83377; AAC42220.1; -;
 DR EMBL; X61476; CAA43704.1; -;
 DR HSSP; P23560; 1BBM.
 DR InterPro: IPR002072; NCF.
 DR Pfam: PF00243; NCF_1.
 DR PRINTS; PR00268; NCF.
 DR ProDom: PD002052; NCF_1.
 DR SMART; SM00140; NCF_1.
 DR PROSITE; PS00248; NCF_1; 1.
 DR PROSITE; PS50270; NCF_2; 1.
 DR Growth factor: Signal
 FT PROPEP 1 18 POTENTIAL.
 FT CHAIN 128 246 BRAIN-DERIVED NEUROTROPHIC FACTOR.
 FT SITE 57 58 CLEAVAGE (BY S1P) (BY SIMILARITY).
 FT DISULFID 140 207 BY SIMILARITY.
 FT DISULFID 185 236 BY SIMILARITY.
 FT DISULFID 195 238 BY SIMILARITY.
 FT CARBOHYD 120 120 N-LINKED (GLCNAC...) (POTENTIAL).
 SO SEQUENCE 246 AA; 27714 MW; CE1D93BE9FDD3BA0 CRC64;
 Query Match 92.6%; Score 592.5; DB 1; Length 246;
 Best Local Similarity 93.3%; Pred. No. 1.5e-55;
 Matches 111; Conservative 3; Mismatches 4; Indels 1; Gaps 1;
 QY 2 HSDPARRGELSYCDISISEMTAAADKRTAVMSGCTVYLEKVPVSGQLOKQFYETKCNP 61
 DB 128 HSDPARRGELSYCDISISEMTAAADKRTAVMSGCTVYLEKVPVSGQLOKQFYETKCNP 187
 QY 62 MGYTKEGCGIDKRRHNSOCRTOSYVVALTMDSKRRIGRFRIDTSCV-TLTIKGR 119
 DB 188 MGYTKEGCGIDKRRHNSOCRTOSYVVALTMDSKRRIGRFRIDTSCVTLTIKGR 246
 RESULT 13
 BDNF_CYPCA STANDARD: PRT: 270 AA.
 AC Q90322;

DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Brain-derived neurotrophic factor precursor (BDNF).
 GN BDNF.
 OS Cyprinus carpio (Common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Cyprinus.
 RN NCBI_TaxID=7962;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Liu T.S., Chang G.D., Huang F.L., Lo T.B.;
 RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS THAT ARE
 ALL LOCATED EITHER IN THE CENTRAL NERVOUS SYSTEM OR DIRECTLY
 CONNECTED TO IT (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE NCF-BETA FAMILY.
 CC -----
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 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: L27171; AAA49204.1; -
 DR HSSP: P23560; 1BBM.
 DR InterPro: IPR002072; NCF.
 DR Pfam: PF00243; NCF. 1.
 DR PRINTS: PR00268; NCF.
 DR PRODOM: PD002052; NCF. 1.
 DR SMART: SM00140; NCF. 1.
 DR PROSITE: PS00248; NCF. 1; 1.
 DR PROSITE: PS00270; NCF_2; 1.
 DR Growth factor; Signal.
 KM Growth factor; Signal.
 FT PROPEP 1 18
 FT CHAIN 152 270
 FT DISULFID 164 231
 FT DISULFID 209 260
 FT DISULFID 219 262
 FT CARBOHYD 144 144
 SQ SEQUENCE 270 AA: 29572 MW: 049DEIECE4742EAA CRC64;
 Query Match 90.5%; Score 579.5; DB 1; Length 270;
 Best Local Similarity 90.8%; Pred. No. 4e-54;
 Matches 108; Conservative 7; Mismatches 3; Indels 1; Gaps 1;
 Oy 2 HSDPARRGELSVCDISISEWYTAADKTAADVMSGCTVYLEKVPVSKQLKQYFETKCNP 61
 DB 152 HSDPARRGELSVCDISISEWYTAADKTAADVMSGCTVYLEKVPVSKQLKQYFETKCNP 211
 Oy 62 MGYTKEGCGRIDKRRHNSOCTTOSYVRALTNDSKKRIGRRIRIDTSCV-TITIKRGR 119
 DB 212 LGYTKGCGRIDKRRHNSOCTTOSYVRALTNDSKKRIGRRIRIDTSCVCTLTIKRGR 270
 RESULT 14
 BDNF_XIPMA STANDARD: PRT: 269 AA.
 ID BDNF_XIPMA
 AC 001193;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Brain-derived neurotrophic factor precursor (BDNF).
 GN BDNF.
 OS Xiphophorus maculatus (Southern platyfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percormorpha; Atherinomorpha;
 OC Cyprinodontiformes; Poeciliidae; Xiphophorus.
 RN NCBI_TaxID=8083;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92333301; PubMed=1629719;
 RA Gatz R., Raulf F., Scharl M.;
 RT "Brain-derived neurotrophic factor is more highly conserved in
 structure and function than nerve growth factor during vertebrate
 evolution.";
 RL J. Neurochem. 59:432-442(1992).
 CC -1- FUNCTION: BDNF PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS THAT
 ARE ALL LOCATED EITHER IN THE CENTRAL NERVOUS SYSTEM OR DIRECTLY
 CONNECTED TO IT.
 CC -1- SIMILARITY: BELONGS TO THE NCF-BETA FAMILY.
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 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: X59943; CAA42567.1; -
 DR HSSP: P23560; 1BBM.
 DR InterPro: IPR002072; NCF.
 DR Pfam: PF00243; NCF. 1.
 DR PRINTS: PR00268; NCF.
 DR PRODOM: PD002052; NCF. 1.
 DR SMART: SM00140; NCF. 1.
 DR PROSITE: PS00248; NCF. 1; 1.
 DR PROSITE: PS00270; NCF_2; 1.
 DR Growth factor; Signal.
 KM Growth factor; Signal.
 FT PROPEP 1 18
 FT CHAIN 151 269
 FT DISULFID 163 230
 FT DISULFID 208 259
 FT DISULFID 218 261
 FT CARBOHYD 143 143
 SQ SEQUENCE 269 AA: 29709 MW: DA6774B7923E5E52 CRC64;
 Query Match 89.1%; Score 570.5; DB 1; Length 269;
 Best Local Similarity 89.1%; Pred. No. 3.5e-53;
 Matches 106; Conservative 7; Mismatches 5; Indels 1; Gaps 1;
 Oy 2 HSDPARRGELSVCDISISEWYTAADKTAADVMSGCTVYLEKVPVSKQLKQYFETKCNP 61
 DB 151 HSDPARRGELSVCDISISEWYTAADKTAADVMSGCTVYLEKVPVSKQLKQYFETKCNP 210
 Oy 62 MGYTKEGCGRIDKRRHNSOCTTOSYVRALTNDSKKRIGRRIRIDTSCV-TITIKRGR 119
 DB 211 MGYTKEGCGRIDKRRHNSOCTTOSYVRALTNDSKKRIGRRIRIDTSCVCTLTIKRGR 269
 RESULT 15
 BDNF_XENLA STANDARD: PRT: 114 AA.
 ID BDNF_XENLA
 AC P23432;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Brain-derived neurotrophic factor (BDNF) (Fragment).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 RN NCBI_TaxID=8355;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91309745; PubMed=1906813;
 RA Isackson P.J., Towne M.D., Huntsman M.M.;

RT *Comparison of mammalian, chicken and Xenopus brain-derived
RT neurotrophic factor coding sequences.*;
RL FEBS Lett. 285:260-264(1991).
RN [2]
RP SEQUENCE OF 58-100 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE-91222573: PubMed-2025430:
RA Halboeck F., Ibanez C.F., Persson H.;
RT *Evolutionary studies of the nerve growth factor family reveal a
RL novel member abundantly expressed in Xenopus ovary.*;
Neuron 6:845-858(1991).
CC -1- FUNCTION: PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS THAT ARE
CC ALL LOCATED EITHER IN THE CENTRAL NERVOUS SYSTEM OR DIRECTLY
CC CONNECTED TO IT.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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CC -----
DR EMBL: X61477; GAA43705.1; -.
DR HSPF: P23560; IBLND.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF; 1.
DR ProDom: PD002052; NGF; 1.
DR SMART: SM00140; NGF; 1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS50270; NGF_2; 1.
KW Growth factor.
FT NON_TER 1 1
FT DISULFID 14 81 BY SIMILARITY.
FT DISULFID 59 110 BY SIMILARITY.
FT DISULFID 69 112 BY SIMILARITY.
FT CONFLICT 73 73 E -> D (IN REF. 2).
FT CONFLICT 96 96 K -> R (IN REF. 2).
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 13031 MW; 409ACFB5B8EAB87 CRC64;

Query Match 87.3% Score 559; DB 1; Length 114;
Best Local Similarity 92.7% Pred. No. 2.3e-52;
Matches 102; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 HSDPARGELSYCDISIKMTAADKKTAVDHSGCTVLEKVPVSKGLKQYFETKCP 61
DB 2 HSDPARGELSYCDISIKMTAADKKTAVDHSGCTVLEKVPVSKGLKQYFETKCP 61
QY 62 MGTKEGCGKRGIDKRHMNSOCRTTOSYVALTMDSKRIGRIFRIDTSCV 111
DB 62 MGTKEGCGKRGIDKRHMNSOCRTTOSYVALTMDSKRIGRIFRIDTSCV 111

Search completed: December 2, 2002, 15:12:43
Job time : 4.88277 secs

GenCore version 5.1.3
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OM protein - protein search, using SW model

Run on: December 2, 2002, 15:05:42 : Search time 18.415 seconds
(without alignments)
1331.501 Million cell updates/sec

Title: US-10-072-681-4

Perfect score: 640
Sequence: 1 PHSDPARRGELGVCSISSEW.....GMRFRIDTSCVLTIRKGR 119

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

Listing first 45 summaries

```

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriophage:*
17: SP archaea:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	622.5	97.3	153	11	09CYL3 mus musculus
2	622.5	97.3	247	6	097759 allurus ful
3	622.5	97.3	249	11	08VH4 mus musculus
4	592.5	92.6	177	13	091812 poephilla gu
5	578.5	90.4	246	13	080675 phrynocephala
6	574.5	89.8	246	13	080676 japalura sp
7	572.5	89.5	270	13	09YH42 brechydano
8	562.5	87.9	246	13	080674 cyclophilops
9	552.5	86.3	247	13	080677 tylosirotito
10	544	85.0	101	6	097722 macaca fusc
11	448	70.0	85	6	002792 notoryctes
12	445	69.5	85	6	013114 isodon mac
13	445	69.5	85	6	013122 tarsipes ro
14	445	69.5	85	6	002795 ornithorhyn
15	445	69.5	85	6	002798 petaurus br
16	445	69.5	85	6	013104 cercartetus

17	445	69.5	85	6	013105	013105 dasyuroides
18	445	69.5	85	6	002801	002801 tachylosus
19	444	69.4	85	6	002803	002803 trichosurus
20	437	68.3	85	6	002790	002790 macropus fu
21	369	57.7	184	6	09BFJ5	09BFJ5 tupia mmo
22	369	57.7	185	6	09BFK5	09BFK5 taipa alta
23	369	57.7	185	6	09BFK5	09BFK5 condylura c
24	369	57.7	186	6	09BFL3	09BFL3 choleopus h
25	369	57.7	186	6	09BFL2	09BFL2 choleopus d
26	369	57.7	186	6	09BFK3	09BFK3 tamandua te
27	369	57.7	186	6	09BFK3	09BFK3 myrmecophag
28	369	57.7	186	6	09BFK4	09BFK4 sorax arane
29	369	57.7	186	6	09BFK2	09BFK2 toxodontia a
30	369	57.7	186	6	09BFK1	09BFK1 oxycerops
31	369	57.7	186	6	09BFJ9	09BFJ9 oxycerops
32	369	57.7	186	6	09BFJ8	09BFJ8 sylviag
33	369	57.7	186	6	09BFJ7	09BFJ7 oclotona hy
34	369	57.7	186	6	09BFJ4	09BFJ4 lemur catla
35	369	57.7	186	6	09BFJ2	09BFJ2 macaca mula
36	369	57.7	186	6	09BFJ1	09BFJ1 hylobates c
37	369	57.7	186	6	09BFJ9	09BFJ9 artibeus ja
38	369	57.7	186	6	09BFJ8	09BFJ8 pteropus gl
39	369	57.7	186	6	09BFJ7	09BFJ7 rousettus ch
40	369	57.7	186	6	09BFJ6	09BFJ6 nycterus ch
41	369	57.7	186	6	09BFJ2	09BFJ2 lama glama
42	369	57.7	186	6	09BFH8	09BFH8 equus cabal
43	369	57.7	186	6	09BFH7	09BFH7 cervatoceri
44	369	57.7	186	6	09BFH6	09BFH6 caprus ind
45	369	57.7	186	6	09BFH5	09BFH5 felis alive

ALIGNMENTS

RESULT 1

09CYL3 PRELIMINARY: PRT: 153 AA.

AC 09CYL3: 01-JUN-2001 (TREMblrel. 17, Created)

DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)

DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)

DE Brain derived neurotrophic factor.

GN BDNF.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RP [1]

RC SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=EMBryo;

RC MEDLINE=21085660; Pubmed=11217851;

RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Aikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I.,

RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochia R.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.H., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boilelli D., Bojunga N., Carlini P., de Bonaldo M.F.,

RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Komdeur P.,

RA Morone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.F.,

RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitlaker C., Wilmig L.,

RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,

RA Hayashizaki Y.

Functional annotation of a full-length mouse cDNA collection.;

RT Nature 409:685-690(2001).

RL EMBL: AK017559; BAB30805.1; -.

DR HSSP: P23560; 188M.

DR MGD: MGI:88145; Bdnf.
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF. 1.
 DR PRINTS: PR00268; NGF. 1.
 DR PRODOM: PD002052; NGF. 1.
 DR SMART: SM00140; NGF. 1.
 DR PROSITE: PS00248; NGF_1; 1.
 DR PROSITE: PS50270; NGF_2; 1.
 DR SEQUENCE 153 AA; 17519 MW; CABEB8944CEE5B37 CRC64;

Query Match 97.3%; Score 622.5; DB 11; Length 153;
 Best Local Similarity 99.2%; Pred. No. 1.4e-62;
 Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARGELSYCDISSEMTAAADKTAVDMSGGTYVLEKVPVSGOLKQYFETKCNP 61
 DB 35 HSDPARGELSYCDISSEMTAAADKTAVDMSGGTYVLEKVPVSGOLKQYFETKCNP 94
 OY 62 MGYTEGCGRIDKRHMNSOCRTTOSYVRLTMDSKKRIGRFRIRIDTSCV-TLTIKRG 119
 DB 95 MGYTEGCGRIDKRHMNSOCRTTOSYVRLTMDSKKRIGRFRIRIDTSCVTLTIKRG 153

RESULT 2

OY 097759 PRELIMINARY; PRT: 247 AA.
 AC 097759;
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE Brain derived neurotrophic factor.
 GN BDNF.
 OS Allurus fulgens (Lesser panda).
 OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Procyonidae; Allurus.
 OX NCBI_Taxid-9649;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Feng L.;
 RT "Giant Panda (GP) and Lesser Panda (LP) BDNF gene sequences and their
 RT deduced amino acid sequences."
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U56639; AAD10843.1; -
 DR HSSP: P23560; 188M.
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF. 1.
 DR PRINTS: PR00268; NGF. 1.
 DR PRODOM: PD002052; NGF. 1.
 DR SMART: SM00140; NGF. 1.
 DR PROSITE: PS00248; NGF_1; 1.
 DR PROSITE: PS50270; NGF_2; 1.
 DR SEQUENCE 247 AA; 27870 MW; FEECGZCFIA6C03EE CRC64;

Query Match 97.3%; Score 622.5; DB 6; Length 247;
 Best Local Similarity 99.2%; Pred. No. 2.4e-62;
 Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARGELSYCDISSEMTAAADKTAVDMSGGTYVLEKVPVSGOLKQYFETKCNP 61
 DB 129 HSDPARGELSYCDISSEMTAAADKTAVDMSGGTYVLEKVPVSGOLKQYFETKCNP 188
 OY 62 MGYTEGCGRIDKRHMNSOCRTTOSYVRLTMDSKKRIGRFRIRIDTSCV-TLTIKRG 119
 DB 189 MGYTEGCGRIDKRHMNSOCRTTOSYVRLTMDSKKRIGRFRIRIDTSCVTLTIKRG 247

RESULT 3

OY 09VHN4 PRELIMINARY; PRT: 249 AA.

AC 09VHN4;
 DT 01-MAR-2002 (TREMblrel. 20, Created)
 DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)

DE Anorexia BDNF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_Taxid-10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-B6C3FE-A/A-ANXA/4A;
 RA Kim S.J., Kim C.S., Cha Y.J., Song K.Y., Yeo M.G.;
 RT Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AF459642; AAL58475.1; -
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF. 1.
 DR PRINTS: PR00268; NGF. 1.
 DR PRODOM: PD002052; NGF. 1.
 DR SMART: SM00140; NGF. 1.
 DR PROSITE: PS00248; NGF_1; UNKNOWN_1.
 DR PROSITE: PS50270; NGF_2; 1.
 DR SEQUENCE 249 AA; 28109 MW; 21CEAE60A235D97 CRC64;

Query Match 97.3%; Score 622.5; DB 11; Length 249;
 Best Local Similarity 99.2%; Pred. No. 2.5e-62;
 Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARGELSYCDISSEMTAAADKTAVDMSGGTYVLEKVPVSGOLKQYFETKCNP 61
 DB 131 HSDPARGELSYCDISSEMTAAADKTAVDMSGGTYVLEKVPVSGOLKQYFETKCNP 190
 OY 62 MGYTEGCGRIDKRHMNSOCRTTOSYVRLTMDSKKRIGRFRIRIDTSCV-TLTIKRG 119
 DB 191 MGYTEGCGRIDKRHMNSOCRTTOSYVRLTMDSKKRIGRFRIRIDTSCVTLTIKRG 249

RESULT 4

OY 091812 PRELIMINARY; PRT: 177 AA.
 AC 091812;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE BDNF (Fragment).
 OS Poephila guttata (zebra finch) (Taeniopygia guttata).
 OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Passeriformes; Estrildidae;
 OC Estrildinae; Taeniopygia.
 OX NCBI_Taxid-59729;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20193595; PubMed-10727739;
 RA Johnson F., Norstrom E., Soderstrom K.;
 RT "Increased expression of endogenous biotin, but not BDNF, in
 RT telencephalic song regions during zebra finch vocal learning."

RL Brain Res. Dev. Brain Res. 120:113-123(2000).
 DR EMBL: AF255389; AAF78050.2; -
 DR HSSP: P23560; 188M.
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF. 1.
 DR PRODOM: PD002052; NGF. 1.
 DR PRINTS: PR00268; NGF. 1.
 DR SMART: SM00140; NGF. 1.
 DR PROSITE: PS00248; NGF_1; 1.
 DR PROSITE: PS50270; NGF_2; 1.
 DR NON_TER 1
 FT 1
 SQ SEQUENCE 177 AA; 20273 MW; BDB9031515BD369D CRC64;

Query Match 92.6%; Score 592.5; DB 13; Length 177;
 Best Local Similarity 93.3%; Pred. No. 4.1e-59;
 Matches 111; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

OY 2 HSDPARGELSYCDISSEMTAAADKTAVDMSGGTYVLEKVPVSGOLKQYFETKCNP 61
 DB 59 HSDPARGELSYCDISSEMTAAADKTAVDMSGGTYVLEKVPVSGOLKQYFETKCNP 118

QY 62 MGYTKEGCGIDKRRHNSOCRTTOSYVRALTMDSKKRIGRFRIRDTSCV-TLTIKGR 119
|||||
DB 119 KGYTKEGCGIDKRRHNSOCRTTOSYVRALTMDSKKRIGRFRIRDTSCVTLTIKGR 117

RESULT 5

ID 080G75 PRELIMINARY; PRT; 246 AA.
AC 080G75;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Brain derived neurotrophic factor.
GN BDNF.
OS Phrynocephalus hongyuanensis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agamini;
OC Phrynocephalus.
OX NCBI_Taxid=171648;
RN [1]
RP SEQUENCE FROM N.A.
RA Cao M., Yang Y.H., Zhang Y.Z.;
RT "Molecular cloning of brain derived neurotrophic factor gene from
RT amphibians and reptiles and its application in the research of
RT phylogeny and taxonomy."
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF497714; AAM18715.1; -
FT CHAIN 128 246 BRAIN DERIVED NEUROTROPHIC FACTOR
FT PRECURSOR.
SQ SEQUENCE 246 AA; 27792 MW; 7709D3058B7AFA30 CRC64;

Query Match 90.4%; Score 578.5; DB 13; Length 246;
Best Local Similarity 91.6%; Pred. No. 2,3e-57;
Matches 109; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 2 HSDPARRGELSYVDSISSEWTAADKRTAVDSGGTVLEKVPVSKGLQKQYETKCNP 61
|||||
DB 128 HSDPARRGELSYVDSISSEWTAADKRTAVDSGGTVLEKVPVSKGLQKQYETKCNP 187
62 MGYTKEGCGIDKRRHNSOCRTTOSYVRALTMDSKKRIGRFRIRDTSCV-TLTIKGR 119
|||||
DB 188 KGYTKEGCGIDKRRHNSOCRTTOSYVRALTMDSKKRIGRFRIRDTSCVTLTIKGR 246

RESULT 6

ID 080G76 PRELIMINARY; PRT; 246 AA.
AC 080G76;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Brain derived neurotrophic factor.
GN BDNF.
OS Japalura splendida.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Japalura.
OX NCBI_Taxid=118209;
RN [1]
RP SEQUENCE FROM N.A.
RA Cao M., Yang Y.H., Zhang Y.Z.;
RT "Molecular cloning of brain derived neurotrophic factor gene from
RT amphibians and reptiles and its application in the research of
RT phylogeny and taxonomy."
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF497713; AAM18714.1; -
FT CHAIN 128 246 BRAIN DERIVED NEUROTROPHIC FACTOR
FT PRECURSOR.
SQ SEQUENCE 246 AA; 27883 MW; 47B1A03DA88EF78 CRC64;

Query Match 89.8%; Score 574.5; DB 13; Length 246;
Best Local Similarity 90.8%; Pred. No. 6,6e-57;

Matches 108; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 2 HSDPARRGELSYVDSISSEWTAADKRTAVDSGGTVLEKVPVSKGLQKQYETKCNP 61
|||||
DB 128 HSDPARRGELSYVDSISSEWTAADKRTAVDSGGTVLEKVPVSKGLQKQYETKCNP 187
62 MGYTKEGCGIDKRRHNSOCRTTOSYVRALTMDSKKRIGRFRIRDTSCV-TLTIKGR 119
|||||
DB 188 KGYTKEGCGIDKRRHNSOCRTTOSYVRALTMDSKKRIGRFRIRDTSCVTLTIKGR 246

RESULT 7

ID 09YH42 PRELIMINARY; PRT; 270 AA.
AC 09YH42;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Brain-derived neurotrophic factor.
GN BDNF.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_Taxid=9955;
RN [1]
RP SEQUENCE FROM N.A.
RA Hashimoto M., Heinrich G.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: U42489; AAD00016.1; -
DR HSP: P23560; 1BRW.
DR ZFIN: ZDB-GENE-000412-1; bdnf.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF; 1.
DR PRINTS: PR00268; NGF.
DR ProDom: PD002052; NGF; 1.
DR SMART: SM00140; NGF; 1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS00270; NGF_2; 1.
SQ SEQUENCE 270 AA; 29482 MW; 6BF136101BAE45C0 CRC64;

Query Match 89.5%; Score 572.5; DB 13; Length 270;
Best Local Similarity 89.9%; Pred. No. 1,2e-56;
Matches 107; Conservative 7; Mismatches 4; Indels 1; Gaps 1;

QY 2 HSDPARRGELSYVDSISSEWTAADKRTAVDSGGTVLEKVPVSKGLQKQYETKCNP 61
|||||
DB 152 HSDPARRGELSYVDSISSEWTAADKRTAVDSGGTVLEKVPVSKGLQKQYETKCNP 211
62 MGYTKEGCGIDKRRHNSOCRTTOSYVRALTMDSKKRIGRFRIRDTSCV-TLTIKGR 119
|||||
DB 212 LGYTKGCGIDKRRHNSOCRTTOSYVRALTMDSKKRIGRFRIRDTSCVTLTIKGR 270

RESULT 8

ID 080G74 PRELIMINARY; PRT; 246 AA.
AC 080G74;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Brain derived neurotrophic factor.
GN BDNF.
OS Cyclophiops major.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubridae;
OC Colubridae; Colubridae; Cyclophiops.
OX NCBI_Taxid=192173;
RN [1]
RP SEQUENCE FROM N.A.
RA Cao M., Yang Y.H., Zhang Y.Z.;
RT "Molecular cloning of brain derived neurotrophic factor gene from
RT amphibians and reptiles and its application in the research of

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RT phylogeny and taxonomy."
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF497715; AAA18716.1;
FT CHAIN 128 246 BRAIN DERIVED NEUROTROPHIC FACTOR
FT SEQUENCE 246 AA; 27773 MW; BA0178034937856 CRC64;
SQ
Query Match
Best Local Similarity 89.1%; Pred. No. 1.5e-55;
Matches 106; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

OY 2 HSDPARGLSVCDSTSEWTAADKKTAVDMGSGTIVLEKVPVSKGLKQYFETKCNP 61
DB 128 HSDPARGLSVCDSTSEWTAADKKTAVDMGSGTIVLEKVPVSKGLKQYFETKCNP 187
OY 62 MGTYKCGRCIGIDKRHMNSOCRTQSYVALTMDSKKRIGRFRIDTSCV-TLTIKGR 119
DB 188 KGAKKCGRCIGIDKRHMNSOCRTQSYVALTMDSKKRIGRFRIDTSCVCTLTIKGR 246

RESULT 9
OY 080G77 PRELIMINARY; PRT: 247 AA.
AC 080G77;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DR 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Brain derived neurotrophic factor.
OS Tylosorion tallangensis.
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidae; Salamandridae;
OC Tylosorion.
OX NCBI_TaxID=12985;
RN 11
RP SEQUENCE FROM N.A.
RA Cao M., Yang Y.H., Zhang Y.Z.;
RT "Cloning and sequence analysis of brain derived neurotrophic factor
RT (BDNF) gene from Sichuan Newt (Tylosorion tallangensis).";
RL Ying Yung Yu Huan Ching Sheng Wu Hsueh Pao 8:0-0(2002).
DR EMBL: AF497712; AAA18076.1;
SQ SEQUENCE 247 AA; 27841 MW; FFCB5F28F620DE0 CRC64;

Query Match
Best Local Similarity 86.3%; Score 552.5; DB 13; Length 247;
Matches 105; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

OY 2 HSDPARGLSVCDSTSEWTAADKKTAVDMGSGTIVLEKVPVSKGLKQYFETKCNP 61
DB 129 HSDPARGLSVCDSTSEWTAADKKTAVDMGSGTIVLEKVPVSKGLKQYFETKCNP 188
OY 62 MGTYKCGRCIGIDKRHMNSOCRTQSYVALTMDSKKRIGRFRIDTSCV-TLTIKGR 119
DB 189 MGTYKCGRCIGIDKRHMNSOCRTQSYVALTMDSKKRIGRFRIDTSCVCTLTIKGR 247

RESULT 10
OY 09TT22 PRELIMINARY; PRT: 101 AA.
AC 09TT22;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DR 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Brain-derived neurotrophic factor (Fragment).
OS BDNF.
OC Macaca fasciata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9542;
RN 11
RP SEQUENCE FROM N.A.
RA Hashimoto T., Okuno H., Tokuyama W., Li Y.-X., Miyashita Y.;

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RT "Expression of brain-derived neurotrophic factor, neurotrophin-3 and
RT their receptor messenger RNAs in monkey rhinal cortex.";
RL Neuroscience 0:0-0(1999).
RN 12
RP SEQUENCE FROM N.A.
RC TISSUE-BLOOD;
RX MEDLINE=99270338; PubMed=10340513;
RA Okuno H., Tokuyama W., Li Y.-X., Hashimoto T., Miyashita Y.;
RT "Quantitative evaluation of neurotrophin and trk mRNA expression in
RT visual and limbic areas along the occipito-temporo-hippocampal pathway
RT in adult macaque monkeys.";
RL J. Comp. Neurol. 408:378-398(1999).
DR EMBL: AF208982; AAF24762.1;
DR HSSP: P23560; 1BND.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF. 1.
DR PRINTS: PR00268; NGF.
DR PRODOM: PD002052; NGF. 1.
DR SMART: SM00140; NGF. 1.
DR PROSITE: PS00248; NGF. 1.
DR PROSITE: PS50270; NGF. 2; 1.
FT NON_TER 1 101
FT SEQUENCE 101 AA; 11476 MW; D6A56BD497961740 CRC64;
SQ
Query Match
Best Local Similarity 85.0%; Score 544; DB 6; Length 101;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 LSVCDISEWTAADKKTAVDMGSGTIVLEKVPVSKGLKQYFETKCNPMGYTKGCR 70
DB 1 LSVCDISEWTAADKKTAVDMGSGTIVLEKVPVSKGLKQYFETKCNPMGYTKGCR 60
OY 71 GIDKRHMNSOCRTQSYVALTMDSKKRIGRFRIDTSCV 111
DB 61 GIDKRHMNSOCRTQSYVALTMDSKKRIGRFRIDTSCV 101

RESULT 11
OY 002792 PRELIMINARY; PRT: 85 AA.
AC 002792;
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DR 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Brain-derived neurotrophic factor (Fragment).
OS Notoryctes typhlops (Marasipal mole).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Notoryctemorphia; Notoryctidae; Notoryctes.
OX NCBI_TaxID=37699;
RN 11
RP SEQUENCE FROM N.A.
RA Kullander K., Carlson B., Hallbook F.;
RT "Molecular phylogeny and evolution of the neurotrophins from
RT Monotremes and Marsupials.";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U93380; AAB5685.1;
DR HSSP: P23560; 1BND.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF. 1.
DR PRINTS: PR00268; NGF.
DR PRODOM: PD002052; NGF. 1.
DR SMART: SM00140; NGF. 1.
DR PROSITE: PS00248; NGF. 1.
DR PROSITE: PS50270; NGF. 2; 1.
FT NON_TER 1 85
FT SEQUENCE 85 AA; 9577 MW; 33754EA015314661 CRC64;
SQ
Query Match
Best Local Similarity 97.6%; Score 448; DB 6; Length 85;
Matches 83; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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OY 16 SISEWTAADKKTAVDMSGGTIVLEKVPVSKGOLKQYFETKCNPMGYTKKCGRCIDKR 75
DB 1 SISEWTAADKKTAVDMSGGTIVLEKVPVSKGOLKQYFETKCNPMGYTKKCGRCIDKR 60
OY 76 HNSOCCRTTOSYVRALTMDSKKRIG 100
DB 61 HNSOCCRTTOSYVRALTMDSKKRIG 85

RESULT 12
OY 013114 PRELIMINARY; PRT; 85 AA.
AC 013114;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Brain-derived neurotrophic factor (Fragment).
GN BDNF.
OS Isodon macrurus (Short-nosed bandicoot).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Peramelomorpha; Peramelidae; Isodon.
OX NCBI_TaxID=37698;
RN [1]
RP SEQUENCE FROM N.A.
RA Kullander K., Carlson B., Hallbook F.;
RT "Molecular phylogeny and evolution of the neurotrophins from
RT Monotremes and Marsupials.";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U93374; AAB58679.1; -.
DR HSSP; P23560; 1BND.
DR InterPro; IPR02072; NGF.
DR Pfam; PF00243; NGF. 1.
DR PRINTS; PR00268; NGF.
DR PRODOM; PD002052; NGF. 1.
DR SMART; SM00140; NGF. 1.
DR PROSITE; PS00248; NGF_1; 1.
DR PROSITE; PS50270; NGF_2; 1.
FT NON_TER 1
FT NON_TER 85
SQ SEQUENCE 85 AA; 9604 MW; 33754EA01520B661 CRC64;

Query Match 69.5%; Score 445; DB 6; Length 85;
Best Local Similarity 96.5%; Pred. No. 8.4e-43;
Matches 82; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 16 SISEWTAADKKTAVDMSGGTIVLEKVPVSKGOLKQYFETKCNPMGYTKKCGRCIDKR 75
DB 1 SISEWTAADKKTAVDMSGGTIVLEKVPVSKGOLKQYFETKCNPMGYTKKCGRCIDKR 60
OY 76 HNSOCCRTTOSYVRALTMDSKKRIG 100
DB 61 HNSOCCRTTOSYVRALTMDSKKRIG 85

RESULT 13
OY 013122 PRELIMINARY; PRT; 85 AA.
AC 013122;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Brain-derived neurotrophic factor (Fragment).
GN BDNF.
OS Tarapetes rostratus (honey possum).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Tarsipedidae; Tarsipes.
OX NCBI_TaxID=38632;
RN [1]
RP SEQUENCE FROM N.A.
RA Kullander K., Carlson B., Hallbook F.;
RT "Molecular phylogeny and evolution of the neurotrophins from
RT Monotremes and Marsupials.";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
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RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U93375; AAB58680.1; -.
DR HSSP; P23560; 1BND.
DR InterPro; IPR02072; NGF.
DR Pfam; PF00243; NGF. 1.
DR PRINTS; PR00268; NGF.
DR PRODOM; PD002052; NGF. 1.
DR SMART; SM00140; NGF. 1.
DR PROSITE; PS00248; NGF_1; 1.
DR PROSITE; PS50270; NGF_2; 1.
FT NON_TER 1
FT NON_TER 85
SQ SEQUENCE 85 AA; 9604 MW; 33754EA01520B661 CRC64;

Query Match 69.5%; Score 445; DB 6; Length 85;
Best Local Similarity 96.5%; Pred. No. 8.4e-43;
Matches 82; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 16 SISEWTAADKKTAVDMSGGTIVLEKVPVSKGOLKQYFETKCNPMGYTKKCGRCIDKR 75
DB 1 SISEWTAADKKTAVDMSGGTIVLEKVPVSKGOLKQYFETKCNPMGYTKKCGRCIDKR 60
OY 76 HNSOCCRTTOSYVRALTMDSKKRIG 100
DB 61 HNSOCCRTTOSYVRALTMDSKKRIG 85

RESULT 14
OY 002795 PRELIMINARY; PRT; 85 AA.
AC 002795;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Brain-derived neurotrophic factor (Fragment).
GN BDNF.
OS Ornithorhynchus anatinus (Duckbill platypus).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
OX NCBI_TaxID=9258;
RN [1]
RP SEQUENCE FROM N.A.
RA Kullander K., Carlson B., Hallbook F.;
RT "Molecular phylogeny and evolution of the neurotrophins from
RT Monotremes and Marsupials.";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U93376; AAB58681.1; -.
DR HSSP; P23560; 1BND.
DR InterPro; IPR02072; NGF.
DR Pfam; PF00243; NGF. 1.
DR PRINTS; PR00268; NGF.
DR PRODOM; PD002052; NGF. 1.
DR SMART; SM00140; NGF. 1.
DR PROSITE; PS00248; NGF_1; 1.
DR PROSITE; PS50270; NGF_2; 1.
FT NON_TER 1
FT NON_TER 85
SQ SEQUENCE 85 AA; 9604 MW; 33754EA01520B661 CRC64;

Query Match 69.5%; Score 445; DB 6; Length 85;
Best Local Similarity 96.5%; Pred. No. 8.4e-43;
Matches 82; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 16 SISEWTAADKKTAVDMSGGTIVLEKVPVSKGOLKQYFETKCNPMGYTKKCGRCIDKR 75
DB 1 SISEWTAADKKTAVDMSGGTIVLEKVPVSKGOLKQYFETKCNPMGYTKKCGRCIDKR 60
OY 76 HNSOCCRTTOSYVRALTMDSKKRIG 100
DB 61 HNSOCCRTTOSYVRALTMDSKKRIG 85

RESULT 15
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002798
ID 002798 PRELIMINARY: PRT: 85 AA.
AC 002798:
DT 01-JUL-1997 (TRENBLREL. 04, Created)
DT 01-JUL-1997 (TRENBLREL. 04, Last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE Brain-derived neurotrophic factor (Fragment).
GN BDNF.
OS Petrus biceps (Australian sugar gilder).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Petauridae; Petrus.
OX NCB:Taxid=34899;
RN (1)
RP SEQUENCE FROM N.A.
RA Kullander K., Carlson B., Hallbook F.;
RT "Molecular phylogeny and evolution of the neurotrophins from
RT Monotremes and Marsupials."
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U93377; AAB58682.1; -.
DR HSSP: P23560; 1BND.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF; 1.
DR PRINTS: PR00268; NGF.
DR PRODOM: PD002052; NGF; 1.
DR SMART: SM00140; NGF; 1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS0270; NGF_2; 1.
FT NON_TER 1
FT NON_TER 85
SQ SEQUENCE 85 AA; 9604 MW; 33754EA01520B661 CRC64;

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Query Match 59.58; Score 445; DB 6; Length 85;
Best Local Similarity 96.58; Pred. No. 8,4e-43;
Matches 82; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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OY 16 SISENTAADKKTAVDMSCGTVLEKVPVSKGOLKQFYETKCNPMGYTKESCRGIDKR 75
Db 1 SISENTAADKKTAVDMSCGTVLEKVPVSKGOLKQFYETKCNPMGYTKESCRGIDKR 60
OY 76 HNSOCTRTOSTYVRLATMDSKKRIG 100
Db 61 HNSOCTRTOSTYVRLATMDSKKRIG 85

```

Search completed: December 2, 2002, 15:12:02
 Job time : 19.415 secs

NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Minipath (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/970,865
FILING DATE: 14-NO. 6005081-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030838
FILING DATE: 11/15/1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047855
FILING DATE: 5/29/1997
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1063R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-970-865-4

Query Match 98.9%: Score 633; DB 3; Length 118;
Best Local Similarity 100.0%; Pred. No. 4.9e-64;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HSDPARGELSVCDISISEWTAADKRTAVDMSCGTIVLEKVPVSKGLKQYFETKCNP 61
DB 1 HSDPARGELSVCDISISEWTAADKRTAVDMSCGTIVLEKVPVSKGLKQYFETKCNP 60

QY 62 MGYTKEGCGIDKRRHNSCCTTOSYVRLTMDSKKRIGRFIRIDTSCVLTITIKRGR 119
DB 61 MGYTKEGCGIDKRRHNSCCTTOSYVRLTMDSKKRIGRFIRIDTSCVLTITIKRGR 118

RESULT 3
US-08-581-662-3
Sequence 3, Application US/08581662
Patent No. 6121235
GENERAL INFORMATION:
APPLICANT: Gao, Wei-Qiang
TITLE OF INVENTION: Treatment of Balance Impairments
FILE REFERENCE: P0981
CURRENT APPLICATION NUMBER: US/08/581,662
CURRENT FILING DATE: 1995-12-29
NUMBER OF SEQ ID NOS: 36
SEQ ID NO 3
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens
US-08-581-662-3

Query Match 98.9%: Score 633; DB 3; Length 118;
Best Local Similarity 100.0%; Pred. No. 4.9e-64;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HSDPARGELSVCDISISEWTAADKRTAVDMSCGTIVLEKVPVSKGLKQYFETKCNP 61
DB 1 HSDPARGELSVCDISISEWTAADKRTAVDMSCGTIVLEKVPVSKGLKQYFETKCNP 60

DB 1 HSDPARGELSVCDISISEWTAADKRTAVDMSCGTIVLEKVPVSKGLKQYFETKCNP 60
QY 62 MGYTKEGCGIDKRRHNSCCTTOSYVRLTMDSKKRIGRFIRIDTSCVLTITIKRGR 119
DB 61 MGYTKEGCGIDKRRHNSCCTTOSYVRLTMDSKKRIGRFIRIDTSCVLTITIKRGR 118

RESULT 4
US-09-363-573-4
Sequence 4, Application US/09363573
Patent No. 6184360
GENERAL INFORMATION:
APPLICANT: Louis E. Burton, Charles H. Schmelzer, Joanne T. Beck
TITLE OF INVENTION: Purification of MGF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Minipath (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,573
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/970,865
FILING DATE: 14-NO. 6184360-1997
APPLICATION NUMBER: 60/030838
FILING DATE: 11/15/1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047855
FILING DATE: 5/29/1997
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1063R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-363-573-4

Query Match 98.9%: Score 633; DB 4; Length 118;
Best Local Similarity 100.0%; Pred. No. 4.9e-64;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HSDPARGELSVCDISISEWTAADKRTAVDMSCGTIVLEKVPVSKGLKQYFETKCNP 61
DB 1 HSDPARGELSVCDISISEWTAADKRTAVDMSCGTIVLEKVPVSKGLKQYFETKCNP 60

QY 62 MGYTKEGCGIDKRRHNSCCTTOSYVRLTMDSKKRIGRFIRIDTSCVLTITIKRGR 119
DB 61 MGYTKEGCGIDKRRHNSCCTTOSYVRLTMDSKKRIGRFIRIDTSCVLTITIKRGR 118

RESULT 5
US-09-664-295-3
Sequence 3, Application US/09664295
Patent No. 6429196
GENERAL INFORMATION:
APPLICANT: Gao, Wei-Qiang
TITLE OF INVENTION: Treatment of Balance Impairments

FILE REFERENCE: GENE 051C1
CURRENT APPLICATION NUMBER: US/09/664,295
CURRENT FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 08/581,662
PRIOR FILING DATE: 1995-12-29
NUMBER OF SEQ ID NOS: 37
SEQ ID NO 3
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens
US-09-664-295-3

Query Match 98.9%: Score 633; DB 4; Length 118;
Best Local Similarity 100.0%: Pred. No. 4,9e-64;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HSDPARRGELSYVCDISSEMTAAADKKTAVDMSGGTVTLKVPVSKGOLKOFYETKCNP 61
DB 1 HSDPARRGELSYVCDISSEMTAAADKKTAVDMSGGTVTLKVPVSKGOLKOFYETKCNP 60
QY 62 MGYTKEGCGIDKRRHNSOCRTTOSYVVALTNDKSKRIGMRFIRIDTSCVTLTIKRG 119
DB 61 MGYTKEGCGIDKRRHNSOCRTTOSYVVALTNDKSKRIGMRFIRIDTSCVTLTIKRG 118

RESULT 6
US-08-440-049-4

Sequence 4, Application US/08440049
Patent No. 5728803
GENERAL INFORMATION:
APPLICANT: Ufer, Roman
APPLICANT: Presta, Leonard G.
APPLICANT: Winshaw, John W.
TITLE OF INVENTION: PANTROPIC NEUTROPHIC FACTORS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Minsalin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,049
FILING DATE: 12-May-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/253937
FILING DATE: 03-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0905C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-440-049-4

Query Match 97.3%: Score 622.5; DB 1; Length 119;
Best Local Similarity 99.2%: Pred. No. 7,6e-63;
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 HSDPARRGELSYVCDISSEMTAAADKKTAVDMSGGTVTLKVPVSKGOLKOFYETKCNP 61
DB 1 HSDPARRGELSYVCDISSEMTAAADKKTAVDMSGGTVTLKVPVSKGOLKOFYETKCNP 60
QY 62 MGYTKEGCGIDKRRHNSOCRTTOSYVVALTNDKSKRIGMRFIRIDTSCV-TLTIKRG 119
DB 61 MGYTKEGCGIDKRRHNSOCRTTOSYVVALTNDKSKRIGMRFIRIDTSCVTLTIKRG 119

RESULT 7
US-08-441-513A-4

Sequence 4, Application US/08441513A
Patent No. 5981480
GENERAL INFORMATION:
APPLICANT: Ufer, Roman
APPLICANT: Presta, Leonard G.
APPLICANT: Winshaw, John W.
TITLE OF INVENTION: Pantropic Neurotrophic Factors
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Minsalin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,513A
FILING DATE: 15-May-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/253937
FILING DATE: 03-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0905C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-441-513A-4

Query Match 97.3%: Score 622.5; DB 2; Length 119;
Best Local Similarity 99.2%: Pred. No. 7,6e-63;
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 HSDPARRGELSYVCDISSEMTAAADKKTAVDMSGGTVTLKVPVSKGOLKOFYETKCNP 61
DB 1 HSDPARRGELSYVCDISSEMTAAADKKTAVDMSGGTVTLKVPVSKGOLKOFYETKCNP 60
QY 62 MGYTKEGCGIDKRRHNSOCRTTOSYVVALTNDKSKRIGMRFIRIDTSCV-TLTIKRG 119
DB 61 MGYTKEGCGIDKRRHNSOCRTTOSYVVALTNDKSKRIGMRFIRIDTSCVTLTIKRG 119

RESULT 8
PCT-US95-06918-4

Sequence 4, Application PC/TUS9506918
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: PANTROPIC NEUTROPHIC FACTORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06918
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Torchio, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 505PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US95-06918-4

Query Match 97.3%; Score 622.5; DB 5; Length 119;
Best Local Similarity 99.2%; Pred. No. 7.6e-63;
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 HSDPARRGELSVCDISSEMTADKKTAVDMGSGTVVLEKVPVSKGLKQYETKCNP 61
DB 1 HSDPARRGELSVCDISSEMTADKKTAVDMGSGTVVLEKVPVSKGLKQYETKCNP 60
QY 62 MGYTKKCGIDKRRHNSCQRTTOSYVRALTMDSKKRIGMFRIDTSCV-TLTIKGR 119
DB 61 MGYTKKCGIDKRRHNSCQRTTOSYVRALTMDSKKRIGMFRIDTSCVCTLIKGR 119

RESULT 9
US-08-502-348-1
Sequence 1, Application US/08502348
Patent No. 5830857
GENERAL INFORMATION:
APPLICANT: Carnahan, Josette F
APPLICANT: Depaulis, Antoine
APPLICANT: Faltz, Paul
APPLICANT: Larnet, Yves
APPLICANT: Marescaux, Christian
APPLICANT: Nawa, Hiroyuki
TITLE OF INVENTION: METHOD OF TREATING EPILEPSY
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Delavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: US
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/502,348

FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Mazza, Richard J.
REFERENCE/DOCKET NUMBER: A-348
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-502-348-1

Query Match 97.3%; Score 622.5; DB 2; Length 120;
Best Local Similarity 99.2%; Pred. No. 7.7e-63;
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 HSDPARRGELSVCDISSEMTADKKTAVDMGSGTVVLEKVPVSKGLKQYETKCNP 61
DB 2 HSDPARRGELSVCDISSEMTADKKTAVDMGSGTVVLEKVPVSKGLKQYETKCNP 61
QY 62 MGYTKKCGIDKRRHNSCQRTTOSYVRALTMDSKKRIGMFRIDTSCV-TLTIKGR 119
DB 62 MGYTKKCGIDKRRHNSCQRTTOSYVRALTMDSKKRIGMFRIDTSCVCTLIKGR 120

RESULT 10
US-09-214-214A-8
Sequence 8, Application US/09214214A
Patent No. 6211150
GENERAL INFORMATION:
APPLICANT: Boone, Thomas C.
APPLICANT: Cheung, Ellen N.
APPLICANT: Herdenson, Susan I.
APPLICANT: Young, John D.
TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS
FILE REFERENCE: A-411A US Revised 073100
CURRENT APPLICATION NUMBER: US/09/214,214A
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: PCT/US97/12609
PRIOR FILING DATE: 1997-07-17
PRIOR APPLICATION NUMBER: US 08/684,353
PRIOR FILING DATE: 1996-07-19
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 120
TYPE: PRT
ORGANISM: Human
US-09-214-214A-8

Query Match 97.3%; Score 622.5; DB 4; Length 120;
Best Local Similarity 99.2%; Pred. No. 7.7e-63;
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 HSDPARRGELSVCDISSEMTADKKTAVDMGSGTVVLEKVPVSKGLKQYETKCNP 61
DB 2 HSDPARRGELSVCDISSEMTADKKTAVDMGSGTVVLEKVPVSKGLKQYETKCNP 61
QY 62 MGYTKKCGIDKRRHNSCQRTTOSYVRALTMDSKKRIGMFRIDTSCV-TLTIKGR 119
DB 62 MGYTKKCGIDKRRHNSCQRTTOSYVRALTMDSKKRIGMFRIDTSCVCTLIKGR 120

RESULT 11
US-08-451-947-3
Sequence 3, Application US/08451947
Patent No. 5702906
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPIC FACTOR

NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,947
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426419
FILING DATE: 19-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030013
FILING DATE: 22-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 1991
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 666P2C1D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-451-947-3

Query Match 97.3%; Score 622.5; DB 1; Length 247;
Best Local Similarity 99.2%; Pred. No. 1.9e-62;
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 HSDPARRGELSYCDISISEVTAAADKRTAVDMSGGTVLEKVPVSKGLQRYETKCNP 61
DB 129 HSDPARRGELSYCDISISEVTAAADKRTAVDMSGGTVLEKVPVSKGLQRYETKCNP 168
QY 62 MGYTEGCGRIDKRRHNSCRRTOGYVRLALTMDSKKRIGRFRIRIDTSCV-TLTIRGR 119
DB 189 MGYTEGCGRIDKRRHNSCRRTOGYVRLALTMDSKKRIGRFRIRIDTSCVTLTIRGR 247

RESULT 12
US-08-424-826A-3
Sequence 3, Application US/08424826A
Patent No. 5830858
GENERAL INFORMATION:
APPLICANT: Rosenthal, Arnon
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,826A
FILING DATE: 19-APR-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240387
FILING DATE: 10-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 25-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0666PIC2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-424-826A-3

Query Match 97.3%; Score 622.5; DB 2; Length 247;
Best Local Similarity 99.2%; Pred. No. 1.9e-62;
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 HSDPARRGELSYCDISISEVTAAADKRTAVDMSGGTVLEKVPVSKGLQRYETKCNP 61
DB 129 HSDPARRGELSYCDISISEVTAAADKRTAVDMSGGTVLEKVPVSKGLQRYETKCNP 188
QY 62 MGYTEGCGRIDKRRHNSCRRTOGYVRLALTMDSKKRIGRFRIRIDTSCV-TLTIRGR 119
DB 189 MGYTEGCGRIDKRRHNSCRRTOGYVRLALTMDSKKRIGRFRIRIDTSCVTLTIRGR 247

RESULT 13
US-08-595-043A-77
Sequence 77, Application US/08595043A
Patent No. 5935824
GENERAL INFORMATION:
APPLICANT: SCARLATO, GREGORY D.
TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/595,043A
FILING DATE: 31-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: SGAR-00371

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 705-8410
 TELEFAX: (415) 397-8338
 INFORMATION FOR SEQ ID NO: 77:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 247 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-595-043A-77

Query Match 97.3% Score 622.5; DB 2; Length 247;
 Best Local Similarity 99.2%; Pred. No. 1.9e-62;
 Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARRGELSYCDISISEMTAAADKTAVDMSGCTVLEKVPVSKGOLKQYFETKCNP 61
 DB 129 HSDPARRGELSYCDISISEMTAAADKTAVDMSGCTVLEKVPVSKGOLKQYFETKCNP 188
 OY 62 MGYTEGCGRIDKRRHNSCCTTOSYVRLATMDSKRRIGRFRIDTSCV-TLTIRGR 119
 DB 189 MGYTEGCGRIDKRRHNSCCTTOSYVRLATMDSKRRIGRFRIDTSCVTLTIRGR 247

RESULT 14
 US-08-928-694-3
 Sequence 3, Application US/08928694
 Patent No. 6037320

GENERAL INFORMATION:
 APPLICANT: ROSENTHAL, ARNON
 TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
 NUMBER OF SEQUENCES: 100
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/928.694
 FILING DATE: 12-Sep-1997

CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/451947
 FILING DATE: 26-MAY-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/426419
 FILING DATE: 19-APR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/030013
 FILING DATE: 22-MAR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/648482
 FILING DATE: 31-JAN

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/587707
 FILING DATE: 1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Torchia, Ph.D., Timothy E.
 REGISTRATION NUMBER: 36,700
 REFERENCE/DOCKET NUMBER: P06662CJDC1
 TELEPHONE: 650/225-8674
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 247 amino acids

TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-928-694-3

Query Match 97.3% Score 622.5; DB 3; Length 247;
 Best Local Similarity 99.2%; Pred. No. 1.9e-62;
 Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARRGELSYCDISISEMTAAADKTAVDMSGCTVLEKVPVSKGOLKQYFETKCNP 61
 DB 129 HSDPARRGELSYCDISISEMTAAADKTAVDMSGCTVLEKVPVSKGOLKQYFETKCNP 188
 OY 62 MGYTEGCGRIDKRRHNSCCTTOSYVRLATMDSKRRIGRFRIDTSCV-TLTIRGR 119
 DB 189 MGYTEGCGRIDKRRHNSCCTTOSYVRLATMDSKRRIGRFRIDTSCVTLTIRGR 247

RESULT 15
 PCT-US91-06950-3
 Sequence 3, Application PC/TUS9106950

GENERAL INFORMATION:
 APPLICANT: GENENTECH, INC.
 TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
 NUMBER OF SEQUENCES: 100
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US91/06950
 FILING DATE: 19910924

CLASSIFICATION: 436
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/648482
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/587707
 ATTORNEY/AGENT INFORMATION:
 NAME: Hensley, Max D.
 REGISTRATION NUMBER: 27,043
 REFERENCE/DOCKET NUMBER: 666P1

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/266-1994
 TELEFAX: 415/952-9881
 TELEEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 247 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 PCT-US91-06950-3

Query Match 97.3% Score 622.5; DB 5; Length 247;
 Best Local Similarity 99.2%; Pred. No. 1.9e-62;
 Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARRGELSYCDISISEMTAAADKTAVDMSGCTVLEKVPVSKGOLKQYFETKCNP 61
 DB 129 HSDPARRGELSYCDISISEMTAAADKTAVDMSGCTVLEKVPVSKGOLKQYFETKCNP 188
 OY 62 MGYTEGCGRIDKRRHNSCCTTOSYVRLATMDSKRRIGRFRIDTSCV-TLTIRGR 119
 DB 189 MGYTEGCGRIDKRRHNSCCTTOSYVRLATMDSKRRIGRFRIDTSCVTLTIRGR 247

Mon Dec 2 15:36:38 2002

us-10-072-681-4.rai

Page 7

Search completed: December 2, 2002, 15:09:43
Job time : 8.23095 secs

GenCore version 5.1.3
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OK protein - protein search, using sw model

Run on: December 2, 2002, 15:08:47 ; Search time 4.18523 Seconds

(Without alignments)
452.778 Million cell updates/sec

Title: US-10-072-681-4

Perfect score: 640

Sequence: 1 PHSDPARRGELSVCSISBM.....GWRFRIRDTSCVLTIRKGR 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 102317 seqs, 15924203 residues

Total number of hits satisfying chosen parameters: 102317

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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13: /cgn2_6/ptodata/1/pubpaa/US06_NEM_PUB pep:*
14: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	640	100.0	119	12 US-10-072-681-4	Sequence 4, Appl1
2	622.5	97.3	120	10 US-09-745-032-8	Sequence 8, Appl1
3	622.5	97.3	120	10 US-09-742-600-8	Sequence 8, Appl1
4	622.5	97.3	247	8 US-08-450-842-3	Sequence 3, Appl1
5	598.5	93.5	120	10 US-09-745-032-9	Sequence 9, Appl1
6	598.5	93.5	120	10 US-09-742-600-9	Sequence 9, Appl1
7	596.5	93.2	120	10 US-09-742-600-10	Sequence 10, Appl1
8	586.5	93.2	120	10 US-09-742-600-10	Sequence 10, Appl1
9	589.5	92.1	120	9 US-09-813-398-10	Sequence 10, Appl1
10	385	60.2	72	10 US-09-848-664-22	Sequence 22, Appl1
11	346	54.1	120	12 US-10-072-681-5	Sequence 1, Appl1
12	344.5	53.8	120	10 US-09-745-032-1	Sequence 1, Appl1
13	344.5	53.8	120	10 US-09-742-600-1	Sequence 1, Appl1
14	344.5	53.8	120	10 US-09-872-090-1	Sequence 1, Appl1
15	344.5	53.8	257	8 US-08-450-842-4	Sequence 4, Appl1
16	340.5	53.2	119	10 US-09-745-032-6	Sequence 6, Appl1
17	340.5	53.2	119	10 US-09-742-600-6	Sequence 6, Appl1
18	340.5	53.2	119	10 US-09-872-090-6	Sequence 6, Appl1
19	340.5	53.2	120	10 US-09-745-032-3	Sequence 3, Appl1

20	340.5	53.2	120	10 US-09-742-600-3	Sequence 3, Appl1
21	340.5	53.2	120	10 US-09-872-090-3	Sequence 3, Appl1
22	338.5	52.9	130	8 US-08-450-842-47	Sequence 47, Appl1
23	338.5	52.9	132	8 US-08-450-842-51	Sequence 51, Appl1
24	336	52.5	117	10 US-09-745-032-7	Sequence 7, Appl1
25	336	52.5	117	10 US-09-742-600-7	Sequence 7, Appl1
26	336	52.5	117	10 US-09-872-090-7	Sequence 7, Appl1
27	336	52.5	118	10 US-09-745-032-5	Sequence 5, Appl1
28	336	52.5	118	10 US-09-872-090-5	Sequence 5, Appl1
29	336	52.5	118	10 US-09-872-090-5	Sequence 5, Appl1
30	335.5	52.4	130	8 US-08-450-842-23	Sequence 23, Appl1
31	334	52.2	120	9 US-09-813-398-11	Sequence 11, Appl1
32	332.5	52.0	130	8 US-08-450-842-22	Sequence 22, Appl1
33	332.5	52.0	131	9 US-09-813-398-12	Sequence 12, Appl1
34	332.5	52.0	168	8 US-08-450-842-6	Sequence 6, Appl1
35	332.5	52.0	210	8 US-08-450-842-2	Sequence 2, Appl1
36	330.5	51.6	130	8 US-08-450-842-60	Sequence 60, Appl1
37	329.5	51.5	130	8 US-08-450-842-59	Sequence 59, Appl1
38	329.5	51.5	130	8 US-08-450-842-61	Sequence 61, Appl1
39	328.5	51.3	130	8 US-08-450-842-62	Sequence 62, Appl1
40	328.5	51.3	130	8 US-08-450-842-68	Sequence 68, Appl1
41	327.5	51.2	130	8 US-08-450-842-64	Sequence 64, Appl1
42	327.5	51.2	130	8 US-08-450-842-69	Sequence 69, Appl1
43	327.5	51.2	130	8 US-08-450-842-20	Sequence 20, Appl1
44	326.5	51.0	130	8 US-08-450-842-20	Sequence 20, Appl1
45	326.5	51.0	130	8 US-08-450-842-65	Sequence 65, Appl1

ALIGNMENTS

RESULT 1
US-10-072-681-4
Sequence 4, Application US/10072681
Patent No. US20020137893A1
GENERAL INFORMATION:
APPLICANT: Burton, Louis E.
APPLICANT: Schmelzer, Charles H.
TITLE OF INVENTION: PURIFICATION OF NCF
FILE REFERENCE: GENENT.037C3
CURRENT APPLICATION NUMBER: US/10/072,681
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/030838
PRIOR FILING DATE: 1996-11-15
PRIOR APPLICATION NUMBER: 60/047855
PRIOR FILING DATE: 1997-05-29
PRIOR APPLICATION NUMBER: 08/970865
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: 08/363573
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: 09/675,503
PRIOR FILING DATE: 2000-09-29
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 119
TYPE: prt
ORGANISM: Homo sapien
US-10-072-681-4
Query Match 100.0%; Score 640; DB 12; Length 119;
Best Local Similarity 100.0%; Pred. No. 5.7e-65;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 PHSDPARRGELSVCSISBMPTADKTAAYVMSGCTVLEKYPVSKGOLKQYFETKCN 60
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61 PMGYTRGCGIDKXRNHNSOCRTTOSYVRALTDNSKRIRGRIKDTSCVLTIRKGR 119
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61 PMGYTRGCGIDKXRNHNSOCRTTOSYVRALTDNSKRIRGRIKDTSCVLTIRKGR 119
|||||

RESULT 2

US-09-745-032-8

Sequence 8, Application US/09745032
Patent No. US20010027179A1

GENERAL INFORMATION:

APPLICANT: Boone, Thomas C.
APPLICANT: Cheung, Ellen N.
APPLICANT: Hershenson, Susan I.

APPLICANT: Young, John D.

TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS

FILE REFERENCE: A-411A US Revised073100

CURRENT FILING DATE: 2000-12-19

CURRENT APPLICATION NUMBER: US/09/745,032

PRIOR FILING DATE: 1998-12-23

PRIOR APPLICATION NUMBER: US 08/684,353

PRIOR FILING DATE: 1996-07-19

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentln Ver. 2.1

SEQ ID NO 8

LENGTH: 120

TYPE: PRT

ORGANISM: Human

US-09-745-032-8

Query Match

Best Local Similarity 97.3%; Score 622.5; DB 10; Length 120;

Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARGELSVCDISSEMTAADKTAVDMSGGTVTYLEKVPVSKGLKQYFETKCNP 61

DB 2 HSDPARGELSVCDISSEMTAADKTAVDMSGGTVTYLEKVPVSKGLKQYFETKCNP 61

OY 62 MGYTKEGCGIDKRRHNSOCCRTTOSYVRLTMDSKKRIGMRFIRIDTSCV-TLTIKGR 119

DB 62 MGYTKEGCGIDKRRHNSOCCRTTOSYVRLTMDSKKRIGMRFIRIDTSCV-TLTIKGR 120

RESULT 3

US-09-742-600-8

Sequence 8, Application US/09742600
Patent No. US2002001035A1

GENERAL INFORMATION:

APPLICANT: Boone, Thomas C.

APPLICANT: Cheung, Ellen N.

APPLICANT: Hershenson, Susan I.

APPLICANT: Young, John D.

TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS

FILE REFERENCE: A-411A US Revised073100

CURRENT FILING DATE: 2000-12-19

CURRENT APPLICATION NUMBER: US/09/742,600

PRIOR FILING DATE: 1998-12-23

PRIOR APPLICATION NUMBER: US 08/684,353

PRIOR FILING DATE: 1996-07-19

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentln Ver. 2.1

SEQ ID NO 8

LENGTH: 120

TYPE: PRT

ORGANISM: Human

US-09-742-600-8

Query Match

Best Local Similarity 97.3%; Score 622.5; DB 10; Length 120;

Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARGELSVCDISSEMTAADKTAVDMSGGTVTYLEKVPVSKGLKQYFETKCNP 61

DB 2 HSDPARGELSVCDISSEMTAADKTAVDMSGGTVTYLEKVPVSKGLKQYFETKCNP 61

OY 62 MGYTKEGCGIDKRRHNSOCCRTTOSYVRLTMDSKKRIGMRFIRIDTSCV-TLTIKGR 119

DB 62 MGYTKEGCGIDKRRHNSOCCRTTOSYVRLTMDSKKRIGMRFIRIDTSCV-TLTIKGR 120

RESULT 4

US-08-450-842-3

Sequence 3, Application US/08450842
Patent No. US20020045576A1

GENERAL INFORMATION:

APPLICANT: GENENTECH, INC.

APPLICANT: ROSENTHAL, ARNON

TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR

NUMBER OF SEQUENCES: 100

CORRESPONDENCE ADDRESS:

ADDRESS: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 KB floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patln (Genentech)

CURRENT APPLICATION DATA: US/08/450,842

APPLICATION NUMBER: 07/587707

FILING DATE: 1991

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: 666P2C1D3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/952-9881

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 247 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-450-842-3

Query Match

Best Local Similarity 97.3%; Score 622.5; DB 8; Length 247;

Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARGELSVCDISSEMTAADKTAVDMSGGTVTYLEKVPVSKGLKQYFETKCNP 61

DB 129 HSDPARGELSVCDISSEMTAADKTAVDMSGGTVTYLEKVPVSKGLKQYFETKCNP 188

OY 62 MGYTKEGCGIDKRRHNSOCCRTTOSYVRLTMDSKKRIGMRFIRIDTSCV-TLTIKGR 119

DB 189 MGYTKEGCGIDKRRHNSOCCRTTOSYVRLTMDSKKRIGMRFIRIDTSCV-TLTIKGR 247

RESULT 5

US-09-745-032-9

Sequence 9, Application US/09745032
Patent No. US20010027179A1

Query Match

Best Local Similarity 97.3%; Score 622.5; DB 10; Length 120;

Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARGELSVCDISSEMTAADKTAVDMSGGTVTYLEKVPVSKGLKQYFETKCNP 61

DB 2 HSDPARGELSVCDISSEMTAADKTAVDMSGGTVTYLEKVPVSKGLKQYFETKCNP 61

OY 62 MGYTKEGCGIDKRRHNSOCCRTTOSYVRLTMDSKKRIGMRFIRIDTSCV-TLTIKGR 119

DB 189 MGYTKEGCGIDKRRHNSOCCRTTOSYVRLTMDSKKRIGMRFIRIDTSCV-TLTIKGR 247

RESULT 9

US-09-813-398-10
Sequence 10, Application US/09813398
Patent No. US20020169292A1
GENERAL INFORMATION:
APPLICANT: Bruce D. Weintraub
APPLICANT: Mariusz W. Skudlinski
APPLICANT: University of Maryland
TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
FILE REFERENCE: US/09/813,398
CURRENT FILING DATE: 2001-03-20
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: PCT/US99/05908
PRIOR FILING DATE: 1998-09-22
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 120
TYPE: PRT
ORGANISM: HOMO SAPIEN
US-09-813-398-10

Query Match 92.1%; Score 589.5; DB 9; Length 120;
Best Local Similarity 93.3%; Pred. NO. 2.7e-59;
Matches 112; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

QY 1 PHSDPARGELSVCSISEMTYADKRTAVDMGSGTIVLEKVPVSKGOLKOFYETKCN 60
DB 1 PHSDPARGELSVCSISEMTYADKRTAVDMGSGTIVLEKVPVSKGOLKOFYETKCN 60
QY 61 PMGYTEGCGIDKRMNSOCTRTQSYVRLTMDSKKRIGRFRIDTSCV-TLTIRGR 119
DB 61 PMGYTEGCGIDKRMNSOCTRTQSYVRLTMDSKKRIGRFRIDTSCV-TLTIRGR 120

RESULT 10

US-09-848-664-22
Sequence 22, Application US/09848664
Patent No. US2002014641A1
GENERAL INFORMATION:
APPLICANT: Sakiyama-Elbert, Shelly E.
APPLICANT: Hubbell, Jeffrey A.
TITLE OF INVENTION: Controlled Release of No. US2002014641A1-Heparin Binding Growth
FILE REFERENCE: ETH 108
CURRENT APPLICATION NUMBER: US/09/848,664
CURRENT FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: 09/298,084
PRIOR FILING DATE: 1999-04-22
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
LENGTH: 72
TYPE: PRT
ORGANISM: Homo sapiens
US-09-848-664-22

Query Match 60.2%; Score 385; DB 10; Length 72;
Best Local Similarity 100.0%; Pred. NO. 1.3e-36;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HSDPARGELSVCSISEMTYADKRTAVDMGSGTIVLEKVPVSKGOLKOFYETKCN 61
DB 1 HSDPARGELSVCSISEMTYADKRTAVDMGSGTIVLEKVPVSKGOLKOFYETKCN 60
QY 62 MGYTEGCGID 73
DB 61 MGYTEGCGID 72

RESULT 11

US-10-072-681-5
Sequence 5, Application US/10072681
Patent No. US20020137893A1
GENERAL INFORMATION:
APPLICANT: Burton, Louis E.
APPLICANT: Schmelzer, Charles H.
APPLICANT: Beck, Joanne T.
TITLE OF INVENTION: PURIFICATION OF NGF
FILE REFERENCE: GENENT. 037C3
CURRENT APPLICATION NUMBER: US/10/072,681
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/030838
PRIOR FILING DATE: 1996-11-15
PRIOR APPLICATION NUMBER: 60/047855
PRIOR FILING DATE: 1997-05-29
PRIOR APPLICATION NUMBER: 08/970865
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: 09/363573
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: 09/675,503
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 120
TYPE: PRT
ORGANISM: Homo sapien
US-10-072-681-5

Query Match 54.1%; Score 346; DB 12; Length 120;
Best Local Similarity 55.4%; Pred. NO. 5.6e-32;
Matches 67; Conservative 21; Mismatches 29; Indels 4; Gaps 3;

QY 1 PHSD-PARGELSVCSISEMTYADKRTAVDMGSGTIVLEKVPVSKGOLKOFYETKCN 59
DB 1 PYAEHKSREYVCSSESLEMT--DKSAIDIRGHVTVLGEIKTGNPVKOLFETKCN 58
QY 60 NPMGYTEGCGIDKRMNSOCTRTQSYVRLTMDSKKRIGRFRIDTSCV-TLTIRGR 118
DB 59 KEARPVNCGRGIDDKRMNSOCTRTQSYVRLTMDSKKRIGRFRIDTSCV-TLTIRGR 118
QY 119 R 119
DB 119 R 119

RESULT 12

US-09-745-032-1
Sequence 1, Application US/09745032
Patent No. US20010027179A1
GENERAL INFORMATION:
APPLICANT: Boone, Thomas C.
APPLICANT: Cheung, Ellen N.
APPLICANT: Hershenson, Susan I.
APPLICANT: Young, John D.
TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS
FILE REFERENCE: A-411A US Revised 073100
CURRENT APPLICATION NUMBER: US/09/745,032
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 09/214,214
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 08/684,353
PRIOR FILING DATE: 1996-07-19
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 120
TYPE: PRT
ORGANISM: Human
US-09-745-032-1

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Query Match      53.8%; Score 344.5; DB 10; Length 120;
Best Local Similarity 57.4%; Pred. No. 8.3e-32;
Matches 66; Conservative 17; Mismatches 29; Indels 3; Gaps 2;

OY 6 ARRGELSYVCDISSEMYTAADKKTAVDMSCGTYVLEKVPVSKGOLKQYFETKCNPMGYT 65
DB 7 SHRGESYVCDSESLMVT--DKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETKCKEARPV 64
OY 66 KEGCGRIDKRNHNSOCTTOSYVRALTMDSKKRIGRFIRIDTSCV-TLTIKGR 119
DB 65 KNGCGRIDKRNHNSOCTTOSYVRALTMDSKKRIGRFIRIDTSCV-CALSRKIGR 119

RESULT 13
US-09-742-600-1
; Sequence 1, Application US/09742600
; Patent No. US20020010135A1
; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C.
; APPLICANT: Cheung, Ellen N.
; APPLICANT: Hershenson, Susan I.
; APPLICANT: Young, John D.
; TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS
; FILE REFERENCE: A-411A US Revised023100
; CURRENT APPLICATION NUMBER: US/09/742,600
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 09/214,214
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 08/684,353
; PRIOR FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Human
US-09-742-600-1

Query Match      53.8%; Score 344.5; DB 10; Length 120;
Best Local Similarity 57.4%; Pred. No. 8.3e-32;
Matches 66; Conservative 17; Mismatches 29; Indels 3; Gaps 2;

OY 6 ARRGELSYVCDISSEMYTAADKKTAVDMSCGTYVLEKVPVSKGOLKQYFETKCNPMGYT 65
DB 7 SHRGESYVCDSESLMVT--DKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETKCKEARPV 64
OY 66 KEGCGRIDKRNHNSOCTTOSYVRALTMDSKKRIGRFIRIDTSCV-TLTIKGR 119
DB 65 KNGCGRIDKRNHNSOCTTOSYVRALTMDSKKRIGRFIRIDTSCV-CALSRKIGR 119

RESULT 14
US-09-872-090-1
; Sequence 1, Application US/09872090
; Patent No. US20020052488A1
; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C.
; APPLICANT: Cheung, Ellen Ngol Yln
; APPLICANT: Hershenson, Susan I.
; APPLICANT: Young, John D.
; TITLE OF INVENTION: Analogs of Nr-3 (As Amended)
; FILE REFERENCE: A-411B
; CURRENT APPLICATION NUMBER: US/09/872,090
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 09/255,953
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: 08/684,353
; PRIOR FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 120
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-872-090-1

Query Match      53.8%; Score 344.5; DB 10; Length 120;
Best Local Similarity 57.4%; Pred. No. 8.3e-32;
Matches 66; Conservative 17; Mismatches 29; Indels 3; Gaps 2;

OY 6 ARRGELSYVCDISSEMYTAADKKTAVDMSCGTYVLEKVPVSKGOLKQYFETKCNPMGYT 65
DB 7 SHRGESYVCDSESLMVT--DKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETKCKEARPV 64
OY 66 KEGCGRIDKRNHNSOCTTOSYVRALTMDSKKRIGRFIRIDTSCV-TLTIKGR 119
DB 65 KNGCGRIDKRNHNSOCTTOSYVRALTMDSKKRIGRFIRIDTSCV-CALSRKIGR 119

RESULT 15
US-08-450-842-4
; Sequence 4, Application US/08450842
; Patent No. US20020045576A1
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; APPLICANT: ROSENTHAL, ARNON
; TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,842
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/426419
; FILING DATE: 19-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/030013
; FILING DATE: 22-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/648482
; FILING DATE: 31-JAN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/587707
; FILING DATE: 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: 666P2C1D3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8674
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-450-842-4

Query Match      53.8%; Score 344.5; DB 8; Length 257;
Best Local Similarity 57.4%; Pred. No. 2.1e-31;
Matches 66; Conservative 17; Mismatches 29; Indels 3; Gaps 2;

OY 6 ARRGELSYVCDISSEMYTAADKKTAVDMSCGTYVLEKVPVSKGOLKQYFETKCNPMGYT 65
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Mon Dec 2 15:36:39 2002

us-10-072-681-4.rapb

Page 6

[illegible]

Search completed: December 2, 2002, 15:14:34
Job time : 4.18523 secs

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GenCore version 5.1.3
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OM protein - protein search, using SW model

Run on: December 2, 2002, 15:05:37 ; Search time 23.9156 Seconds

668.605 Million cell updates/sec

Perfect score: 653

Sequence: 1 PYAEHKSHRGEYSVCDSESL.....RWIRIDTSCVSAISRKIGRT 120

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

1. /SI052/gcgcdatA/genseq/genseqcp-emb1/AA1980.DAT.*
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22. /SI052/gcgcdatA/genseq/genseqcp-emb1/AA2001.DAT.*
23. /SI052/gcgcdatA/genseq/genseqcp-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	646	98.9	119	19	AAM48889	Human neurotrophin-3
2	646	98.9	119	21	AAB29113	Human neurotrophin-3
3	646	98.9	281	12	AAR11359	Neurotrophin-3, H
4	646	98.9	201	14	AAR37800	Human NT-3, Homo
5	641	98.2	119	13	AAR29495	NT-3, mouse, Mus
6	641	98.2	119	15	AAR54086	Neurotrophin-3, R
7	641	98.2	119	20	AAW81118	Neurotrophin-3, w
8	641	98.2	119	22	AAG64995	Nerve growth facto
9	641	98.2	119	22	AAB35946	NT-3 amino acid se
10	641	98.2	120	17	AAW29392	Conjugate of neuro

11	6.1	98.2	120	18	AAH10014
12	6.1	98.2	120	21	AAH10455
13	6.1	98.2	120	22	AAE03868
14	6.1	98.2	136	12	AAH13306
15	6.1	98.2	240	13	AAE32375
16	98.2		240	14	AAE32375
17	6.1	98.2	240	15	AAH34937
18	6.1	98.2	257	12	AAH14032
19	6.1	98.2	257	13	AAE32372
20	6.1	98.2	257	14	AAH43936
21	6.1	98.2	257	16	AAH85078
22	6.1	98.2	257	20	AAH05594
23	6.1	98.2	257	22	AAE65927
24	6.1	98.2	257	23	AAE20262
25	6.1	98.2	258	11	AAE05847
26	6.1	98.2	258	12	AAH1357
27	6.1	98.2	258	22	AAE65928
28	6.1	98.2	258	23	AAE65928
29	6.1	98.2	271	11	AAE06493
30	6.1	98.2	271	12	AAH11307
31	6.1	98.2	271	11	AAH11307
32	6.1	98.2	257	15	AAE65067
33	6.1	98.2	257	14	AAE65067
34	6.1	98.2	257	14	AAE65067
35	6.1	98.2	257	14	AAE65067
36	6.1	98.2	257	14	AAE65067
37	6.1	98.2	257	14	AAE65067
38	6.1	98.2	257	14	AAE65067
39	6.1	98.2	257	14	AAE65067
40	6.1	98.2	257	14	AAE65067
41	6.1	98.2	257	14	AAE65067
42	6.1	98.2	257	14	AAE65067
43	6.1	98.2	257	14	AAE65067
44	6.1	98.2	257	14	AAE65067
45	6.1	98.2	257	14	AAE65067

ALIGNMENTS

RESULT 1

ID	AAW48889	standard; Protein; 119 AA.
----	----------	----------------------------

AC AAW48889;

DT 12-OCT-1998 (first entry)
yy

Human neurotrophin-3.

KW Neurotrophin-3; NT-3; human; purification
KW Neurotrophin-3; NT-3; human; purification
KW Neurotrophin-3; NT-3; human; purification

Homocysteine
XX
XX
US

xx	xx	Key	Location/Qualifiers
----	----	-----	---------------------

ET	Region	5/-.6/	conserved C	/note=
ET				

E1	Region	Cys knob motif
ET	108..110	

7.4 /note- conserved cys-containing region involved in
ET Cys knot motif

PN W09821234-A2.

PD 22-MAY-1998.

PF 14-NOV-1997; 97WO-US21068.

PR	29-MAY-1997;	97US-0047855.
PR	15-MAY-1996;	06US-0030030.

XX
XX
DA (CETHU) CENEHEBCHU TUC

PA (GETH) GENENTECH INC.

XX Beck JT, Burton LE, Schmelzer CH;
 XX WPI: 1998-322333/28.
 DR
 XX
 XX Isolation of neurotrophin(s) from, e.g. mis-folded or glycosylated
 PT variant(s) - using hydrophobic interaction chromatography,
 PT optionally in combination with high performance cation exchange
 chromatography
 XX
 XX
 PS Disclosure: Page 37-38; 59pp: English.
 XX
 CC This polypeptide comprises human neurotrophin-3 (NT-3) mature
 CC polypeptide. Methods are provided for large-scale purification of
 CC neurotrophins. Including mature NT-3, suitable for clinical use. A
 CC claimed method comprises: (1) separating the neurotrophin from the
 CC other proteins using a hydrophobic interaction chromatography resin
 CC (HICR); and optionally (2) separating the neurotrophin from a
 CC chemical variant by high performance cation exchange chromatography
 CC (HPEC). The processes can also be used for purification of e.g.
 CC human nerve growth factor (NGF) (see AAM4886), mouse NGF (see
 CC AAM4887), brain-derived neurotrophic factor (see AAM4888) and
 CC neurotrophin-4/5 (see AAM4890). The processes allow separation of
 CC neurotrophins from various undesirable misprocessed, misfolded,
 CC size, glycosylated or charge forms. They allow selective
 CC separation from variants and other molecules, and from other
 CC polypeptides with high pI. The processes are applicable to
 CC starting materials from various sources, including fermentation
 CC broths or lysed bacterial or mammalian cells.
 XX
 SO Sequence 119 AA:
 Query Match 98.9%; Score 646; DB 19; Length 119;
 Best Local Similarity 100.0%; Pred. No. 1.3e-60;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 YAEKSHRGEYSVCDESLMTDKSSAIDIRGHQVTVLGEIKTNSPVKQYFETRCKEA 61
 DB 1 YAEKSHRGEYSVCDESLMTDKSSAIDIRGHQVTVLGEIKTNSPVKQYFETRCKEA 60
 OY 62 RPYKNCGRGIDKHMNSCKTSQTYVRALTSNNKLVGMRRIRIDTSCVSLSRKIGRT 120
 DB 61 RPYKNCGRGIDKHMNSCKTSQTYVRALTSNNKLVGMRRIRIDTSCVSLSRKIGRT 119

RESULT 2
 AAB29113
 ID AAB29113 standard; Protein: 119 AA.
 XX
 AC AAB29113;
 XX
 DT 02-FEB-2001 (first entry)
 XX
 XX Human neurotrophin-3.
 DE
 XX
 XX Neurotrophin: trkB, trkC; ototoxicity-related balance impairment;
 KW Meniere's syndrome; myringitis; otitis media;
 KW acute vestibular neuronitis; herpes zoster oticus; labyrinthitis;
 KW middle; labyrinthine tumour; petrositis; otosclerosis; bacteria.
 XX
 OS Homo sapiens.
 XX
 PN US6121235-A.
 XX
 PD 19-SEP-2000.
 XX
 PF 29-DEC-1995; 95US-0581662.
 XX
 PR 29-DEC-1995; 95US-0581662.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Gao W;

XX
 DR WPI: 2000-618200/59.
 XX
 XX Treating ototoxin-induced neuronal-related balance impairment and
 PT promoting vestibular ganglion neuron survival prior to, upon or after
 PT exposure to an ototoxin, comprises administering a trkB or trkC agonist
 PT
 XX
 XX
 PS Disclosure: Column 47-50; 40pp: English.
 XX
 CC The present invention relates to treating ototoxin-induced
 CC neuronal-related balance impairment in a mammal by administering a
 CC trkB or trkC agonist, particularly neurotrophin-4/5 (NT-4/5).
 CC ototoxicity-related balance impairments include Meniere's syndrome,
 CC myringitis, otitis media, acute vestibular neuronitis, herpes zoster
 CC oticus, labyrinthitis, middle or labyrinthine tumours, petrositis and
 CC otosclerosis. NT-4/5 may also be used to treat diseases
 CC induced by gram positive, gram negative and acid-fast bacteria. The
 CC present sequence is a protein used in the invention.
 XX
 SO Sequence 119 AA:
 Query Match 98.9%; Score 646; DB 21; Length 119;
 Best Local Similarity 100.0%; Pred. No. 1.3e-60;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 YAEKSHRGEYSVCDESLMTDKSSAIDIRGHQVTVLGEIKTNSPVKQYFETRCKEA 61
 DB 1 YAEKSHRGEYSVCDESLMTDKSSAIDIRGHQVTVLGEIKTNSPVKQYFETRCKEA 60
 OY 62 RPYKNCGRGIDKHMNSCKTSQTYVRALTSNNKLVGMRRIRIDTSCVSLSRKIGRT 120
 DB 61 RPYKNCGRGIDKHMNSCKTSQTYVRALTSNNKLVGMRRIRIDTSCVSLSRKIGRT 119

RESULT 3
 AAR11359
 ID AAR11359 standard; Protein: 281 AA.
 XX
 AC AAR11359;
 XX
 DT 31-MAY-1991 (first entry)
 XX
 XX Neurotrophin-3.
 DE
 XX
 XX NT-3; nerve growth factor; NGF; brain derived neurotrophic factor;
 KW BDNF; Alzheimers disease; Parkinsonism; central nervous system; CNS;
 KW neuropathy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Protein 25..281
 FT /label= prepro NT3
 FT Protein 163..281
 FT /label= mature NT3
 XX
 XX W09103569-A.
 XX
 PD 21-MAR-1991.
 XX
 PF 29-AUG-1990; 90MO-0504916.
 XX
 PR 20-AUG-1990; 90US-0570189.
 PR 30-AUG-1989; 89US-0400591.
 PR 07-MAR-1990; 90US-0490004.
 XX
 PA (PLAC) MAX PLANCK GES WISSENSCH.
 PA (REG-) REGENERON PHARM INC.
 XX
 XX Hohn A, Leibrock J, Bailey K, Barde YA, Thoenen H;
 PI Malsenplacrie PC, Furchme, Lindsay RW;

XX A comparison of the mature NT-4 protein (Xenopus) to the mature
CC NGF, BDNF, and NT-3 proteins from mouse revealed 51%, 60% and 58%
CC amino acid identity respectively. See sequences AAR29491 and
CC AAR29493-95.
XX
SO Sequence 119 AA:

Query Match 98.2%; Score 641; DB 13; Length 119;
Best Local Similarity 99.2%; Pred. No. 4.3e-60;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 YAEHSHRGEYSCDSESLAWTDKSSAIDIRGHQVTVLGEIRKGNSPVKQYFETRCKEA 61
DB 1 YAEHSHRGEYSCDSESLAWTDKSSAIDIRGHQVTVLGEIRKGNSPVKQYFETRCKEA 60
OY 62 RPKVKGCGIDDKHNSCKTSQTYVRLALTSNNKLVGNMIRIDPSVLSRLKIGRT 120
DB 61 RPKVKGCGIDDKHNSCKTSQTYVRLALTSNNKLVGNMIRIDPSVLSRLKIGRT 119

RESULT 6

AAR54086
ID AAR54086 standard; protein: 119 AA.
XX
AC AAR54086;
XX
DT 10-NOV-1994 (first entry)
XX
DE Neurotrophin-3.

XX Nerve growth factor: NGF; chimeric neurotrophin; neurotrophic factor;
KM brain-derived neurotrophic factor; BDNF; neurotrophin-3; NF-3;
KM TrkA; TrkB; TrkC; receptor; neurological disorder;
KM Parkinson disease; Alzheimer disease.

XX Rattus sp.

XX W09412539-A.

XX 09-JUN-1994.

XX 19-NOV-1993; 93MO-US11292.

XX 20-NOV-1992; 92US-0979630.

XX (MCIN/) MCINTYRE K R.

XX Ibanez CFM, Persson HB;

XX WPI: 1994-200202/24.

XX New chimeric neurotrophic factors and DNA - used to develop
PT prods. for use in the treatment and diagnosis of neurological
PT disorders

XX Disclosure: Page 50; 79pp; English.

XX Sequences are provided for rat nerve growth factor (AAR54084), rat
CC brain-derived neurotrophic factor (AAR54085) and rat neurotrophin-3
CC (AAR54086). Chimeric neurotrophins capable of binding TrkA, TrkB and
CC TrkC are obtained by substituting amino acids 3-9, 28-37, 40-49,
CC 61-66, 81-88, 94-98 or 95-97 of a neurotrophin with corresponding
CC amino acids from NGF, BDNF or NT-3. Recombinant chimeric
CC neurotrophins are used to treat e.g. Alzheimer disease and
CC Parkinson disease.

XX Sequence 119 AA:

Query Match 98.2%; Score 641; DB 13; Length 119;
Best Local Similarity 99.2%; Pred. No. 4.3e-60;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 YAEHSHRGEYSCDSESLAWTDKSSAIDIRGHQVTVLGEIRKGNSPVKQYFETRCKEA 61
DB 1 YAEHSHRGEYSCDSESLAWTDKSSAIDIRGHQVTVLGEIRKGNSPVKQYFETRCKEA 60
OY 62 RPKVKGCGIDDKHNSCKTSQTYVRLALTSNNKLVGNMIRIDPSVLSRLKIGRT 120
DB 61 RPKVKGCGIDDKHNSCKTSQTYVRLALTSNNKLVGNMIRIDPSVLSRLKIGRT 119

RESULT 7

AAR81118
ID AAR81118 standard; protein: 119 AA.

XX AAR81118;

XX 01-MAR-1999 (first entry)

XX Neurotrophin-3 wild type.

XX Nerve growth factor: trkC; neuron; neural disease; animal feed;
KM neurotrophin assay; nerve cell culture media; neurotrophic factor; NT-3;
KM TrkA; TrkB.

XX Homo sapiens.

XX W09849308-A1.

XX 05-NOV-1998.

XX 23-APR-1998; 98MO-US08242.

XX 29-APR-1997; 97US-0841045.

XX 25-APR-1997; 97US-0845541.

XX (GETH) GENENTECH INC.

XX Presta LG, Urfer R, Winslow JW;

XX WPI: 1999-009429/01.

XX New variants of nerve growth factor able to bind trkC - contain
PT specified mutations and have multiple neurotrophic activities in a
PT single molecule, used for treating, e.g. peripheral neuropathy

XX Example 1; Page 33; 53pp; English.

XX Neurotrophin-3 was used in the production of new variants of nerve growth
CC factor (NGF) with substitutions at amino acid positions: 623 and 884, and
CC one or both of V18 and V20, so that it acquires the ability to bind trkC.
CC The variants can be used to promote development, maintenance and
CC regeneration of neurons in vivo or in vitro, so can be used to treat a
CC wide range of neural diseases, e.g. Alzheimer's, Parkinson's,
CC Huntington's and Meniere's diseases; stroke; amyotrophic lateral
CC sclerosis; epilepsy; Down's syndrome; nerve deafness; Bell's palsy, or
CC specifically, peripheral neuropathy. They are also used as cognitive
CC enhancers and can also be used for diagnosis: in animal feeds; as
CC standards for neurotrophin assays; as additives for nerve cell culture
CC media; and for generation of specific antibodies. By introducing trkC
CC binding/signaling inducing activity, the variants acquire the activity of
CC neurotrophic factor NT-3 while optionally retaining ability to bind trkA
CC and/or B and therefore provide several activities in a single molecule,
CC with more predictable pharmacokinetic and other properties than a mixture
CC of agents each with a single activity, and better pan-neurotrophic
CC activity than known compounds.

XX Sequence 119 AA:

Query Match 98.2%; Score 641; DB 20; Length 119;
Best Local Similarity 99.2%; Pred. No. 4.3e-60;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 YAEHSHRGEYSCDSESLAWTDKSSAIDIRGHQVTVLGEIRKGNSPVKQYFETRCKEA 61
|||||


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DB      1 YAEKSHRGEYSVCDSESLMTVDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 60
OY      62 RPYKNGCRGIDDKHNSQCKTSQTYVRALTSENKLVGRWIRIDTSCVSAISRKIGRT 120
        |||||||
DB      61 RPYKNGCRGIDDKHNSQCKTSQTYVRALTSENKLVGRWIRIDTSCVSAISRKIGRT 119

RESULT 8
ID      AAG64995
        AAG64995 standard; protein: 119 AA.
XX
AC      AAG64995;
XX
DT      25-SEP-2001 (first entry)
XX
DE      Nerve growth factor variant related protein SEQ ID NO: 2.
XX
XX      Nerve growth factor; NGF; trkC-binding activity; trkA; trkB; neuropathy;
KM      neuronal disorder; neurotrophin; variant; mutant; Bell's palsy;
KM      amyotrophic lateral sclerosis; paralysis; neurodegenerative disease;
KM      Parkinson's disease; Alzheimer's disease; multiple sclerosis.
XX
OS      Unidentified.
XX
PM      US2001012625-A1.
XX
PD      09-AUG-2001.
XX
PF      24-APR-1998; 98US-0066065.
XX
PR      25-APR-1997; 97US-0044918.
XX
PA      (PRES/) PRESTA L G.
PA      (UREE/) UREER R.
PA      (WINS/) WINSLOW J W.
XX
PI      Presta LG, Ureer R, Winslow JW;
XX
DR      WPI: 2001-466388/50.
XX
PT      Nerve growth factor variants which have trkC-binding activity and
PT      trkC-signal inducing activity, useful for treating a neural disorder in
PT      a mammal such as peripheral neuropathy (e.g. diabetic peripheral
PT      neuropathy) -
XX
PS      Disclosure: Page 19-20; 34pp; English.
XX
XX      The present invention provides a number of nerve growth factor (NGF)
CC      variants with trkC-binding activity and trkC-signal inducing activity.
CC      They may also be capable of binding to trkA and trkB. The variants are
CC      useful in the treatment of neuronal disorders, including peripheral
CC      neuropathy and motor-neurone disorders, such as amyotrophic lateral
CC      sclerosis, Bell's palsy, and various conditions involving spinal muscular
CC      atrophy, or paralysis. They are also useful for treating other human
CC      neurodegenerative disorders, such as Alzheimer's disease, Parkinson's
CC      disease, epilepsy, multiple sclerosis, Huntington's disease, Down's
CC      syndrome, nerve deafness, Meniere's disease and other conditions
CC      characterized by necrosis or loss of neurones, whether central,
CC      peripheral, or motor neurones.
XX
SO      Sequence 119 AA;
XX
Query Match      98.2%; Score 641; DB 22; Length 119;
Best Local Similarity 99.2%; Pred. No. 4.3e-60;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB      1 YAEKSHRGEYSVCDSESLMTVDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 61
OY      62 RPYKNGCRGIDDKHNSQCKTSQTYVRALTSENKLVGRWIRIDTSCVSAISRKIGRT 120
        |||||||
DB      61 RPYKNGCRGIDDKHNSQCKTSQTYVRALTSENKLVGRWIRIDTSCVSAISRKIGRT 119

RESULT 9
ID      AAB35946
        AAB35946 standard; protein: 119 AA.
XX
AC      AAB35946;
XX
DT      26-FEB-2001 (first entry)
XX
DE      NT-3 amino acid sequence.
XX
KM      Heparin binding; vascular graft; matrix; cell adhesion; growth factor;
KM      wound healing; dermal wound; wound healing; NT-3.
XX
OS      Unidentified.
XX
PM      WO200064481-A1.
XX
PD      02-NOV-2000.
XX
PF      22-APR-1999; 99WO-IB00800.
XX
PR      22-APR-1999; 99WO-IB00800.
XX
PA      (ETHZ-) ETH ZURICH & UNIV ZURICH.
XX
PI      Sakiyama SE, Hubbell JA;
XX
DR      WPI: 2001-024627/03.
XX
PT      Matrix for controlled release of growth factor for wound healing, has
PT      substrate that attaches heparin binding peptide, protein growth factor
PT      that bind heparin with low affinity, and heparin or heparin-like
PT      polymer -
XX
PS      Example 5; Page 21; 48pp; English.
XX
XX      This invention relates to a matrix comprising a substrate capable of
CC      providing attachment of a heparin binding peptide (HBP), a peptide
CC      comprising a binding domain which binds heparin with high affinity,
CC      heparin or heparin-like polymer, and a protein growth factor or peptide
CC      fragment which has a domain that binds heparin with low affinity.
CC      Included in the invention is a vascular graft comprising the matrix,
CC      which is capable of supporting cell adhesion. The matrix is used for
CC      delivering low heparin binding affinity growth factor proteins or
CC      peptides in a controlled manner suitable for wound healing. The matrix
CC      can be used in an article for treating dermal wounds, and in an
CC      implantable sterilized composition capable of supporting cell adhesion.
CC      The present sequence represents a growth factor protein. The protein is
CC      used in an example illustrating that non-heparin-binding growth factors
CC      systems based on their low affinity for heparin.
XX
SO      Sequence 119 AA;
XX
Query Match      98.2%; Score 641; DB 22; Length 119;
Best Local Similarity 99.2%; Pred. No. 4.3e-60;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

AC AAW29392;
 XX 20-FEB-1998 (first entry)
 DT XX
 DE Conjugate of neurotrophin-3 with polyethylene glycol.
 XX
 XX Brain derived growth factor conjugate; BDNF; polyethylene glycol;
 XX water-soluble polymer; neurotrophin-3; NT-3; methoxypolyethylene glycol;
 XX trophic factor; neurodegenerative disease; Parkinson's disease;
 XX amyotrophic lateral sclerosis; Huntington's disease;
 XX retinal degeneration; peripheral neuropathies; Alzheimer's disease.
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 XX Misc-difference 1 /note= "optionally absent"
 FT
 FT Modified-site 120 /note= "alpha amino group of Thr modified with
 FT 120 methoxypolyethylene glycol"
 XX
 XX M09615146-A1.
 XX
 XX 23-MAY-1996.
 XX
 XX 13-NOV-1995; 95MO-US14658.
 XX
 XX 14-NOV-1994; 94US-0340131.
 XX
 XX (AMGE-) AMGEN INC.
 XX
 XX Kinzler OF, Yan Q;
 XX
 XX WPI: 1996-259779/26.
 XX
 XX Conjugates of brain derived growth factor or neurotrophin-3 with
 XX water soluble polymer - having improved migration through brain
 XX tissue compared with the free peptide, useful e.g. for promoting
 XX survival and maintenance of neurons
 XX
 XX Claim 2: Pages 36-7; 54pp; English.
 XX
 XX This sequence represents a new conjugate of neurotrophin-3 (NT-3)
 XX and methoxypolyethylene glycol, a water soluble polymer. The modification
 XX may be at the N-terminal alpha-amino group of NT-3 or on one or several
 XX of the lysine epsilon-amino acid groups of NT-3. These derivatives, and
 XX similar derivatives of brain derived growth factor (BDGF) have the
 XX same uses as the trophic factors BDNF and NT-3. They are useful for
 XX promoting the survival and maintenance of neurons in vitro and in vivo,
 XX and for treating neurodegenerative diseases, e.g. Parkinson's disease,
 XX amyotrophic lateral sclerosis, Huntington's disease, retinal
 XX degeneration, peripheral neuropathies or Alzheimer's disease. Use of the
 XX derivatives improves migration of BDNF or NT-3 through brain tissue,
 XX resulting in easier delivery to targets within the brain.
 XX
 XX Sequence 120 AA:
 SQ
 Query Match 98.2%; Score 641; DB 17; Length 120;
 Best Local Similarity 99.2%; Pred. No. 4,3e-60;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 2 YAEKSHRGEYSVCDSESLMTVDKSSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEA 61
 DB 2 YAEKSHRGEYSVCDSESLMTVDKSSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEA 61
 Oy 62 RPKVNCGRGIDDKHMNSOCKTSQTYVRALTSNNKLVGMRIRIDTSCVSLSRKIGRT 120
 DB 62 RPKVNCGRGIDDKHMNSOCKTSQTYVRALTSNNKLVGMRIRIDTSCVSLSRKIGRT 120
 RESULT 11
 AAW10014
 ID AAW10014 standard; protein: 120 AA.

XX AAW10014;
 AC 15-SEP-1997 (first entry)
 XX
 DT XX
 DE Human neurotrophin-3.
 XX
 XX NT-3; neurotrophin 3; active; refolded; differentiation; research;
 XX expression; protein induction; enzyme expression.
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 XX Disulfide-bond 15..80
 XX Disulfide-bond 58..109
 XX Disulfide-bond 68..111
 XX
 XX JP09121886-A.
 XX
 XX 13-MAY-1997.
 XX
 XX 22-AUG-1996; 96JP-0220963.
 XX
 XX 25-AUG-1995; 95JP-0217032.
 XX
 XX (TAKE) TAKEDA CHEM IND LTD.
 XX
 XX WPI: 1997-314237/29.
 XX
 XX Preparation of active correctly folded neurotrophin-3 - which can be
 XX used in cell differentiation, and protein expression research
 XX
 XX Disclosure; Fig 1; 15pp; Japanese.
 XX
 XX This sequence is human neurotrophin 3 (NT-3). Active NT-3 is produced by
 XX the method of the invention, which comprises transforming a prokaryotic
 XX host cell with an NT-3 gene to express the NT-3, and then NT-3 produced
 XX is refolded correctly in a redox buffer. The active NT-3 produced by the
 XX method can be used as a reagent for research on the differentiation of
 XX cells, genetic expression and induction of protein and enzyme expression.
 XX
 XX Sequence 120 AA:
 SQ
 Query Match 98.2%; Score 641; DB 18; Length 120;
 Best Local Similarity 99.2%; Pred. No. 4,3e-60;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 2 YAEKSHRGEYSVCDSESLMTVDKSSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEA 61
 DB 2 YAEKSHRGEYSVCDSESLMTVDKSSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEA 61
 Oy 62 RPKVNCGRGIDDKHMNSOCKTSQTYVRALTSNNKLVGMRIRIDTSCVSLSRKIGRT 120
 DB 62 RPKVNCGRGIDDKHMNSOCKTSQTYVRALTSNNKLVGMRIRIDTSCVSLSRKIGRT 120
 RESULT 12
 AAB10455
 ID AAB10455 standard; protein: 120 AA.
 XX
 XX AAB10455;
 XX
 XX 01-DEC-2000 (first entry)
 XX
 XX Human R-methuM protein.
 XX
 XX Human; R-methuM; gastrointestinal hypomotility; constipation; diarrhea;
 XX trk neurotrophin-3 receptor; surgery; neuropathy; Parkinson's disease;
 XX multiple sclerosis; irritable bowel syndrome; spinal cord injury;
 XX paraplegia; quadriplegia; antididiarrheic; laxative.
 XX
 XX Homo sapiens.
 OS
 OS Synthetic.

[illegible]

FT		This protein is expressed without the methionine residue when occurring naturally in mammalian cells"
XX		
XX	0562711364-B1.	
XX		
PD	07-AUG-2001.	
XX		
Pf	23-FEB-1999; .	99US-0255953.
XX		
PR	23-FEB-1999; .	99US-0255953.
XX		
PA	(AMGE-) AMGEN INC.	
XX		
PI	Cheung ENT, Boone TC, Hershenson SI, Young JD:	
DR	WPI; 2001-464215/50.	
XX		
PT	Polypeptide analogs of the neurotrophin factor (NT-3) and its recombinant production method -	
PS	Disclosure; Fig 1: 24pp: English.	
XX		
CC	The present invention relates to a method for production of a polypeptide analogue of a cationic polypeptide selected from 4 fully defined polypeptide sequences, where the polypeptide analogue has an isoelectric point which is lower and an in vivo circulating life and/or absorption which is increased relative to those properties in unmodified neurotrophic factor-3 (NT-3). The method is useful for producing certain analogues of NT-3 which have a relatively lower pI, yet retain the structure and biological activity of the protein in its 'native' state, to assess the impact of the pI on the pharmacokinetic behaviour of proteins. The present sequence is human recombinant neurotrophic factor-3 (NT-3), r-methuNT-3. This sequence is recombinantly produced in E. coli bacterial cells and thus expressing the methionine residue at its N-terminus.	
CC		
CC		
CC		
CC		
SO	Sequence 120 AA:	
	Query Match 98.2%; Score 641; DB 22; Length 120;	
	Best Local Similarity 99.2%; Pred. No. 4,3e-60;	
	Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
OY	2 YAEKSHRGEYSVCDESLMTWTDKSSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEA 61 2 YAEKSHRGEYSVCDESLMTWTDKSSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEA 61	
Dd	2 RPYAKNGCRGIDDKHNNSOCTSGTYVRALTSNNKLVGKKRIKIDTSCVSALSRIKIGRT 120 62 RPYAKNGCRGIDDKHNNSOCTSGTYVRALTSNNKLVGKKRIKIDTSCVSALSRIKIGRT 120	
Dd	62 RPYAKNGCRGIDDKHNNSOCTSGTYVRALTSNNKLVGKKRIKIDTSCVSALSRIKIGRT 120	
RESULT 14		
ID	AAR11306 standard; Protein: 136 AA.	
AC	AAR11306;	
XX		
DT	29-MAY-1991 (first entry)	
XX		
DE	Nerve Growth Factor-like pro-protein from human glioma cells.	
XX		
KX	nerve growth factor; NGF; cell proliferation; glioma cell.	
OS	Homo sapiens.	
FH	Key Location/Qualifiers	
FT	Peptide 1..17	
FT	/label= propeptide 18..136	
FT	Protein /label= NGF-like polypeptide 18..31	
FT	Peptide /label= claimed partial peptide /note= "12-14 successive amino acids from this	

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OM protein - protein search, using SW model

Run on: December 2, 2002, 15:05:43 ; Search time 9.56624 Seconds
(without alignments)
1205.921 Million cell updates/sec

Title: US-10-072-681-5

Perfect score: 653
Sequence: 1 PYAEKSHRGVSVCSDSL.....RMIRIDTSCVSLSRKIGRT 120

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	641	98.2	257	2 C40304	neurotrophin-3 pre
2	641	98.2	258	2 S09155	neurotrophin-3 pre
3	641	98.2	282	2 A35781	hippocampus-derive
4	638	97.7	257	2 I50400	neurotrophin-3 pre
5	392.5	60.1	243	2 A26311	nerve growth facto
6	385	59.0	235	2 S14481	nerve growth facto
7	382.5	58.6	229	2 I46614	nerve growth facto
8	378.5	58.0	245	2 I56570	beta-nerve growth
9	378	57.9	236	2 JH0400	neurotrophin-4 pre
10	375.5	57.5	125	2 A26312	nerve growth facto
11	373.5	57.2	286	1 NGHUBM	nerve growth facto
12	371.5	56.9	241	2 J10097	nerve growth facto
13	370	56.7	303	1 NGPRBA	nerve growth facto
14	368.5	56.4	307	1 NGKSKG	nerve growth facto
15	354	54.2	247	2 A40504	brain-derived neur
16	354	54.2	249	2 S12555	brain-derived neur
17	354	54.2	249	2 B40304	brain-derived neur
18	354	54.2	252	2 A30361	brain-derived neur
19	352.5	54.0	243	2 I51193	nerve growth facto
20	352	53.9	209	2 B42687	neurotrophin-4 pre
21	350	53.6	210	2 A42687	neurotrophin-4 pre
22	350	53.6	248	2 JG6183	brain-derived neur
23	349	53.4	117	2 S28161	nerve growth facto
24	349	53.4	269	2 I51708	brain-derived neur
25	345	52.8	114	2 I50606	brain-derived neur
26	343	52.5	114	2 I84765	brain-derived neur
27	326	49.9	114	2 I51599	brain-derived neur
28	323.5	49.5	116	1 NGNXXI	nerve growth facto
29	317.5	48.6	116	2 A58565	nerve growth facto

30	317.5	48.6	246	2 A59218	nerve growth facto
31	295.5	45.3	194	2 I51709	nerve growth facto
32	266	40.7	286	2 S50855	neurotrophin-6 - s
33	78	11.9	1268	2 B88209	protein R02A2.6 (1
34	72	11.0	390	2 JG4023	transforming growt
35	71.5	10.9	145	2 S74292	hypothetical prote
36	71.5	10.9	647	2 C87693	acetyl-CoA synthet
37	71	10.9	326	2 T10166	restriction endonu
38	71	10.9	498	2 B83884	beta-xylosidase /
39	71	10.9	783	2 B91124	probable isomerase
40	71	10.9	783	2 A85969	probable isomerase
41	70.5	10.8	718	2 T05840	subtilisin-like pr
42	70	10.7	759	2 S53922	phosphoprotein C -
43	70	10.7	1099	2 T18257	phospholipase C -
44	69.5	10.6	195	2 A13153	hypothetical prote
45	69.5	10.6	230	2 A98134	hypothetical prote

ALIGNMENTS

RESULT 1

C40304 neurotrophin-3 precursor - human

M:Alternate names: nerve growth factor 2; NGF-2

C:Species: Homo sapiens (man)

C:Date: 03-Apr-1992 #sequence, revision 30-Sep-1993 #text, change 16-Jul-1999

C:Accession: A36208; JH0141; C40304; S10719; C60536

R:Jones, K.R.; Reichardt, L.F.

Proc. Natl. Acad. Sci. U.S.A. 87, 8060-8064, 1990

A:Title: Molecular cloning of a human gene that is a member of the nerve growth facto

A:Reference number: A36208; MUID:91045937; PMID:2236018

A:Accession: A36208

A:Molecule type: DNA

A:Residues: 1-257 <JUN>

A:Cross-references: GB:M37763; NID:g189300; PIDN:AA59953.1; PID:g189301

R:Rosenthal, A.; Goeddel, D.V.; Nguyen, T.; Lewis, M.; Shih, A.; Laramee, G.R.; Nixol

Neuron 4, 767-773, 1990

A:Title: Primary structure and biological activity of a novel human neurotrophic fact

A:Reference number: JH0141; MUID:90265727; PMID:2344409

A:Accession: JH0141

A:Molecule type: DNA

A:Residues: 1-257 <ROS>

R:Malomplere, P.C.; Le Beau, M.M.; Espinosa III, R.; Ip, N.Y.; Belluscio, L.; de la

Genomics 10, 558-568, 1991

A:Title: Human and rat brain-derived neurotrophic factor and neurotrophin-3: gene str

A:Reference number: A40304; MUID:91365361; PMID:1898806

A:Accession: C40304

A:Molecule type: DNA

A:Residues: 1-257 <MAL>

A:Cross-references: GB:M61180; NID:g189302; PIDN:AA63231.1; PID:g189303

R:Kishino, Y.; Yoshimura, K.; Nakahama, K.

FEBS Lett. 266, 187-191, 1990

A:Title: Cloning and expression of a cDNA encoding a novel human neurotrophic factor.

A:Reference number: S10719; MUID:90306351; PMID:2365067

A:Accession: S10719

A:Molecule type: mRNA

A:Residues: 1-257 <KAT>

A:Cross-references: GB:X53655; NID:g287794; PIDN:CAA7703.1; PID:g287795

R:Rancopoles, G.D.; Malomplere, P.C.; Ip, N.Y.; Aldrich, T.H.; Belluscio, L.; Boul

Cold Spring Harb. Symp. Quant. Biol. 55, 371-379, 1990

A:Title: Neurotrophic factors, their receptors, and the signal transduction pathways

A:Reference number: A60536; MUID:92111157; PMID:1966766

A:Accession: C60536

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-73, 'O', '75-77', 'R', '79-108', 'T', '110-257' <KAN>

C:Genetics:

A:Gene: GDB:MTF3

A:Cross-references: GDB:125917; OMIM:162660

A:Map position: 12p13-12p13

C:Superfamily: nerve growth factor beta chain

C:Keywords: glycoprotein

F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-138/Domain: propeptide #status predicted <PRO>
 F:139-237/Product: neurotrophin-3 #status predicted <NT>
 F:131/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 98.2%; Score 641; DB 2; Length 257;
 Best Local Similarity 99.2%; Pred. No. 2.4e-57;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 YAEKSHRGEYSVCDSESLWTDKSSAIDIRGHQVTVLGEITGNSPVKQYFETRCKEA 61
 DB 139 YAEKSHRGEYSVCDSESLWTDKSSAIDIRGHQVTVLGEITGNSPVKQYFETRCKEA 198
 OY 62 RPYVNGRCGIDDKHNSOCTTSQTYVRALTSNNKLVGWRWIRIDTSCVLSRRKIGRT 120
 DB 199 RPYVNGRCGIDDKHNSOCTTSQTYVRALTSNNKLVGWRWIRIDTSCVLSRRKIGRT 257

RESULT 2

509155
 neurotrophin-3 precursor - mouse
 C:Species: Mus musculus (house mouse)

C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999
 C:Accession: S09155; S51179
 R:Hohn, A.; Leibrock, J.; Bailey, K.; Barde, Y.A.

A:Title: Identification and characterization of a novel member of the nerve growth factor family
 A:Reference number: S09155; MUID:90190865; PMID:2314473
 A:Accession: S09155

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-258 <NO>
 A:Cross-references: GB:X53257; MTD:953451; PIDN:CAA37348.1; PID:953452

R:Kotobek, R.; Jungbluth, S.; Barde, Y.A.

A:Title: Characterisation of neurotrophin dimers and monomers.
 A:Reference number: S51179; MUID:95045576; PMID:7957235

A:Accession: S51179

A:Status: preliminary

A:Molecule type: protein

A:Residues: 140-152 <KO>
 A:Superfamily: nerve growth factor beta chain

C:Keywords: glycoprotein
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:140-258/Product: neurotrophin-3 #status predicted <NT>
 F:131/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 98.2%; Score 641; DB 2; Length 258;
 Best Local Similarity 99.2%; Pred. No. 2.5e-57;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 YAEKSHRGEYSVCDSESLWTDKSSAIDIRGHQVTVLGEITGNSPVKQYFETRCKEA 61
 DB 140 YAEKSHRGEYSVCDSESLWTDKSSAIDIRGHQVTVLGEITGNSPVKQYFETRCKEA 199
 OY 62 RPYVNGRCGIDDKHNSOCTTSQTYVRALTSNNKLVGWRWIRIDTSCVLSRRKIGRT 120
 DB 200 RPYVNGRCGIDDKHNSOCTTSQTYVRALTSNNKLVGWRWIRIDTSCVLSRRKIGRT 258

RESULT 3

A35781
 hippocampus-derived neurotrophic factor precursor - rat

C:Species: Rattus norvegicus (Norway rat)
 C>Date: 05-Oct-1990 #sequence_revision 05-Oct-1990 #text_change 16-Jul-1999

C:Accession: A35781; A40094
 R:Ernfors, P.; Ibanez, C.F.; Ebendal, T.; Olson, L.; Persson, H.

A:Title: Molecular cloning and neurotrophic activities of a protein with structural simi-

A:Reference number: A35781; MUID:90319130; PMID:2164684

A:Accession: A35781
 A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-282 <EN>
 A:Cross-references: GB:M34643

R:Malsonpiere, P.C.; Belluscio, L.; Squinto, S.; Ip, N.Y.; Furch, M.E.; Lindsay, R.M.

A:Title: Neurotrophin-3: a neurotrophic factor related to NGF and BDNF.

A:Reference number: A40094; MUID:90208301; PMID:2321006

A:Accession: A40094

A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 25-282 <NA>
 A:Cross-references: GB:M33968; MTD:9205771; PIDN:AAA1127.1; PID:9205772

C:Superfamily: nerve growth factor beta chain

Query Match 98.2%; Score 641; DB 2; Length 282;
 Best Local Similarity 99.2%; Pred. No. 2.7e-57;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 YAEKSHRGEYSVCDSESLWTDKSSAIDIRGHQVTVLGEITGNSPVKQYFETRCKEA 61
 DB 164 YAEKSHRGEYSVCDSESLWTDKSSAIDIRGHQVTVLGEITGNSPVKQYFETRCKEA 223
 OY 62 RPYVNGRCGIDDKHNSOCTTSQTYVRALTSNNKLVGWRWIRIDTSCVLSRRKIGRT 120
 DB 224 RPYVNGRCGIDDKHNSOCTTSQTYVRALTSNNKLVGWRWIRIDTSCVLSRRKIGRT 282

RESULT 4

150400
 neurotrophin-3 precursor - chicken

C:Species: Gallus gallus (chicken)
 C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999

C:Accession: 150400; S42227
 R:Malsonpiere, P.C.; Belluscio, L.; Conover, J.C.; Yancopoulos, G.D.

A:Title: Gene sequences of chicken BDNF and NT-3.
 A:Reference number: 150400; MUID:93091238; PMID:1457809

A:Accession: 150400

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-257 <NA>
 A:Cross-references: GB:M83378; MTD:9212464; PIDN:AA68880.1; PID:9212465

R:Hallboeck, F.; Ibanez, C.F.; Ebendal, T.; Persson, H.

A:Title: Cellular localization of brain-derived neurotrophic factor and neurotrophin-3.
 A:Reference number: S42227; MUID:94084226; PMID:8074744

A:Accession: S42227

A:Status: preliminary

A:Molecule type: mRNA
 A:Residues: 32-257 <NA>
 A:Cross-references: EMBL:230092; MTD:9455531; PIDN:CAA82908.1; PID:9927570

C:Superfamily: nerve growth factor beta chain

Query Match 97.7%; Score 638; DB 2; Length 257;
 Best Local Similarity 98.3%; Pred. No. 4.9e-57;
 Matches 117; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 YAEKSHRGEYSVCDSESLWTDKSSAIDIRGHQVTVLGEITGNSPVKQYFETRCKEA 61
 DB 139 YAEKSHRGEYSVCDSESLWTDKSSAIDIRGHQVTVLGEITGNSPVKQYFETRCKEA 198
 OY 62 RPYVNGRCGIDDKHNSOCTTSQTYVRALTSNNKLVGWRWIRIDTSCVLSRRKIGRT 120
 DB 199 RPYVNGRCGIDDKHNSOCTTSQTYVRALTSNNKLVGWRWIRIDTSCVLSRRKIGRT 257

RESULT 5

A26311
 nerve growth factor beta chain precursor - chicken (fragment)

C:Species: Gallus gallus (chicken)
 C>Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 21-Jul-2000

neurotrophin-4 precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999

C:Accession: J04000
R:Hallboeck, F.; Ibanez, C.F.; Persson, H.
Nucleon 6, 845-858, 1991

A>Title: Evolutionary studies of the nerve growth factor family reveal a novel member at A:Reference number: J04000; MUID:9122573; PMID:2025430

A:Accession: J04000
A:Molecule type: DNA

A:Residues: 1-236 <NA>
A:Cross-references: GB:Z30090; NID:g455533; PIDN:CA02906.1; PID:g455534
C:Comment: This protein belongs to the nerve growth factor family.

C:Superfamily: nerve growth factor beta chain
C:Keywords: glycoprotein
F:1-18/Domain: signal sequence \$status predicted <SIG>
F:19-113/Domain: propeptide \$status predicted <PRO>
F:114-236/Product: neurotrophin-4 \$status predicted <NA>
F:106/Binding site: carbohydrate (asn) (covalent) \$status predicted

Query Match 57.9%; Score 378; DB 2; Length 236;
Best Local Similarity 59.6%; Pred. No. 9e-31;
Matches 68; Conservative 16; Mismatches 30; Indels 0; Gaps 0;

OY 7 SHRGVSVCDSESLAWTDKSSAIDIRGHQVTGLCEITGNSPVOXYETRECKEARPVKN 66
+ + + + + :
Db 123 SRGELSVCDISVMWTDKRTAVDDRKGIATVNSEIQTLPGLKGYFFERKCNPSSTR 182
+ + + + + :
OY 67 GCRRIDDKHMSOCKTSQTYVRALTSNNKLIVGNRIIRDTSQVSALSRIKGT 120
+ + + + + :
Db 183 GCRGVDDKKMISECKAKOSYVRALPIDANKLVGRNIRIDTACVCULSRTGRT 236

RESULT 10
A26312
nerve growth factor beta chain precursor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 16-Jul-1999
C:Accession: A26312
R:Meier, R.; Becker-Andre, M.; Goetz, R.; Heumann, R.; Shaw, A.; Thoenen, H.
EMBO J. 5, 1489-1493, 1986

A>Title: Molecular cloning of bovine and chick nerve growth factor (NGF): delineation of A:Reference number: A26312; MUID:86300647; PMID:2427334

A:Accession: A26312
A:Molecule type: mRNA
A:Residues: 1-125 <ME>
A:Cross-references: GB:M26809; NID:g163419; PIDN:AAA30666.1; PID:g163420
C:Comment: Nerve growth factor stimulates neurite outgrowth from sympathetic and embryonic C:Superfamily: nerve growth factor beta chain
C:Keywords: growth factor; homodimer; seminal vesicle
F:6-125/Product: nerve growth factor \$status predicted <NA>
F:20-85;63-113 73-115/Disulfide bonds: \$status predicted

Query Match 57.5%; Score 375.5; DB 2; Length 125;
Best Local Similarity 59.8%; Pred. No. 8.1e-31;
Matches 67; Conservative 19; Mismatches 25; Indels 1; Gaps 1;

OY 8 HRGEYSVCDSESLAWTDKSSAIDIRGHQVTGLCEITGNSPVOXYETRECKEARPVKN 67
+ + + + + :
Db 13 HRGFSVCDISVMWTDKRTADIRKGKVMVLGEVININSVFVKGFYETRCKRPNDPSG 72
+ + + + + :

OY 68 CRGIDDKHMSOCKTSQTYVRALTSNNKLIVGNRIIRDTSQVSALSRIKGT 119
+ + + + + :
Db 73 CGRIDAKHMNSTCTTHRTFKALTMQ-GKQAAMAFIRIDTACVCULSRKTGO 123

RESULT 11
NGHUBM
nerve growth factor beta chain precursor - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 18-Jun-1999
C:Accession: A01939; S10253
R:Ullrich, A.; Gray, A.; Berman, C.; Dull, T.J.

```

Nature 303, 821-825, 1983
A:Title: Human beta-nerve growth factor gene sequence highly homologous to that of mouse
A:Reference number: A93305; MUID:83244969; PMID:5668123
A:Accession: A01399
A:Molecule type: DNA
A:Residues: 1-286 <OLD>
R:Bornsl, G.; Pizzutti, A.; Ruggeri, E.L.; Fallini, A.; Silani, V.; Sidoli, A.; Scarla
Nucleic Acids Res. 18, 4020, 1990
A:Title: cDNA sequence of human beta-NGF.
A:Reference number: S10253; MUID:90326556; PMID:2314737
A:Accession: S10253
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 46-286 <BOB>
A:Cross-references: EMBL:X52599; NID:q29476; PIDN:CA36832.1; PID:q29477
A:Map position: 1p13.1-1p13.1
A:Inserts: 41/3
C:Complex: nerve growth factor is composed of two alpha chains, two beta chains, and
C:Superfamily: nerve growth factor beta chain
C:Keywords: glycoprotein; growth factor; submandibular gland
F:1-166/Domain: signal sequence and propeptide (fragment) #status predicted <SIG>
F:167-284/Product: nerve growth factor beta chain #status predicted <MAT>
F:26,114,159,211/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:181-246,224-274,234-276/Disulfide bonds: #status predicted

Query Match 57.2%; Score 373.5; DB 1; Length 286;
Best Local Similarity 59.8%; Pred. No. 3.1e-30;
Matches 67; Conservative 18; Mismatches 26; Indels 1; Gaps 1;

Oy 8 HRGESVCSDESLMTDKSSADIRGHQTVYGEIKTGNSPVRYEFTCKEARPVNG 67
Db 174 HRGESVCSDESVSWAGKTTATDIDKEKETVLAEEVNNVNNKRYEFTCKRDPNPDVG 233

Oy 68 CRGIDRHNNSOCTSOYVVRALTSENNKLVGMWRIRIDSCVSAISRKR 119
Db 234 CRGIDSRHNNSYCTTHTFEVKALTYD-GKQAMRFRIIDTACVLSRKAVR 284

RESULT 12
JL0097
nerve growth factor beta chain precursor - guinea pig
C:Species: Cavia porcellus (guinea pig)
C:Date: 07-Jun-1990 #sequence-revision 07-Jun-1990 #text-change 15-Mar-1996
C:Accession: JL0097
R:Schwarz, M.A.; Fisher, D.; Bradshaw, R.A.; Isaacson, P.J.
J. Neurochem. 52, 1203-1209, 1989
A:Title: Isolation and sequence of a cDNA clone of beta-nerve growth factor from the
A:Reference number: JL0097; MUID:89177243; PMID:2926397
A:Accession: JL0097
A:Molecule type: mRNA
A:Residues: 1-241 <CCH>
A>Note: the authors translated the codon GCU for residue 214 as Asp
C:Genetics:
A:Gene: Beta-NGF
C:Superfamily: nerve growth factor beta chain
C:Keywords: glycoprotein; growth factor; hormone
F:1-121/Domain: propeptide #status predicted <PRO>
F:122-241/Product: nerve growth factor beta chain #status predicted <MAT>
F:114-134/Region: receptor binding #status predicted
F:69,114/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 56.9%; Score 371.5; DB 2; Length 241;
Best Local Similarity 58.0%; Pred. No. 4.2e-30;
Matches 65; Conservative 20; Mismatches 26; Indels 1; Gaps 1;

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A:Molecule type: mRNA
A:Residues: 1-247 <NAM>
A:Cross-references: GB:M61176; NID:g179404; PIDN:AAA6805.1; PID:q896463
A:Note: the sequence in GenBank entry HUMBDNF, release 106.0, (PID:q896463) begins tran
J.Yamamoto, H.; Gurney, M.E.
J. Neurosci. 10, 3469-3478, 1990
A:Title: Human platelets contain brain-derived neurotrophic factor.
A:Reference number: A37218; MUID:91038253; PMID:2210938
A:Accession: A37218
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 138-236 <YAM>
R.Koschenthal, A.; Goeddel, D.V.; Nguyen, T.; Martin, E.; Burton, L.E.; Smith, A.; Laramee
Endocrinology 129, 1285-1294, 1991
A:Title: Primary structure and biological activity of human brain-derived neurotrophic f
A:Reference number: A61115; MUID:91339743; PMID:1874171
A:Accession: A61115
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-65; 'M', 67-247 <ROS>
R.Shintani, A.; Ono, Y.; Katsuo, Y.; Igarashi, K.
Biochem. Biophys. Res. Commun. 182, 325-332, 1992
A:Title: Characterization of the 5'-flanking region of the human brain-derived neurotro
A:Reference number: I38072; MUID:92118032; PMID:1339267
A:Accession: I38072
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-247 <SHI>
A:Cross-references: EMBL:M6201; NID:q3928269; PIDN:CAA42761.1; PID:q496626
A:Note: the authors do not discuss this mRNA sequence in this reference; attribution is
C:Genetics:
A:Gene: GDN:BDNF
A:Cross-references: GDB:125916; OMIM:113505
A:Map position: 11p13-11p13
A:Superfamily: nerve growth factor beta chain
C:Keywords: dimer; glycoprotein
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-138/Domain: propeptide #status predicted <PRO>
F:139-247/Product: brain-derived neurotrophic factor #status predicted <NAT>
F:1/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match      54.2%  Score 354;  DB 2;  Length 247;
Best Local Similarity 57.4%  Pred. No. 2.5e-28;
Matches 66;  Conservative 17;  Mismatches 30;  Indels 2;  Gaps 1;

Oy      7  SHREYVCSDELAWT--DKSAIDIRGHQTVGEIKTNSPNKYQPYETRECKEARPV 64
      :  ||| ||||| |||  || :||:|  ||| ::  :||| ||||| :|
Db      133 ARRELISVCSISEMWTAAADKTAIVDMSCGYTVLEKYPVSKGOLKQYFETCKNPMGYT 192

Oy      65  KNGCGIDDKHNSOCKTSQTVYRALTSENNKLVGMWRIRIDTSCVSLAKRIQR 119
      |  ||||| :||| ||| :| :||| ||||| ||| :| ||
Db      193  KEGCRGIDKRNHNSOCCRTQSYVALTMSKKRIQMFRIRIDTSCVCTLIKRCR 247

Search completed: December 2, 2002, 15:14:00
Job time : 10.5662 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 2, 2002, 15:05:43 ; Search time 4.9238 seconds
(without alignments)
1010.837 Million cell updates/sec

Title: US-10-072-681-5

Perfect score: 653
Sequence: 1 PYAEKSHRGESVCSSESL.....RWIRIDTSVLSALSRIGRT 120

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SWISSProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	641	98.2	257 1	NT3_HUMAN
2	641	98.2	258 1	NT3_MOUSE
3	641	98.2	258 1	NT3_RAT
4	638	97.7	257 1	NT3_CHICK
5	638	97.7	257 1	NT3_FELCA
6	619	94.8	260 1	NT3_XENLA
7	392.5	60.1	243 1	NGF_XENLA
8	385	59.0	231 1	NGF_CHICK
9	382.5	58.6	229 1	NGF_PIG
10	378.5	58.0	241 1	NGF_RAT
11	378	57.9	236 1	NGF_XENLA
12	373.5	57.2	241 1	NGF_HUMAN
13	372.5	57.0	231 1	NGF_BOVIN
14	371.5	56.9	241 1	NGF_BOVIN
15	370	56.7	241 1	NGF_CAVPO
16	368.5	56.4	241 1	NGF_PANA
17	356	54.5	246 1	BDNF_MOUSE
18	355	54.4	255 1	BDNF_CHICK
19	354	54.2	247 1	BDNF_CAVPO
20	354	54.2	247 1	BDNF_HUMAN
21	354	54.2	247 1	BDNF_PROLO
22	354	54.2	247 1	BDNF_ORSAR
23	354	54.2	249 1	BDNF_ORSML
24	354	54.2	249 1	BDNF_MOUSE
25	354	54.2	252 1	BDNF_PIG
26	352.5	54.0	243 1	NGF_BUNMU
27	352	53.9	209 1	NT5_RAT
28	350	53.6	210 1	NT5_HUMAN
29	350	53.6	247 1	BDNF_FELCA
30	350	53.6	248 1	BDNF_BOVIN
31	350	53.6	270 1	BDNF_CYPCA
32	349	53.4	117 1	NGF_DABRR
33	349	53.4	269 1	BDNF_XIPMA

34	343	52.5	114 1	BDNF_MACMU	006225 macaca mufa
35	326	49.9	116 1	BDNF_XENLA	P25432 xenopus lae
36	320.5	49.1	116 1	NGF_NAJNA	P01140 naja naja (
37	314.5	48.2	116 1	NGF_NAJNA	P21377 naja atra (
38	308	47.2	140 1	NT7_CYPCA	003479 cyprinus ca
39	299	45.8	233 1	NT7_BRARE	071797 brachydonto
40	295.5	45.3	194 1	NGF_XIPMA	P34129 xiphophorus
41	244.5	37.4	257 1	NT66_HUMAN	P34133 homo sapien
42	241.5	37.0	186 1	NT66_HUMAN	P34134 homo sapien
43	238.5	36.5	257 1	NT3_RATCL	P25434 raja clavac
44	212	32.5	43 1	NGF_VIPLE	P25428 vipera lebe
45	147	22.5	42 1	NGF_VIPLE	

ALIGNMENTS

RESULT 1	NT3_HUMAN	STANDARD:	PRT:	257 AA.
AC	P20783:			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (BDNF)			
DE	(Nerve growth factor 2) (NGF-2).			
GN	NT3.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606:			
RX	SEQUENCE FROM N.A.			
RX	MEDLINE=90262727; PubMed=2344409;			
RA	Rosenthal A., Goeddel D.V., Nguyen T., Lewis M., Shih A.,			
RA	Laramee G.R., Nikolic K., Winslow J.W.;			
RT	"Primary structure and biological activity of a novel human			
RT	neurotrophic factor.";			
RL	Neuron 4:767-773(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=91045937; PubMed=2236018;			
RX	Jones K.R., Reichardt L.F.;			
RA	Kaisho Y., Yoshimura K., Nakahama K.;			
RT	"Cloning and expression of a cDNA encoding a novel human neurotrophic			
RT	factor.";			
RL	FEBS Lett. 266:187-191(1990).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=91365361; PubMed=1889806;			
RA	Malsompierre P.C., Le Beau M.M., Espinosa R. III, Ip N.Y.,			
RA	Belluscio L., de la Monte S.M., Squitito S., Furch M.E.,			
RT	"Human and rat brain-derived neurotrophic factor and neurotrophin-3:			
RT	gene structures, distributions, and chromosomal localizations.";			
RL	Genomics 10:558-568(1991).			
RN	[5]			
RP	SEQUENCE OF 194-236 FROM N.A.			
RP	TISSUE=Leukocyte; PubMed=2025430;			
RX	MEDLINE=91222573; PubMed=2025430;			
RA	Hallboeek F., Ibanez C.F., Persson H.;			
RT	"Evolutionary studies of the nerve growth factor family reveal a			
RT	novel member abundantly expressed in xenopus ovary.";			
RL	Neuron 6:845-858(1991).			
RN	[6]			
RP	X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).			
RX	MEDLINE=95211877; PubMed=7703225;			

RA Robinson R.C., Redziejewski C., Stuart D.I., Jones E.Y.;
RT "Structure of the brain-derived neurotrophic factor/neurotrophin 3
RT heterodimer";
RT Biochemistry 34:4139-4146(1995).
RN (7)
RP VARIANT GLU-76.
RX MEDLINE-95251647; PubMed-7733919;
RA Hattori M., Nenko S.;
RT "Association of neurotrophin-3 gene variant with severe forms of
RT schizophrenia";
RT Biochem. Biophys. Res. Commun. 209:513-518(1995).
RN (8)
RP VARIANT GLU-76.
RX MEDLINE-96253892; PubMed-8925252;
RA Arihama T., Takekoshi K., Itohawa M., Hameguchi H., Toru M.;
RT "Failure to find associations of the CA repeat polymorphism in the
RT first intron and the GLU-63/GLU-63 polymorphism of the neurotrophin-3
RT gene with schizophrenia";
RT Psychiatr. Genet. 6:13-15(1996).
CC -1- FUNCTION: SEEMS TO PROMOTE THE SURVIVAL OF VISCERAL AND
CC PROPRIOCEPTIVE SENSORY NEURONS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: BRAIN AND PERIPHERAL TISSUES.
CC -1- POLYMORPHISM: Variant Glu-76 (frequently reported as Glu-63) was
CC thought to be associated with severe forms of schizophrenia. This
CC does not seem to be the case.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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CC -----
DR EMBL: X53555; CAA37703.1; -
DR EMBL: X57763; AAA59953.1; -
DR EMBL: M6180; AAA63231.1; -
DR PIR: JH0141; JH0141.
DR PIR: A36208; A36208.
DR PIR: S10719; S10719.
DR PIR: CA0304; CA0304.
DR PDB: 1BND; 04-APR-96.
DR PDB: 1BRK; 09-FEB-99.
DR Genew; MGC:8023; NTF3.
DR MIM: 162660; -
DR InterPro: IPR002400; GF_cysknob.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF.1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRINTS: PR00268; NGF.
DR PRODOM: PD002052; NGF.1.
DR SMART: SM00140; NGF.1.
DR PROSITE: PS00248; NGF.1; 1.
DR PROSITE: PS0270; NGF.2; 1.
KW Growth factor; Signal; Polymorphism; 3D-structure.
KW SIGNAL
FT SIGNAL 1 16
FT PROPEP 17 138
FT CHAIN 139 257
FT DISULFID 152 217
FT DISULFID 195 246
FT DISULFID 205 248
FT CARBOHYD 131 131
FT VARIANT 76 76
FT SEQUENCE 257 AA; 29354 MW; 39A5BB3B28E25E03 CRC64;
FT /FTID=VAR_012084.
FT G->E.
FT N-LINKED (GLCNAC...) (POTENTIAL).
Query Match 98.2%; Score 641; DB 1; Length 257;
Best Local Similarity 99.2%; Pred. No. 2,2e-59;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 2 YAEHSHRGESVCDSESLMTWTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 61

DB 139 YAEHSHRGESVCDSESLMTWTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 198
OY 62 RPYKNGCRGIDDKHNSOCKTSQTVYRALTSNNKLVGMRIIRIDTSCVSLSKRT 120
DB 199 RPYKNGCRGIDDKHNSOCKTSQTVYRALTSNNKLVGMRIIRIDTSCVSLSKRT 257
RESULT 2
NT3_MOUSE STANDARD; PRT; 258 AA.
ID NT3_MOUSE
AC P20181;
DT 01-FEB-1991 (Rel. 17, Created)
DT 30-FEB-1991 (Rel. 17, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (HDNF)
DE (Nerve growth factor 2) (NGF-2).
GN NTF3 OR NTF-3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE-90190865; PubMed-2314473;
RA Hohn A., Leibrock J., Bailey K., Barde Y.-A.;
RT "Identification and characterization of a novel member of the nerve
RT growth factor/brain-derived neurotrophic factor family";
RT Nature 344:339-341(1990).
CC -1- FUNCTION: SEEMS TO PROMOTE THE SURVIVAL OF VISCERAL AND
CC PROPRIOCEPTIVE SENSORY NEURONS.
CC -1- SUBCELLULAR LOCATION: secreted.
CC -1- TISSUE SPECIFICITY: BRAIN AND PERIPHERAL TISSUES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL: X53257; CAA37348.1; -
DR PIR: S09155; S09155.
DR HSSP: P20783; 1BRK.
DR MGD: MGI:97380; NTF3.
DR InterPro: IPR002400; GF_cysknob.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF.1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRINTS: PR00268; NGF.
DR PRODOM: PD002052; NGF.1.
DR SMART: SM00140; NGF.1.
DR PROSITE: PS00248; NGF.1; 1.
DR PROSITE: PS0270; NGF.2; 1.
KW Growth factor; Signal.
KW SIGNAL
FT SIGNAL 1 16
FT PROPEP 17 139
FT CHAIN 140 258
FT DISULFID 153 218
FT DISULFID 196 247
FT DISULFID 206 249
FT CARBOHYD 131 131
FT SEQUENCE 258 AA; 29587 MW; 7180D064EBAE6042 CRC64;
Query Match 98.2%; Score 641; DB 1; Length 258;
Best Local Similarity 99.2%; Pred. No. 2,2e-59;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 2 YAEHSHRGESVCDSESLMTWTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 61
DB 140 YAEHSHRGESVCDSESLMTWTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 199

OY 62 RPVKNCGRIDKHNNSCKTSQTYVRLTSENKLVGMRIIDTSCVLSRKIGRT 120
 DB 200 RPVKNCGRIDKHNNSCKTSQTYVRLTSENKLVGMRIIDTSCVLSRKIGRT 258

RESULT 3
 NT3_RAT STANDARD: PRT: 258 AA.
 AC P16280:
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (HDMF)
 DE (Nerve growth factor 2) (NGF-2).
 GN NT3 OR NT3-3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-90319130; PubMed-2164684;
 RA Ertfola P., Ibanez C.F., Ebdendal T., Olson L., Persson H.;
 RT "Molecular cloning and neurotrophic activities of a protein with
 RT structural similarities to nerve growth factor: developmental and
 RT topographical expression in the brain";
 RT Proc. Natl. Acad. Sci. U.S.A. 87:5454-5458(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-90208301; PubMed-2321006;
 RA Maisonnier P.C., Belluscio L., Squinto S., Ip N.Y., Furch M.E.,
 RA Lindsay R.M., Yancopoulos G.D.;
 RT "Neurotrophin-3: a neurotrophic factor related to NGF and BDNF";
 RT Science 247:1446-1451(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-91365361; PubMed-1899806;
 RA Maisonnier P.C., le Beau M.M., Espinosa R. III, Ip N.Y.,
 RA Belluscio L., de la Monte S.M., Squinto S., Furch M.E.,
 RA Yancopoulos G.D.;
 RT "Human and rat brain-derived neurotrophic factor and neurotrophin-3:
 RT gene structures, distributions, and chromosomal localizations";
 RT Genomics 10:558-568(1991).
 RN [4]
 RP SEQUENCE OF 195-237 FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE-liver;
 RX MEDLINE-9122573; PubMed-2025430;
 RA Hallboeek F., Ibanez C.F., Persson H.;
 RT "Evolutionary studies of the nerve growth factor family reveal a
 RT novel member abundantly expressed in Xenopus ovary";
 RT Neuron 6:845-858(1991).
 CC -1- FUNCTION: SEEMS TO PROMOTES THE SURVIVAL OF VISCERAL AND
 CC PROPRIOCEPTIVE SENSOR NEURONS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: BRAIN AND PERIPHERAL TISSUES.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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 DR EMBL: M34643; AAA1313.1; -;
 DR EMBL: M33968; AAA1727.1; -;
 DR EMBL: M51179; AAA63497.1; -;
 DR PIR: A35781; A35781;
 DR PIR: A40094; A40094;
 DR HSSP: P20783; 188X;
 DR InterPro: IPR002400; GF_cysknot.

DR InterPro: IPR002072; NGF.
 DR Pfam: PR0043; NGF; 1.
 DR PRINTS: PR00438; GF_CYSKNOT.
 DR PRINTS: PR00268; NGF.
 DR PRODOM: PD002052; NGF; 1.
 DR SMART: SM00140; NGF; 1.
 DR PROSITE: PS00248; NGF_1; 1.
 DR PROSITE: PS50370; NGF_2; 1.
 KR Growth factor; Signal.
 FT SIGNAL 1
 FT PROPEP 17 139
 FT CHAIN 140 258
 FT DISULFID 153 218
 FT DISULFID 196 247
 FT CARBOHYD 131 131
 SO SEQUENCE 258 AA; 29644 MW; 7AD537CF8518A1CE CRC64; N-LINKED (GLYCAC...) (POTENTIAL).

Query Match 98.2%; Score 641; DB 1; Length 258;
 Best Local Similarity 99.2%; Pred. No. 2,2e-59;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 YAEKSHREYGVCSSESLMTDSSAIDIRGHOTVYGEITGNSPVKQYETCKEA 61
 DB 140 YAEKSHREYGVCSSESLMTDSSAIDIRGHOTVYGEITGNSPVKQYETCKEA 199
 OY 62 RPVKNCGRIDKHNNSCKTSQTYVRLTSENKLVGMRIIDTSCVLSRKIGRT 120
 DB 200 RPVKNCGRIDKHNNSCKTSQTYVRLTSENKLVGMRIIDTSCVLSRKIGRT 258

RESULT 4
 NT3_CHICK STANDARD: PRT: 257 AA.
 ID NT3_CHICK
 AC P23433;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (HDMF)
 DE (Nerve growth factor 2) (NGF-2).
 GN NT3.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_Taxid=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-91091238; PubMed-1457809;
 RA Maisonnier P., Belluscio L., Conover J.C., Yancopoulos G.D.;
 RT "Gene sequences of chicken BDNF and NT-3";
 RT DNA Seq. 3:49-54(1992).
 RN [2]
 RP SEQUENCE OF 194-236 FROM N.A.
 RX MEDLINE-9122573; PubMed-2025430;
 RA Hallboeek F., Ibanez C.F., Persson H.;
 RT "Evolutionary studies of the nerve growth factor family reveal a
 RT novel member abundantly expressed in Xenopus ovary";
 RT Neuron 6:845-858(1991).
 CC -1- FUNCTION: SEEMS TO PROMOTES THE SURVIVAL OF VISCERAL AND
 CC PROPRIOCEPTIVE SENSOR NEURONS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
 CC -----
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 CC -----
 DR EMBL: M63378; AAA68880.1; -;

DR HSSP: P20783; 188K.
DR InterPro: IPR002400; GF_cysknot.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF_1.
DR PRINTS: PR00438; GFCSNMOT.
DR PRINTS: PR00268; NGF.
DR ProDom: PD02052; NGF_1.
DR SMART: SM00140; NGF_1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS50270; NGF_2; 1.
KW Growth factor; Signal.
FT SIGNAL 1 16
FT PROPEP 17 138
FT CHAIN 139 257
FT DISULFID 152 217
FT DISULFID 195 246
FT DISULFID 205 248
FT CARBOHYD 131 131
SQ SEQUENCE 257 AA; 29701 MW; E8043BA2A005C1E7 CRC64;

Query Match 97.7%; Score 638; DB 1; Length 257;
Best Local Similarity 98.3%; Pred. No. 4; Se-59;
Matches 117; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 YAEKSHRGESVCSSESLMTDKSSAIDIRGHQVTVLGEIKTGNSPVKNQYFETRCKEA 61
DB 139 YAEKSHRGESVCSSESLMTDKSSAIDIRGHQVTVLGEIKTGNSPVKNQYFETRCKEA 198
OY 62 RPYKNGCGRIDDKHNSCKTSQTYVRLTSENKLVGMWRIRIDTSCVLSRKIGRT 120
DB 199 RPYKNGCGRIDDKHNSCKTSQTYVRLTSENKLVGMWRIRIDTSCVLSRKIGRT 257

RESULT 5
NT3_FELCA STANDARD; PRT: 257 AA.
ID NT3_FELCA
AC G9T5T2;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (HDNF)
DE (Nerve growth factor 2) (NGF-2).
GN NT-3.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Feliidae; Felis.
OC NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20211727; PubMed=10745216;
RA Lein E.S., Hohn A., Shatz C.J.;
RT "Dynamic regulation of BDNF and NT-3 expression during visual system development."
RL J. Comp. Neurol. 420:1-18(2000).
CC -1- FUNCTION: SEEMS TO PROMOTES THE SURVIVAL OF VISCERAL AND
CC PHOTORECEPTIVE SENSOR NEURONS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF192538; AAF03424.1; -
DR HSSP: P20783; 188K.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF_1.
DR PRINTS: PR00268; NGF.
DR ProDom: PD02052; NGF_1.

DR SMART: SM00140; NGF_1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS50270; NGF_2; 1.
KW Growth factor; Signal.
FT SIGNAL 1 16
FT PROPEP 17 138
FT CHAIN 139 257
FT DISULFID 152 217
FT DISULFID 195 246
FT DISULFID 205 248
FT CARBOHYD 131 131
SQ SEQUENCE 257 AA; 29403 MW; E853FE59C5113E4 CRC64;

Query Match 97.1%; Score 634; DB 1; Length 257;
Best Local Similarity 97.5%; Pred. No. 1; Se-58;
Matches 116; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 YAEKSHRGESVCSSESLMTDKSSAIDIRGHQVTVLGEIKTGNSPVKNQYFETRCKEA 61
DB 139 YAEKSHRGESVCSSESLMTDKSSAIDIRGHQVTVLGEIKTGNSPVKNQYFETRCKEA 198
OY 62 RPYKNGCGRIDDKHNSCKTSQTYVRLTSENKLVGMWRIRIDTSCVLSRKIGRT 120
DB 199 RPYKNGCGRIDDKHNSCKTSQTYVRLTSENKLVGMWRIRIDTSCVLSRKIGRT 257

RESULT 6
NT3_XENLA STANDARD; PRT: 260 AA.
ID NT3_XENLA
AC P25435;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (HDNF) (Nerve
DE growth factor 2) (NGF-2).
DE Xenopus laevis (African clawed frog).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodidae; Xenopus.
OC NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RC MEDLINE=97252639; PubMed=9096131;
RX Xie K., Wang T., Olaisson P., Mizuno K., Lu B.;
RA "Activity-dependent expression of NT-3 in muscle cells in culture:
RT implications in the development of neuromuscular junctions."
RL J. Neurosci. 17:2947-2958(1997).
RN [2]
RP SEQUENCE OF 197-217 FROM N.A.
RX TISSUE=Liver;
RC MEDLINE=91225273; PubMed=2025430;
RX Hallboeek E., Ibanez C.F., Persson H.;
RA "Evolutionary studies of the nerve growth factor family reveal a
RT novel member abundantly expressed in Xenopus ovary."
RL Neuron 6:845-858(1991).
CC -1- FUNCTION: SEEMS TO PROMOTES THE SURVIVAL OF VISCERAL AND
CC PHOTORECEPTIVE SENSOR NEURONS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D27576; AAB17723.1; -
DR HSSP: P20783; 188K.
DR InterPro: IPR002400; GF_cysknot.
DR InterPro: IPR002072; NGF.

DR Pfam: PF00243; NGF; 1.
 DR PRINTS: PRO0268; NGF.
 DR PRODOM: PRO0268; NGF; 1.
 DR SMART: SM00140; NGF; 1.
 DR PROSITE: PS00248; NGF_1; 1.
 DR PROSITE: PS50270; NGF_2; 1.
 KM Growth factor; signal.
 FT SIGNAL 1 16
 FT PROPEP 17 141 POTENTIAL.
 FT CHAIN 142 260 NEUROTROPHIN-3.
 FT DISULFID 153 220 BY SIMILARITY.
 FT DISULFID 198 249 BY SIMILARITY.
 FT DISULFID 208 251 BY SIMILARITY.
 FT CARBOHYD 134 134 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 260 AA; 30022 MW; FFB8507A5EA930C5 CRC64;

Query Match 94.88; Score 619; DB 1; Length 260;
 Best Local Similarity 94.18; Pred. No. 4, 2e-57;
 Matches 112; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 2 YAEKSHRGEXVCDSESLWVTDKSSAIDIRGHQVTLGEIKTGNSPVQYFETRCKEA 61
 DB 142 FAEHKSHRGEXVCDSESLWVTDKMAIDIRGHQVTLGEIKTGNSPVQYFETRCKEA 201
 OY 62 RPKNGCGRIDKHNNSCKTSOTYVRLTSENKLVGWRHRIIDTSCVSALSRIKGR 120
 DB 202 RPKNGCGRIDKHNNSCKTSOTYVRLTSENKLVGWRHRIIDTSCVSALSRIKGRS 260

RESULT 7

NGF_CHICK
 ID NGF_CHICK STANDARD; PRT; 243 AA.

AC P03200;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 13-JUN-2002 (Rel. 41, Last annotation update)
 DE Beta-nerve growth factor precursor (Beta-NGF).
 CN NGFB.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;
 RX MEDLINE=86300646; PubMed=3017695;
 RA Ebendahl T., Lachmar D., Persson H.;
 RT Structure and expression of the chicken beta nerve growth factor gene.
 RL EMBO J. 5:1483-1487(1986).
 RN [12]

RP SEQUENCE OF 118-243 FROM N.A.
 RX MEDLINE=86248129; PubMed=3720959;
 RA Wilson D., Perret C., Frechin N., Keller A., Behar G., Brachet P.,
 RA Aulicay C.;
 RT "Molecular cloning of the avian beta-nerve growth factor gene:
 RT transcription in brain."
 RL FEBS Lett. 203:82-86(1986).
 RN [13]

RP SEQUENCE OF 121-243 FROM N.A.
 RX MEDLINE=86300647; PubMed=2427334;
 RA Meier R., Becker-Andre M., Gotz R., Heumann R., Shaw A., Thoenen H.;
 RT "Molecular cloning of bovine and chick nerve growth factor (NGF):
 RT delineation of conserved and unconserved domains and their
 RT relationship to the biological activity and antigenicity of NGF."
 RL EMBO J. 5:1489-1493(1986).
 RN [14]

RP SEQUENCE OF 181-222 FROM N.A.
 RX MEDLINE=91225573; PubMed=2035430;
 RA Hallboeck F., Ibanez C.F., Persson H.;
 RT "Evolutionary studies of the nerve growth factor family reveal a
 RT novel member abundantly expressed in Xenopus ovary."
 RN [2]

RL Neuron 6:845-858(1991).
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 CC EMBRYONIC SENSORY NEURONS.
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
 CC -----
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 CC -----

DR EMBL: X04003; CAA27633.1; ALT_INIT.
 DR EMBL: X04067; CAA27703.1;
 DR EMBL: M26810; AAA48984.1;
 DR PIR: A24857; A24857.
 DR PIR: A26311; A26311.
 DR HSSP: P01139; 1BET.
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF; 1.
 DR PRINTS: PRO0268; NGF.
 DR PRODOM: PRO02052; NGF; 1.
 DR SMART: SM00140; NGF; 1.
 DR PROSITE: PS00248; NGF_1; 1.
 DR PROSITE: PS50270; NGF_2; 1.
 KM Growth factor; signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT PROPEP 23 125
 FT CHAIN 126 243 BETA-NERVE GROWTH FACTOR.
 FT DISULFID 139 204 BY SIMILARITY.
 FT DISULFID 182 232 BY SIMILARITY.
 FT DISULFID 192 234 BY SIMILARITY.
 SQ SEQUENCE 243 AA; 27138 MW; 74C306CB2079DA07 CRC64;

Query Match 60.14; Score 392.5; DB 1; Length 243;
 Best Local Similarity 62.58; Pred. No. 1, 2e-13;
 Matches 70; Conservative 18; Mismatches 23; Indels 1; Gaps 1;

OY 8 HNGEYVCDSESLWVTDKSSAIDIRGHQVTLGEIKTGNSPVQYFETRCKEARPKNG 67
 DB 132 HNGEYVCDSESLWVTDKSSAIDIRGHQVTLGEIKTGNSPVQYFETRCKEARPKNG 119
 OY 68 CRGIDKHNNSCKTSOTYVRLTSENKLVGWRHRIIDTSCVSALSRIKGR 119
 DB 192 CRGIDKHNNSCKTSOTYVRLTSENKLVGWRHRIIDTSCVSALSRIKGRS 242

RESULT 8

NGF_XENLA
 ID NGF_XENLA STANDARD; PRT; 231 AA.

AC P21617;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Nerve growth factor precursor (NGF).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 NCBI_TaxID=8355;
 RX MEDLINE=91362944; PubMed=1888511;
 RA Carriero F., Campioni M., Pierandrei-Amaldi P.;
 RT "Structure and expression of the nerve growth factor gene in Xenopus
 RT oocytes and embryos."
 RL Mol. Reprod. Dev. 29:313-322(1991).
 RN [2]

RP SEQUENCE OF 170-211 FROM N.A.
 RX MEDLINE=91362944; PubMed=1888511;
 RA Carriero F., Campioni M., Pierandrei-Amaldi P.;
 RT "Structure and expression of the nerve growth factor gene in Xenopus
 RT oocytes and embryos."
 RL Mol. Reprod. Dev. 29:313-322(1991).
 RN [2]

RL J. Neurosci. Res. 20:403-410(1988).

RP [2] SEQUENCE OF 178-219 FROM N.A.

RC STRAIN-Sprague-Dawley; TISSUE-Liver;

RX MEDLINE-91222573; PubMed-2025430;

RA Haliboeck F., Ibanez C.F., Persson H.;

RT "Evolutionary studies of the nerve growth factor family reveal a novel member abundantly expressed in Xenopus ovary."

RL Neuron 5:845-858(1991).

CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND MAINTENANCE OF THE SYMPATHETIC AND SENSORY NEPOTUS SYSTEMS. IT STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND EMBRYONIC SENSORY NEURONS.

CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.

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CC EMBL: M36589; AAA41697.1; ALT_INIT.

DR HSSP: P01139; 18ET.

DR InterPro: IPR002072; NGF.

DR Pfam: PF00243; NGF; 1.

DR PRINTS: PR00268; NGF.

DR ProDom: PD002052; NGF; 1.

DR SMART: SM00140; NGF; 1.

DR PROSITE: PS00248; NGF_1; 1.

DR PROSITE: PS0270; NGF_2; 1.

KM Growth factor: Signal.

FT SIGNAL 1 18

FT PROPEP 19 121

FT CHAIN 122 241

FT DISULFID 136 201

FT DISULFID 179 229

FT DISULFID 189 231

FT CARBOHYD 69 69

FT CARBOHYD 114 114

FT CARBOHYD 166 166

SO SEQUENCE 241 AA: 27009 MW: 665423715632130 CRC64;

Query Match 58.0%; Score 378.5; DB 1; Length 241;

Best Local Similarity 59.8%; Pred. No. 3.5e-32;

Matches 67; Conservative 20; Mismatches 24; Indels 1; Gaps 1;

OY 8 HNGEVSVDSESLWYTDKSSAIDIRGHQVYVIGETKNGSPVQYFETRECKEAPVKN 67

DB 129 HNGEVSVDSESLWYTDKSSAIDIRGHQVYVIGETKNGSPVQYFETRECKEAPVKN 188

OY 68 GCGIDDKHNSCKTSQTYVALTSNNKLVGRNIRIDTSCVSAISRIGT 119

DB 189 GCGIDDKHNSCKTSQTYVALTSNNKLVGRNIRIDTSCVSAISRIGT 239

RESULT 11

NT4_XENLA STANDARD: PRT: 236 AA.

AC P24727;

DT 01-MAR-1992 (Rel. 21, Created)

DT 01-MAR-1992 (Rel. 21, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Neurotrophin-4 precursor (NT-4).

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI_Taxid-9355;

RA NCBI_Taxid-9355;

RP SEQUENCE FROM N.A.

RC TISSUE-Ovary;

RX MEDLINE-91222573; PubMed-2025430;

RA Haliboeck F., Ibanez C.F., Persson H.;

RT "Evolutionary studies of the nerve growth factor family reveal a novel member abundantly expressed in Xenopus ovary."

RL Neuron 5:845-858(1991).

CC -1- FUNCTION: NT-4 COULD PLAY A ROLE IN OOCYTESIS AND/OR EARLY AND ELICITS NEURITE OUTGROWTH FROM EXPLANTED DORSAL ROOT GANGLIA WITH NO AND LOWER ACTIVITY IN SYMPATHETIC AND NODOSE GANGLIA, RESPECTIVELY.

CC -1- TISSUE SPECIFICITY: OVARY.

CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.

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CC EMBL: Z30090; CAA82906.1; "

DR PIR: JH0400; JH0400.

DR HSSP: P34130; 1B98.

DR InterPro: IPR002072; NGF.

DR Pfam: PF00243; NGF; 1.

DR PRINTS: PR00268; NGF.

DR ProDom: PD002052; NGF; 1.

DR SMART: SM00140; NGF; 1.

DR PROSITE: PS00248; NGF_1; 1.

DR PROSITE: PS0270; NGF_2; 1.

KM Growth factor: Signal.

FT SIGNAL 1 18

FT PROPEP 19 113

FT CHAIN 114 236

FT DISULFID 131 196

FT DISULFID 174 225

FT DISULFID 184 227

FT CARBOHYD 47 47

FT CARBOHYD 106 106

SO SEQUENCE 236 AA: 26213 MW: A210F97F2016357D CRC64;

Query Match 57.9%; Score 378; DB 1; Length 236;

Best Local Similarity 59.6%; Pred. No. 3.8e-32;

Matches 68; Conservative 16; Mismatches 30; Indels 0; Gaps 0;

OY 7 SHNGEVSVDSESLWYTDKSSAIDIRGHQVYVIGETKNGSPVQYFETRECKEAPVKN 66

DB 123 SHNGEVSVDSESLWYTDKSSAIDIRGHQVYVIGETKNGSPVQYFETRECKEAPVKN 182

OY 67 GCGIDDKHNSCKTSQTYVALTSNNKLVGRNIRIDTSCVSAISRIGT 120

DB 183 GCGIDDKHNSCKTSQTYVALTSNNKLVGRNIRIDTSCVSAISRIGT 235

RESULT 12

NGF_HUMAN STANDARD: PRT: 241 AA.

AC P01138;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Beta-nerve growth factor precursor (beta-NGF).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_Taxid-9605;

RA NCBI_Taxid-9605;

RP SEQUENCE FROM N.A.

RX MEDLINE-83244969; PubMed-6688123;

RA Ullrich A., Gray A., Berman C., Dull T.J.;

RT "Human beta-nerve growth factor gene sequence highly homologous to
 RT that of mouse."
 RL Nature 303:821-825(1983).
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE-84206565; PubMed-6327169;
 RA Ullrich A., Gray A., Berman C., Coussens L., Dull T.J.;
 RT "Sequence homology of human and mouse beta-NGF subunit genes."
 RL Cold Spring Harb. Symp. Quant. Biol. 48:435-442(1983).
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE-90326556; PubMed-2374737;
 RA Boreani G., Pizzuti A., Ruggeri E.I., Falini A., Silani V.,
 RA Sidoli A., Scariato G., Baralle F.E.;
 RT "cDNA sequence of human beta-NGF."
 RL Nucleic Acids Res. 18:4020-4020(1990).
 RN
 RP SEQUENCE OF 178-219 FROM N.A.
 RC TISSUE-Leukocyte;
 RX MEDLINE-9122573; PubMed-2025430;
 RA Halboeck F., Idanez C.F., Persson H.;
 RT "Evolutionary studies of the nerve growth factor family reveal a
 RT novel member abundantly expressed in Xenopus ovary."
 RL Neuron 6:845-858(1991).
 CC
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 CC EMBRYONIC SENSORY NEURONS.
 CC
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
 CC
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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 CC
 CC -----
 DR EMBL: V01511; CAA24755.1;
 DR EMBL: M21062; AAA5931.1;
 DR EMBL: X52599; CAA36832.1;
 DR PIR: A01399; NCIDBM.
 DR PIR: S10253; S10253.
 DR HSP: P01139; 1BET.
 DR Gene: HGNC:7808; NGFB.
 DR MIM: 162030;
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF.1.
 DR PRINTS: PR00268; NGF.
 DR PRODOM: PD002052; NGF.1.
 DR SMART: SM00140; NGF.1.
 DR PROSITE: PS00248; NGF.1;
 DR PROSITE: PS0270; NGF_2; 1.
 DR Growth factor, Signal.
 KM
 FT SIGNAL 1 18
 FT PROPEP 19 121
 FT CHAIN 122 241
 FT DISULFID 136 201
 FT DISULFID 179 229
 FT DISULFID 189 231
 FT CARBOHYD 69 69
 FT CARBOHYD 114 114
 SQ SEQUENCE 241 AA; 26987 MW; CFIADADCSB736BDF CRC64;
 Query Match 57.2%; Score 373.5; DB 1; Length 241;
 Best Local Similarity 59.8%; Pred. No. 1,1e-31;
 Matches 67; Conservative 18; Mismatches 26; Indels 1; Gaps 1;
 Qy 8 HRRGVSYCDSESLWYDKSSAIDIRGHQVTVYGEIKRTNSPVKQYFETTRCKEAPRKNG 67
 Db 129 HRRGVSYCDSESLWYDKSSAIDIRGHQVTVYGEIKRTNSPVKQYFETTRCKEAPRKNG 188

Oy 68 CRGIDCKHNSOCTQSYRYALTSNNKLYGMRIRIDTSCVSALSRKIGR 119
 Db 189 CRGIDCKHNSYCTTTRITFKALTNM-GKQAMRRIRIDTACVCLSRKAVR 239
 RESULT 13
 NGF_BOVIN STANDARD: PRT: 231 AA.
 ID NGF_BOVIN
 AC P13600; 018969;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Beta-nerve growth factor precursor (beta-NGF) (Fragment).
 GN NGFB.
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 CC NCBI_TaxID=9913;
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE-Blood;
 RX MEDLINE-97430845; PubMed-9284944;
 RA Elduque C., Laurent P., Hayes H., Rodellar C., Laveziell H.,
 RA Zaragoza P.;
 RT "Assignment of the beta-nerve growth factor (NGFB) to bovine
 RT chromosome 3 band q23 by in situ hybridization."
 RL Cytogenet. Cell Genet. 77:306-307(1997).
 RN
 RP SEQUENCE OF 107-231 FROM N.A.
 RX MEDLINE-96306647; PubMed-2427334;
 RA Meier R., Becker-Andre M., Gotz R., Heumann R., Shaw A., Thoenen H.;
 RT "Molecular cloning of bovine and chick nerve growth factor (NGF):
 RT delineation of conserved and unconserved domains and their
 RT relationship to the biological activity and antigenicity of NGF."
 RL EMBO J. 5:1489-1493(1986).
 CC
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 CC EMBRYONIC SENSORY NEURONS.
 CC
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
 CC
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC
 CC -----
 DR EMBL: Y09566; CAA70759.1;
 DR EMBL: M26809; AAA30666.1;
 DR PIR: A26312; A26312.
 DR HSP: P01139; 1BET.
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF.1.
 DR PRODOM: PD002052; NGF.1.
 DR SMART: SM00140; NGF.1.
 DR PROSITE: PS00248; NGF.1;
 DR PROSITE: PS0270; NGF_2; 1.
 DR Growth factor, Signal.
 KM
 FT NON_TER 1 8
 FT SIGNAL 9 111
 FT PROPEP 9 111
 FT CHAIN 112 231
 FT DISULFID 126 191
 FT DISULFID 169 221
 FT DISULFID 179 221
 FT CARBOHYD 156 156
 FT CARBOHYD 118 118
 FT CONFLICT 161 161
 FT CONFLICT 161 161
 R -> K (IN REF. 2).
 POTENTIAL.
 BETA-NERVE GROWTH FACTOR.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 L -> F (IN REF. 2).
 R -> K (IN REF. 2).

FT CONFLICT 230 231 AP -> RA (IN REF. 2).
 SO SEQUENCE 231 AA: 25437 MM: 01605099291AA18C CRC64:

Query Match
 Best Local Similarity 58.9%; Score 372.5; DB 1; Length 231;
 Matches 66; Conservative 20; Mismatches 25; Indels 1; Gaps 1;

OY 8 HRCGVSQDSESLWYTDSSAIDRGHOVTLGEITGNSPVKQYFETKCEARPYKNG 67
 DB 119 HRCGVSQDSESLWYTDSSAIDRGHOVTLGEITGNSPVKQYFETKCEARPYKNG 178
 OY 68 CRGIDKHMNSOCTSTYVRLTSENKLVGMWRIRIDTSCVLSLRTRIG 119
 DB 179 CRGIDKHMNSOCTSTYVRLTSENKLVGMWRIRIDTSCVLSLRTRIG 229

RESULT 14
 NGF_CAVPO STANDARD: PRT: 241 AA.

AC P19093;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Beta-nerve growth factor precursor (Beta-NGF).
 GN NGF.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriognathii; Cavidae; Cavia.
 OX NCBI_TaxID-10141;
 RN 11
 RP SEQUENCE FROM N.A.
 RC Tissue-Procate;
 RA MEDLINE-8917743; PubMed-2926397;
 RA Scharr M.A., Fisher D., Bradshaw R.A., Jackson P.J.;
 RT Isolation and sequence of a cDNA clone of beta-nerve growth factor
 RT from the guinea pig prostate gland.
 RL J. Neurochem. 52:1203-1209(1989).
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 CC EMBRYONIC SENSORY NEURONS.
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
 DR PIR: J0097; J0097.
 DR HSP: P01139; 1BET.
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF. 1.
 DR PRINTS: PR00268; NGF.
 DR PRODOM: PD002052; NGF. 1.
 DR SMART: SM00140; NGF. 1.
 DR PROSITE: PS00248; NGF. 1.
 DR PROSITE: PS50270; NGF. 2; 1.
 KM Growth factor; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 121
 FT CHAIN 122 241
 FT DISULEID 136 201
 FT DISULEID 179 229
 FT DISULEID 189 231
 FT CARBOHYD 69 69
 FT CARBOHYD 114 114
 SQ SEQUENCE 241 AA: 26821 MM: 2F4E26B197804BF4 CRC64:

Query Match
 Best Local Similarity 56.9%; Score 371.5; DB 1; Length 241;
 Matches 65; Conservative 20; Mismatches 26; Indels 1; Gaps 1;

OY 8 HRCGVSQDSESLWYTDSSAIDRGHOVTLGEITGNSPVKQYFETKCEARPYKNG 67
 DB 119 HRCGVSQDSESLWYTDSSAIDRGHOVTLGEITGNSPVKQYFETKCEARPYKNG 188
 OY 68 CRGIDKHMNSOCTSTYVRLTSENKLVGMWRIRIDTSCVLSLRTRIG 119
 DB 179 CRGIDKHMNSOCTSTYVRLTSENKLVGMWRIRIDTSCVLSLRTRIG 229

DB 189 CRGIDKHMNSOCTSTYVRLTSENKLVGMWRIRIDTSCVLSLRTRIG 239

RESULT 15
 NGF_PRANA STANDARD: PRT: 241 AA.

AC P20675;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Beta-nerve growth factor precursor (Beta-NGF).
 GN NGF.
 OS Praomys natalensis (African soft-furred rat) (Mastomys natalensis).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciuromorphi; Muridae; Murinae;
 OC Mastomys.
 OX NCBI_TaxID-10112;
 RN 11
 RP SEQUENCE FROM N.A.
 RC MEDLINE-89172070; PubMed-3234767;
 RA Fahnestock M., Bell R.A.;
 RT Molecular cloning of a cDNA encoding the nerve growth factor
 RT precursor from Mastomys natalensis.
 RL Gene 69:257-264(1989).
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 CC EMBRYONIC SENSORY NEURONS.
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
 DR EMBL: M22748; AAA40599.1; ALT_INIT.
 DR PIR: J0343; NGRTBA.
 DR HSP: P01139; 1BET.
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF. 1.
 DR PRINTS: PR00268; NGF.
 DR PRODOM: PD002052; NGF. 1.
 DR SMART: SM00140; NGF. 1.
 DR PROSITE: PS00248; NGF. 1.
 DR PROSITE: PS50270; NGF. 2; 1.
 KM Growth factor; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 121
 FT CHAIN 122 241
 FT DISULEID 136 201
 FT DISULEID 179 229
 FT DISULEID 189 231
 FT CARBOHYD 69 69
 FT CARBOHYD 114 114
 FT CARBOHYD 166 166
 SQ SEQUENCE 241 AA: 27035 MM: 8BF8B207A1F82F7 CRC64:

Query Match
 Best Local Similarity 56.7%; Score 370; DB 1; Length 241;
 Matches 67; Conservative 24; Mismatches 23; Indels 10; Gaps 2;

OY 5 HKSRR-----GCVSVDSESLWYTDSSAIDRGHOVTLGEITGNSPVKQYFETK 55
 DB 117 HKSRRSTHVPFGVSGVSDSVVWGKTRTIDIKGEVTLGEVNNNSVRFKFFE 176
 OY 56 TRCEARPVKNGCRGIDKHMNSOCTSTYVRLTSENKLVGMWRIRIDTSCVLSLR 115
 DB 177 TRCEARPVKNGCRGIDKHMNSOCTSTYVRLTSENKLVGMWRIRIDTSCVLSLR 235

Mon Dec 2 15:36:41 2002

us-10-072-681-5.rsp

Page 10

OY 116 KIGR 119
|
DB 236 KAPR 239

Search completed: December 2, 2002, 15:12:44
Job time : 5.9238 secs

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OM protein - protein search, using sw model

Run on: December 2, 2002, 15:05:42 ; Search time 18.5698 seconds
(without alignments)
1331.301 Million cell updates/sec

Title: US-10-072-681-5

Perfect score: 653
Sequence: 1 PYAEHKSRRGEYSVDSSESL.....RWIRIDTSCVSLSRKRGRT 120

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_PROTOZOA:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	583	89.3	241	6	09N182 macaca fusc
2	373.5	57.2	241	4	09P208 09P248 homo sapien
3	373.5	57.2	241	4	09UKL8 09UKL8 homo sapien
4	373.5	57.2	241	6	09N2F1 09N2F1 pan troglod
5	373.5	57.2	241	6	09N2F0 09N2F0 gorilla gor
6	373.5	57.2	241	6	09N2E9 09N2E9 pongo pygma
7	370.5	56.7	241	4	09B6E0 09B6E0 homo sapien
8	356	54.5	177	13	0918L2 0918L2 poephila gu
9	355	54.4	246	13	08Q6T6 08Q6T6 japalura sp
10	354	54.2	153	11	09CYL3 09CYL3 mus musculu
11	354	54.2	241	13	09O6J8 09O6J8 bochrups ja
12	354	54.2	247	6	097759 097759 allurus ful
13	354	54.2	249	11	08VNH4 08VNH4 mus musculu
14	352	53.9	246	13	08Q6T4 08Q6T4 cyclophiops
15	351	53.8	246	13	08Q6T5 08Q6T5 phyncncepha
16	350	53.6	241	13	09DEZ9 09DEZ9 cirotatus du

17	344	52.7	270	13	09YH42	09YH42 brachydanto
18	341.5	52.3	217	6	09N183	09N183 macaca fusc
19	336.5	51.5	294	11	091XB4	091XB4 mus musculu
20	334	51.1	247	13	08Q6T7	08Q6T7 lytolotrito
21	324.5	49.7	324	13	09XY95	09XY95 lampetra fl
22	324	49.6	101	6	09TT22	09TT22 macaca fusc
23	276	42.3	87	4	09P224	09P224 homo sapien
24	274.5	42.0	87	6	09PTC3	09PTC3 cervus elap
25	265	40.7	286	13	0919E8	0919E8 xiphophorus
26	247	37.8	85	6	013114	013114 isodon mac
27	247	37.8	85	6	013122	013122 taraipea ro
28	247	37.8	85	6	002795	002795 ornithorhyn
29	247	37.8	85	6	002798	002798 petaurus br
30	247	37.8	85	6	013104	013104 cercartetus
31	247	37.8	85	6	002790	002790 macropus fu
32	247	37.8	85	6	013105	013105 dasypodides
33	247	37.8	85	6	002801	002801 tachyglissu
34	246	37.7	85	6	002803	002803 trichosurus
35	242	37.1	85	6	002792	002792 notoryctes
36	226.5	34.2	186	12	09J5D9	09J5D9 fowlpox vir
37	210	32.2	43	13	013117	013117 protopteris
38	169	25.9	185	6	09BFR7	09BFR7 erinaceus c
39	166	25.4	185	11	09N9Y9	09N9Y9 pedetes cap
40	165	25.3	184	6	09BFR5	09BFR5 tupia mino
41	165	25.3	185	6	09BFR6	09BFR6 talpa alai
42	165	25.3	185	6	09BFR5	09BFR5 condylura c
43	165	25.3	186	6	09BFL3	09BFL3 choiopeus d
44	165	25.3	186	6	09BFL2	09BFL2 tamandua te
45	165	25.3	186	6	09BFR9	09BFR9

ALIGNMENTS

RESULT 1

ID 09N182 PRELIMINARY: PRT: 241 AA.

AC 09N182;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE Neurotrophin-3 (Fragment).
OS Macaca fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
CC Cercopithecoidea; Macaca.
OX NCBI_TaxID:9542;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BLOOD;
RX MEDLINE-92270338; PubMed-10340513;
RA Okuno H., Tokuyama W., Li Y.X., Hashimoto T., Miyashita Y.;
RT "Quantitative evaluation of neurotrophin and trk mRNA expression in
RT visual and limbic areas along the occipito-temporo-hippocampal pathway
RT in adult macaque monkeys.";
RL J. Comp. Neurol. 408:378-396(1999).
RM [2]
RN SEQUENCE FROM N.A.
RP TISSUE-BLOOD;
RA Hashimoto T., Okuno H., Tokuyama W., Li Y.X., Miyashita Y.;
RT "Expression of brain-derived neurotrophic factor, neurotrophin-3 and
RT their receptor messenger RNAs in monkey rhinal cortex.";
RL ENBL; AF222683; AF33791.1; -;
DR HSSP; P20783; 188K.
DR InterPro; IPR002072; NGF.
DR Pfam; PF00243; NGF.1.
DR PRINTS; PR00268; NGF.
DR PRODOM; PD002052; NGF.1.
DR SMART; SM00140; NGF.1.
DR PROSITE; PS00248; NGF.1.
DR PROSITE; PS00270; NGF.2; 1.
FT NON_TER 1 1


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FT NON_TER 241 241
SQ SEQUENCE 241 AA: 27803 MW: AB95E457CB07113 CRC64:

Query Match
Best Local Similarity 100.0%; Score 583; DB 6; Length 241;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 YAEHSHRGESVCDSESLMTYDKSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEA 61
DB 136 YAEHSHRGESVCDSESLMTYDKSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEA 195

OY 62 RPYKNCRCRIDDKHNSCKTSQTYVRALTSNNKLVGMWRIRDT 107
DB 196 RPYKNCRCRIDDKHNSCKTSQTYVRALTSNNKLVGMWRIRDT 241

RESULT 2
O9P208 PRELIMINARY: PRT: 241 AA.
AC 09P208:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Beta-nerve growth factor (Fragment).
GN BETA-NGF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Kikano T., Kobayakawa H., Saitou N.;
RT "Silver Project."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB037517; BAA90437.1; -.
DR HSSP: P01139; 1BET.
DR InterPro: IPR002072; NCF.
DR Pfam: PF00243; NCF.1.
DR PRINTS: PR00268; NCF.
DR PRODOM: PD002052; NCF.1.
DR SMART: SM00140; NCF.1.
DR PROSITE: PS00248; NCF.1; 1.
DR PROSITE: PS50270; NCF.2; 1.
FT NON_TER 241
SQ SEQUENCE 241 AA: 26998 MW: D5531ED825D96C14 CRC64:

Query Match
Best Local Similarity 57.2%; Score 373.5; DB 4; Length 241;
Matches 67; Conservative 18; Mismatches 26; Indels 1; Gaps 1;

OY 8 HRGEYSVCDSESLMTYDKSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEARPYKNG 67
DB 129 HRGEYSVCDSESLMTYDKSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEARPYKNG 188

OY 68 CRGIDSKHNSCKTSQTYVRALTSNNKLVGMWRIRDTSCVSLSKRIR 119
DB 189 CRGIDSKHNSCKTSQTYVRALTSNNKLVGMWRIRDTSCVSLSKRIR 239

RESULT 3
O9UKL8 PRELIMINARY: PRT: 241 AA.
AC 09UKL8:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Nerve growth factor B.
GN NGFB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN (1)

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RP SEQUENCE FROM N.A.
RX MEDLINE=99256269; PubMed=10322959;
RA Tong Y., Wang H., Chen W.;
RT "Cloning and sequencing of the gene for premature beta nerve growth
factor B."
RL Chung Kuo ying yung Sheng Li Hsueh Tsa Chih 13:316-318(1997).
RN (1)
RP SEQUENCE FROM N.A.
RA Tong Y., Wang H.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF150960; AAD55975.1; -.
DR HSSP: P01139; 1BET.
DR InterPro: IPR002072; NCF.
DR Pfam: PF00243; NCF.1.
DR PRINTS: PR00268; NCF.1.
DR PRODOM: PD002052; NCF.1.
DR SMART: SM00140; NCF.1.
DR PROSITE: PS00248; NCF.1; 1.
DR PROSITE: PS50270; NCF.2; 1.
SQ SEQUENCE 241 AA: 26959 MW: 619DFC65EB3BD671 CRC64:

Query Match
Best Local Similarity 57.2%; Score 373.5; DB 4; Length 241;
Matches 67; Conservative 18; Mismatches 26; Indels 1; Gaps 1;

OY 8 HRGEYSVCDSESLMTYDKSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEARPYKNG 67
DB 129 HRGEYSVCDSESLMTYDKSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEARPYKNG 188

OY 68 CRGIDSKHNSCKTSQTYVRALTSNNKLVGMWRIRDTSCVSLSKRIR 119
DB 189 CRGIDSKHNSCKTSQTYVRALTSNNKLVGMWRIRDTSCVSLSKRIR 239

RESULT 4
O9N2F1 PRELIMINARY: PRT: 241 AA.
AC 09N2F1:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Beta-nerve growth factor (Fragment).
GN BETA-NGF.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_Taxid=9598;
RN (1)
RP SEQUENCE FROM N.A.
RA Kikano T., Kobayakawa H., Saitou N.;
RT "Silver Project."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB037518; BAA90438.1; -.
DR HSSP: P01139; 1BET.
DR InterPro: IPR002072; NCF.
DR Pfam: PF00243; NCF.1.
DR PRINTS: PR00268; NCF.1.
DR PRODOM: PD002052; NCF.1.
DR SMART: SM00140; NCF.1.
DR PROSITE: PS00248; NCF.1; 1.
DR PROSITE: PS50270; NCF.2; 1.
FT NON_TER 241
SQ SEQUENCE 241 AA: 26868 MW: B39FAA8912C00A0B CRC64:

Query Match
Best Local Similarity 57.2%; Score 373.5; DB 6; Length 241;
Matches 67; Conservative 18; Mismatches 26; Indels 1; Gaps 1;

OY 8 HRGEYSVCDSESLMTYDKSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEARPYKNG 67
DB 129 HRGEYSVCDSESLMTYDKSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEARPYKNG 188

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RX MEDLINE-10727739:
RA Johnson F., Norstrom E., Soderstrom K.;
RT "Increased expression of endogenous biotin, but not BDNF, in
RL telencephalic song regions during zebra finch vocal learning.";
RL Brain Res. Dev. Brain Res. 120:113-123(2000).
DR EMBL: AF255389; AAF78050.2; -
DR HSSP: P23560; 1BM.
DR InterPro: IPR002072; NCF.
DR Pfam: PF00243; NCF; 1.
DR PRINTS: PR00268; NCF.
DR PRODOM: PD002052; NCF; 1.
DR SMART: SM00140; NCF; 1.
DR PROSITE: PS00248; NCF; 1; 1.
DR PROSITE: PS50270; NCF; 2; 1.
FT NON_TER
SQ SEQUENCE 177 AA; 20273 MW; BDB9031515BD369D CRC64;

Query Match
Best Local Similarity 54.5%; Score 356; DB 13; Length 177;
Matches 67; Conservative 16; Mismatches 30; Indels 2; Gaps 1;

OY 7 SHRGESVCDSESLWT--DKSSAIDIRGHQVTVLGEITGNSPVKQYFETRCKEARPV 64
DB 63 ARRGESVCDSTSEWTALEKKTAVDMGATVTVLEKVPVKGQLKQFETKCNPKGYT 122
OY 65 KNGCRGIDDKHNSOCTKSTQTVYRALTSNNKLVGMWRIRIDTSCVSLSRKIGR 119
DB 123 KEGCRGIDKRNHNSOCTKSTQSYVYRALTMNKKRVGMFRIRIDTSCVTLTKRGR 177

RESULT 9
O80C76 PRELIMINARY: PRT; 246 AA.
AC O80G76;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Brain derived neurotrophic factor.
GN BDNF.
OS Japalura splendide.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Actodontia; Agamidae; Dipsosaurus;
OC Japalura.
OC NCBI_TaxID=118209;
RN [1]
RP SEQUENCE FROM N.A.
RA Cao M., Yang Y.H., Zhang Y.Z.;
RT "Molecular cloning of brain derived neurotrophic factor gene from
RT amphibians and reptiles and its application in the research of
RL phylogeny and taxonomy.";
RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF497713; MAM18714.1; -
FT CHAIN 128 246
FT PRECURSOR.
SQ SEQUENCE 246 AA; 27883 MW; 47B1A03DA838FD8 CRC64;

Query Match
Best Local Similarity 54.4%; Score 355; DB 13; Length 246;
Matches 66; Conservative 18; Mismatches 29; Indels 2; Gaps 1;

OY 7 SHRGESVCDSESLWT--DKSSAIDIRGHQVTVLGEITGNSPVKQYFETRCKEARPV 64
DB 132 ARRGESVCDSTSEWTALEKKTAVDMGATVTVLEKVPVKGQLKQFETKCNPKGYT 191
OY 65 KNGCRGIDDKHNSOCTKSTQTVYRALTSNNKLVGMWRIRIDTSCVSLSRKIGR 119
DB 192 KEGCRGIDKRNHNSOCTKSTQSYVYRALTMNKKRVGMFRIRIDTSCVTLTKRGR 246

RESULT 10
O9C7L3 PRELIMINARY: PRT; 153 AA.
AC O9C7L3;

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DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Brain derived neurotrophic factor.
GN BDNF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE-EMBRIO;
RX MEDLINE-21085660; Pubmed-11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Machi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glasl C., King B., Kochwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Mashio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Burt C., Fletcher C., Fujita M., Gariboldi M.,
RA Guncionich S., Hill D., Holman M., Hume D.A., Kamya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombert P.,
RA Nadore P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata C., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weiss C., Whitlaker C., Wilming L.,
RA Wyszynski B., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK017559; BAB30805.1; -
DR HSSP: P23560; 1BM.
DR MGD: MGI:88145; Bdnf.
DR InterPro: IPR002072; NCF.
DR Pfam: PF00243; NCF; 1.
DR PRINTS: PR00268; NCF.
DR PRODOM: PD002052; NCF; 1.
DR SMART: SM00140; NCF; 1.
DR PROSITE: PS00248; NCF; 1; 1.
DR PROSITE: PS50270; NCF; 2; 1.
SQ SEQUENCE 153 AA; 17519 MW; CABEB944CE5B37 CRC64;

Query Match
Best Local Similarity 54.2%; Score 354; DB 11; Length 153;
Matches 66; Conservative 17; Mismatches 30; Indels 2; Gaps 1;

OY 7 SHRGESVCDSESLWT--DKSSAIDIRGHQVTVLGEITGNSPVKQYFETRCKEARPV 64
DB 39 ARRGESVCDSTSEWTALEKKTAVDMGATVTVLEKVPVKGQLKQFETKCNPKGYT 98
OY 65 KNGCRGIDDKHNSOCTKSTQTVYRALTSNNKLVGMWRIRIDTSCVSLSRKIGR 119
DB 99 KEGCRGIDKRNHNSOCTKSTQSYVYRALTMNKKRVGMFRIRIDTSCVTLTKRGR 153

RESULT 11
O90W38 PRELIMINARY: PRT; 241 AA.
AC O90W38;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Putative neurotrophic growth factor.
GN NGF.
OS Bothrops jararacussu (Jararacussu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8726;
RN [1]

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SEQUENCE FROM N.A.
 RC TISSUE-VENOM GLAND:
 RA Koshima S., Pereira J.O., Astolifi Filho S., Soares A.M.,
 RA Cinctra A.C.O., Giglio J.R., Franca S.C.;
 RT "Molecular cloning and cDNA sequence of a nerve growth factor
 RT precursor from Bothrops jararacussu venomous gland."
 RL Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AY007318; AAG12169.1;
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF.1.
 DR ProDom: PD002052; NGF.1.
 DR PROSITE: PS00248; NGF.1;
 DR PROSITE: PS0270; NGF.2; 1.
 SO SEQUENCE 241 AA; 27161 MW; AC57F2A4A6531A8P CRC64;

Query Match 54.2%; Score 354; DB 13; Length 241;
 Best Local Similarity 55.3%; Pred. No. 6.2e-32;
 Matches 63; Conservative 22; Mismatches 27; Indels 2; Gaps 2;

OY 4 EKHSH-NGEYSVCDSESLMT--DKSSAIDIRGHQVTVLGEITGNSPVKQYFETRCKEAR 62
 DB 124 DHPVHNGEYSVCDSESLMT--DKSSAIDIRGHQVTVLGEITGNSPVKQYFETRCKEAR 183
 OY 63 PVKNGCRGIDKHMNSOCKTSQTYVRLTSENKLVGNRMIRIDTSCVLSLRK 116
 DB 184 PVPTGCRGIDKHMNSOCKTSQTYVRLTSENKLVGNRMIRIDTSCVLSLRK 236

RESULT 12
 OY97759 PRELIMINARY; PRT; 247 AA.

ID 080674;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE Brain derived neurotrophic factor.
 GN BDNF.
 OS Allurus fulgens (lesser panda).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Flapsipedia; Procyonidae; Allurus.
 OX NCBI_TaxID=9649;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Feng L.;
 RT "Clont Panda (GP) and Lesser Panda (LP) BDNF gene sequences and their
 RT deduced amino acid sequences."
 RL Submitted (APR-1996) to the EMBL/Genbank/DBJ databases.
 DR EMBL: U56639; AAD10843.1;
 DR HSSP: P23560; 188M.
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF.1.
 DR PRINTS: PR00268; NGF.
 DR ProDom: PD002052; NGF.1.
 DR SMART: SM00140; NGF.1.
 DR PROSITE: PS00248; NGF.1;
 DR PROSITE: PS0270; NGF.2; 1.
 SO SEQUENCE 247 AA; 27870 MW; FEB6C62CF1A6C03EE CRC64;

Query Match 54.2%; Score 354; DB 6; Length 247;
 Best Local Similarity 57.4%; Pred. No. 6.4e-32;
 Matches 66; Conservative 17; Mismatches 30; Indels 2; Gaps 1;

OY 7 SHRGEYSVCDSESLMT--DKSSAIDIRGHQVTVLGEITGNSPVKQYFETRCKEARPV 64
 DB 133 ARRGELSVCDSESLMT--DKSSAIDIRGHQVTVLGEITGNSPVKQYFETRCKEARPV 192
 OY 65 KNGCRGIDKHMNSOCKTSQTYVRLTSENKLVGNRMIRIDTSCVLSLRK 119
 DB 193 KEGCRGIDKHMNSOCKTSQTYVRLTSENKLVGNRMIRIDTSCVLSLRK 247

RESULT 13
 OY97H14

ID 08VH14 PRELIMINARY; PRT; 249 AA.
 AC 08VH14;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Anorexia BDNF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-B6C3FE-A/A-ANXA/+A;
 RA Kim S.J., Kim C.S., Cha Y.J., Song K.Y., Yeo H.G.;
 RT "Anorexia mouse ORF BDNF."
 RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF459642; AAL58475.1;
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF.1.
 DR PRINTS: PR00268; NGF.
 DR ProDom: PD002052; NGF.1.
 DR SMART: SM00140; NGF.1.
 DR PROSITE: PS00248; NGF.1;
 DR PROSITE: PS0270; NGF.2; 1.
 SO SEQUENCE 249 AA; 28109 MW; 21CEAE6A0A235D97 CRC64;

Query Match 54.2%; Score 354; DB 11; Length 249;
 Best Local Similarity 57.4%; Pred. No. 6.5e-32;
 Matches 66; Conservative 17; Mismatches 30; Indels 2; Gaps 1;

OY 7 SHRGEYSVCDSESLMT--DKSSAIDIRGHQVTVLGEITGNSPVKQYFETRCKEARPV 64
 DB 135 ARRGELSVCDSESLMT--DKSSAIDIRGHQVTVLGEITGNSPVKQYFETRCKEARPV 194
 OY 65 KNGCRGIDKHMNSOCKTSQTYVRLTSENKLVGNRMIRIDTSCVLSLRK 119
 DB 195 KEGCRGIDKHMNSOCKTSQTYVRLTSENKLVGNRMIRIDTSCVLSLRK 249

RESULT 14
 ID 080674 PRELIMINARY; PRT; 246 AA.

ID 080674;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Brain derived neurotrophic factor.
 GN BDNF.
 OS Cyclophlops major.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
 OC Colubridae; Colubrinae; Cyclophlops.
 OX NCBI_TaxID=192173;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cao M., Yang Y.H., Zhang Y.Z.;
 RT "Molecular cloning of brain derived neurotrophic factor gene from
 RT amphibians and reptiles and its application in the research of
 RT phylogeny and taxonomy."
 RL Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF497715; AAM18716.1;
 DR CHAIN 128 246
 SO SEQUENCE 246 AA; 27773 MW; BA01780349F37856 CRC64;

Query Match 53.9%; Score 352; DB 13; Length 246;
 Best Local Similarity 57.4%; Pred. No. 1.1e-31;
 Matches 66; Conservative 18; Mismatches 29; Indels 2; Gaps 1;

OY 7 SHRGEYSVCDSESLMT--DKSSAIDIRGHQVTVLGEITGNSPVKQYFETRCKEARPV 64
 DB 132 ARRGELSVCDSESLMT--DKSSAIDIRGHQVTVLGEITGNSPVKQYFETRCKEARPV 191

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 2, 2002, 15:05:42 ; Search time 8.30012 seconds
(without alignments)
425.366 Million cell updates/sec

Title: US-10-072-681-5

Perfect score: 653
Sequence: 1 PRAEKSRRGERSVCDSESL.....RWIRDTSCVSLSRKIGRT 120

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents, AA: *
1: /cgn2_6/pdata/1/laa/5A.COMB.pep: *
2: /cgn2_6/pdata/1/laa/5B.COMB.pep: *
3: /cgn2_6/pdata/1/laa/6A.COMB.pep: *
4: /cgn2_6/pdata/1/laa/6B.COMB.pep: *
5: /cgn2_6/pdata/1/laa/PCITUS.COMB.pep: *
6: /cgn2_6/pdata/1/laa/Backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	653	100.0	120	4	US-09-675-503-5
2	646	98.9	119	3	US-08-970-865-5
3	646	98.9	119	3	US-08-581-662-2
4	646	98.9	119	4	US-09-363-573-5
5	646	98.9	119	4	US-09-664-295-2
6	641	98.2	119	1	US-07-979-630-3
7	641	98.2	119	1	US-08-440-049-2
8	641	98.2	119	1	US-08-340-131-3
9	641	98.2	119	2	US-08-441-513A-2
10	641	98.2	119	3	US-08-910-691-12
11	641	98.2	119	4	US-08-845-541B-2
12	641	98.2	119	4	US-09-066-065A-2
13	641	98.2	119	5	PCR-US93-11292-3
14	641	98.2	119	5	PCR-US95-06918-2
15	641	98.2	119	5	PCR-US95-06918-5
16	641	98.2	120	1	US-08-340-131-4
17	641	98.2	120	4	US-09-214-214A-1
18	641	98.2	120	4	US-09-255-953-1
19	641	98.2	120	4	US-09-872-090-1
20	641	98.2	120	3	US-08-910-691-11
21	641	98.2	257	2	US-08-451-947-4
22	641	98.2	257	2	US-08-424-826A-4
23	641	98.2	257	3	US-08-910-691-7
24	641	98.2	257	3	US-08-928-694-4
25	641	98.2	257	5	PCR-US91-05950-4
26	629	96.3	119	4	US-09-214-214A-6
27	629	96.3	119	4	US-09-235-953-6

28	629	96.3	119	4	US-09-872-090-6	Sequence 6, Appl 1
29	629	96.3	120	4	US-09-214-214A-3	Sequence 3, Appl 1
30	629	96.3	120	4	US-09-255-953-3	Sequence 3, Appl 1
31	629	96.3	120	4	US-09-872-090-3	Sequence 3, Appl 1
32	629	96.3	117	4	US-09-214-214A-7	Sequence 7, Appl 1
33	619	94.8	117	4	US-09-255-953-7	Sequence 7, Appl 1
34	619	94.8	117	4	US-09-872-090-7	Sequence 7, Appl 1
35	619	94.8	118	4	US-09-214-214A-5	Sequence 5, Appl 1
36	619	94.8	118	4	US-09-255-953-5	Sequence 5, Appl 1
37	619	94.8	118	4	US-09-872-090-5	Sequence 5, Appl 1
38	613	93.9	120	3	US-08-581-662-32	Sequence 32, Appl 1
39	613	93.9	120	4	US-09-664-295-32	Sequence 32, Appl 1
40	416.5	63.8	120	4	US-08-845-541B-9	Sequence 9, Appl 1
41	416.5	63.8	120	4	US-09-066-065A-9	Sequence 9, Appl 1
42	411.5	63.0	120	4	US-08-845-541B-7	Sequence 7, Appl 1
43	411.5	63.0	120	4	US-09-066-065A-7	Sequence 7, Appl 1
44	408.5	62.6	120	4	US-08-845-541B-8	Sequence 8, Appl 1
45	408.5	62.6	120	4	US-09-066-065A-8	Sequence 8, Appl 1

ALIGNMENTS

```

RESULT 1
US-09-675-503-5
; Sequence 5, Application US/09675503
; Patent No. 6423831
; GENERAL INFORMATION:
; APPLICANT: Burton, Louis E.
; APPLICANT: Schmelzer, Charles H.
; APPLICANT: Beck, Joanne T.
; TITLE OF INVENTION: ISOLATION OF NEUROTROPINS FROM A
; TITLE OF INVENTION: MIXTURE CONTAINING OTHER PROTEINS AND NEUROTROPIN VARIANTS
; FILE REFERENCE: GENENT-037C2
; CURRENT APPLICATION NUMBER: US/09/675,503
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/030838
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: 60/047855
; PRIOR FILING DATE: 1997-05-29
; PRIOR APPLICATION NUMBER: 08/970865
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 09/363573
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-675-503-5

Query Match      100.0%; Score 653; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 3.4e-70;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 PRAEKSRRGERSVCDSESLVYTKSSAIDIRGHOVYVGEITGNSPKQOFTYTRCKE 60
DB      1 PRAEKSRRGERSVCDSESLVYTKSSAIDIRGHOVYVGEITGNSPKQOFTYTRCKE 60
OY      61 ABPVNCGRGIDDKHMSQCTSTQYVRAVLTSENKLVGNRYRIDTSCVSLSRKIGRT 120
DB      61 ABPVNCGRGIDDKHMSQCTSTQYVRAVLTSENKLVGNRYRIDTSCVSLSRKIGRT 120

RESULT 2
US-08-970-865-5
; Sequence 5, Application US/08970865
; Patent No. 6005081
; GENERAL INFORMATION:
; APPLICANT: Louis E. Burton, Charles H. Schmelzer, Joanne T. Beck
; TITLE OF INVENTION: Purification of NGF

```

NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA

ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/970,865
FILING DATE: 14-NO. 6005081-1997

CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030838

FILING DATE: 11/15/1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047855

FILING DATE: 5/29/1997

ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: P1063R2

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-08-970-865-5

Query Match 98.9% Score 646; DB 3; Length 119;
Best Local Similarity 100.0%; Pred. No. 2,3e-69;

Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YAEHSHRGEYSVCDSESLWYTDKSSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEA 61
DB 1 YAEHSHRGEYSVCDSESLWYTDKSSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEA 60
QY 62 RPKVNCRCGIDDKHNNCKTSQTYVRALTSNNKLVGMWRIRIDTSCVSLSRKIGRT 120
DB 61 RPKVNCRCGIDDKHNNCKTSQTYVRALTSNNKLVGMWRIRIDTSCVSLSRKIGRT 119

RESULT 3
US-08-581-662-2

Sequence 2, Application US/08581662

Patent No. 6121235

GENERAL INFORMATION:

APPLICANT: Gao, Wei-Qiang

TITLE OF INVENTION: Treatment of Balance Impairments

FILE REFERENCE: P0981

CURRENT APPLICATION NUMBER: US/08/581,662

CURRENT FILING DATE: 1995-12-29

NUMBER OF SEQ ID NOS: 36

SEQ ID NO 2

LENGTH: 119

TYPE: PRT

ORGANISM: Homo sapiens

US-08-581-662-2

Query Match 98.9% Score 646; DB 3; Length 119;

Best Local Similarity 100.0%; Pred. No. 2,3e-69;

Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YAEHSHRGEYSVCDSESLWYTDKSSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEA 61
DB 1 YAEHSHRGEYSVCDSESLWYTDKSSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEA 60

DB 1 YAEHSHRGEYSVCDSESLWYTDKSSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEA 60
QY 62 RPKVNCRCGIDDKHNNCKTSQTYVRALTSNNKLVGMWRIRIDTSCVSLSRKIGRT 120
DB 61 RPKVNCRCGIDDKHNNCKTSQTYVRALTSNNKLVGMWRIRIDTSCVSLSRKIGRT 119

RESULT 4
US-09-363-573-5

Sequence 5, Application US/09363573

Patent No. 6184360

GENERAL INFORMATION:

APPLICANT: Louis E. Burton, Charles H. Schmelzer, Joanne T. Beck

TITLE OF INVENTION: Purification of NGF

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,573

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/970,865

FILING DATE: 14-NO. 6184360-1997

APPLICATION NUMBER: 60/030838

FILING DATE: 11/15/1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047855

FILING DATE: 5/29/1997

ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: P1063R2

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-09-363-573-5

Query Match 98.9% Score 646; DB 4; Length 119;

Best Local Similarity 100.0%; Pred. No. 2,3e-69;

Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YAEHSHRGEYSVCDSESLWYTDKSSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEA 61
DB 1 YAEHSHRGEYSVCDSESLWYTDKSSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEA 60
QY 62 RPKVNCRCGIDDKHNNCKTSQTYVRALTSNNKLVGMWRIRIDTSCVSLSRKIGRT 120
DB 61 RPKVNCRCGIDDKHNNCKTSQTYVRALTSNNKLVGMWRIRIDTSCVSLSRKIGRT 119

RESULT 5
US-09-664-295-2

Sequence 2, Application US/09664295

Patent No. 6429196

GENERAL INFORMATION:

APPLICANT: Gao, Wei-Qiang

TITLE OF INVENTION: Treatment of Balance Impairments

FILE REFERENCE: GENENT.051C1
CURRENT APPLICATION NUMBER: US/09/664.295
CURRENT FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 08/581.662
PRIOR FILING DATE: 1995-12-29
NUMBER OF SEQ ID NOS: 37
SEQ ID NO 2
LENGTH: 119
TYPE: PRP
ORGANISM: Homo sapiens
US-09-664-295-2

Query Match 98.9%; Score 646; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 2, 3e-69;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 YAEKSHRGEYSVCDSESLMTYDSSAIDIRGHQVTVLGEITGNSPVKQYFETRCKEA 61
DB 1 YAEKSHRGEYSVCDSESLMTYDSSAIDIRGHQVTVLGEITGNSPVKQYFETRCKEA 60
OY 62 RPYKNCRCGIDDKHNSOCTSOYTVRALTSENKLVGMWIRIDTSCVLSRKIGRT 120
DB 61 RPYKNCRCGIDDKHNSOCTSOYTVRALTSENKLVGMWIRIDTSCVLSRKIGRT 119

RESULT 6

US-07-979-630-3
Sequence 3, Application US/07979630
Patent No. 5488099

GENERAL INFORMATION:

APPLICANT: Persson, et al.

TITLE OF INVENTION: Multifunctional Neurotrophic Factors

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Regeneron Pharmaceuticals, Inc.

STREET: 777 Old Saw Mill River Road

CITY: Tarrytown

STATE: New York

COUNTRY: U.S.A.

ZIP: 10591

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/979.630

FILING DATE: 20-NOV-1992

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/847,369

FILING DATE: 06-MAR-1992

NAME:

ATTORNEY/AGENT INFORMATION:

NAME: Kempner Ph.D., Gail M.

REGISTRATION NUMBER: 32,143

REFERENCE/DOCKET NUMBER: REG 41

TELEPHONE: 914-347-7000

TELEFAX: 914-347-2113

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-07-979-630-3

Query Match 98.2%; Score 641; DB 1; Length 119;
Best Local Similarity 99.2%; Pred. No. 8, 9e-69;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 YAEKSHRGEYSVCDSESLMTYDSSAIDIRGHQVTVLGEITGNSPVKQYFETRCKEA 61
DB 1 YAEKSHRGEYSVCDSESLMTYDSSAIDIRGHQVTVLGEITGNSPVKQYFETRCKEA 60
OY 62 RPYKNCRCGIDDKHNSOCTSOYTVRALTSENKLVGMWIRIDTSCVLSRKIGRT 120
DB 61 RPYKNCRCGIDDKHNSOCTSOYTVRALTSENKLVGMWIRIDTSCVLSRKIGRT 119

RESULT 7

US-08-440-049-2
Sequence 2, Application US/08440049
Patent No. 5728803

GENERAL INFORMATION:

APPLICANT: Ufer, Roman

APPLICANT: Presta, Leonard G.

APPLICANT: Winslow, John W.

TITLE OF INVENTION: PANROTIC NEUROTROPHIC FACTORS

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: WinPacIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/440,049

FILING DATE: 12-May-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/253937

FILING DATE: 03-JUN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: P0905C2

TELEPHONE: 415/225-8674

TELEFAX: 415/952-9881

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-08-440-049-2

Query Match 98.2%; Score 641; DB 1; Length 119;
Best Local Similarity 99.2%; Pred. No. 8, 9e-69;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 YAEKSHRGEYSVCDSESLMTYDSSAIDIRGHQVTVLGEITGNSPVKQYFETRCKEA 61
DB 1 YAEKSHRGEYSVCDSESLMTYDSSAIDIRGHQVTVLGEITGNSPVKQYFETRCKEA 60
OY 62 RPYKNCRCGIDDKHNSOCTSOYTVRALTSENKLVGMWIRIDTSCVLSRKIGRT 120
DB 61 RPYKNCRCGIDDKHNSOCTSOYTVRALTSENKLVGMWIRIDTSCVLSRKIGRT 119

RESULT 8

US-08-340-131-3
Sequence 3, Application US/08340131
Patent No. 5770577

GENERAL INFORMATION:

APPLICANT: Kinsler, Olaf B

APPLICANT: Yan, Qiao


```
Best Local Similarity 99.2%: Pred. No. 8.9e-69;
Matches 118: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 YAEHKSHERGEYVCDSSESLWYTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 61
DB 1 YAEHKSHERGEYVCDSSESLWYTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 60
OY 62 RPYKNCRCGIDDKHNSCKTSOTYVVALTSENKLVGMRIIRIDTSCVCAISRKIGRT 120
DB 61 RPYKNCRCGIDDKHNSCKTSOTYVVALTSENKLVGMRIIRIDTSCVCAISRKIGRT 119

RESULT 11
US-08-845-541B-2
; Sequence 2, Application US/08845541B
; Patent No. 6333310
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard
; APPLICANT: Urfer, Roman
; APPLICANT: Winslow, John
; TITLE OF INVENTION: NGF VARIANTS
; FILE REFERENCE: GENEHT.039A
; CURRENT APPLICATION NUMBER: US/08/845,541B
; CURRENT FILING DATE: 1999-04-25
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 119
; TYPE: PRT
; ORGANISM: homo sapien
US-08-845-541B-2

Query Match 98.2%: Score 641; DB 4; Length 119;
Best Local Similarity 99.2%: Pred. No. 8.9e-69;
Matches 118: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 YAEHKSHERGEYVCDSSESLWYTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 61
DB 1 YAEHKSHERGEYVCDSSESLWYTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 60
OY 62 RPYKNCRCGIDDKHNSCKTSOTYVVALTSENKLVGMRIIRIDTSCVCAISRKIGRT 120
DB 61 RPYKNCRCGIDDKHNSCKTSOTYVVALTSENKLVGMRIIRIDTSCVCAISRKIGRT 119

RESULT 12
US-09-066-065A-2
; Sequence 2, Application US/09066065A
; Patent No. 6365373
; GENERAL INFORMATION:
; APPLICANT: Leonard G. Presta, Roman Urfer, John W. Winslow
; TITLE OF INVENTION: NGF Variants
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/066,065A
; FILING DATE: 24-Apr-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/0445918
; FILING DATE: 25-Apr-1999
; ATTORNEY/AGENT INFORMATION:

NAME: Torchia, PND., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1098R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: Linear
US-09-066-065A-2

Query Match 98.2%: Score 641; DB 4; Length 119;
Best Local Similarity 99.2%: Pred. No. 8.9e-69;
Matches 118: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 YAEHKSHERGEYVCDSSESLWYTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 61
DB 1 YAEHKSHERGEYVCDSSESLWYTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 60
OY 62 RPYKNCRCGIDDKHNSCKTSOTYVVALTSENKLVGMRIIRIDTSCVCAISRKIGRT 120
DB 61 RPYKNCRCGIDDKHNSCKTSOTYVVALTSENKLVGMRIIRIDTSCVCAISRKIGRT 119

RESULT 13
PCT-US93-11292-3
; Sequence 3, Application PC/TUS9311292
; GENERAL INFORMATION:
; APPLICANT: Persson, et al.
; TITLE OF INVENTION: Multifunctional Neurotrophic Factors
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11292
; FILING DATE: 19-NOV-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,369
; FILING DATE: 06-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kempler Ph.D., Gail N.
; REGISTRATION NUMBER: 32,143
; REFERENCE/DOCKET NUMBER: REG 41
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 914-347-7000
; TELEFAX: 914-347-2113
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
PCT-US93-11292-3

Query Match 98.2%: Score 641; DB 5; Length 119;
Best Local Similarity 99.2%: Pred. No. 8.9e-69;
Matches 118: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 YAEHKSHERGEYVCDSSESLWYTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 61
```

DB 1 YAEKSHRGESVCDSESLWYTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 60
OY 62 RPYKNGCRGIDDKHMSOCTSTQTYVRALTSNNKLVGWRIRIDTSCVLSALSRKIGRT 120
DB 61 RPYKNGCRGIDDKHMSOCTSTQTYVRALTSNNKLVGWRIRIDTSCVLSALSRKIGRT 119

RESULT 14

PCT-US95-06918-2
Sequence 2, Application PC/TUS9506918

GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: PANITROPIC NEUROTROPIC FACTORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 Inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06918
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 905PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US95-06918-2

Query Match 98.2%; Score 641; DB 5; Length 119;
Best Local Similarity 99.2%; Pred. No. 8.9e-69;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 YAEKSHRGESVCDSESLWYTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 61
DB 1 YAEKSHRGESVCDSESLWYTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 60
OY 62 RPYKNGCRGIDDKHMSOCTSTQTYVRALTSNNKLVGWRIRIDTSCVLSALSRKIGRT 120
DB 61 RPYKNGCRGIDDKHMSOCTSTQTYVRALTSNNKLVGWRIRIDTSCVLSALSRKIGRT 119

RESULT 15

PCT-US95-06918-5
Sequence 5, Application PC/TUS9506918

GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: PANITROPIC NEUROTROPIC FACTORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco

STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 Inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06918
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 905PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US95-06918-5

Query Match 98.2%; Score 641; DB 5; Length 119;
Best Local Similarity 99.2%; Pred. No. 8.9e-69;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 YAEKSHRGESVCDSESLWYTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 61
DB 1 YAEKSHRGESVCDSESLWYTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 60
OY 62 RPYKNGCRGIDDKHMSOCTSTQTYVRALTSNNKLVGWRIRIDTSCVLSALSRKIGRT 120
DB 61 RPYKNGCRGIDDKHMSOCTSTQTYVRALTSNNKLVGWRIRIDTSCVLSALSRKIGRT 119

Search completed: December 2, 2002, 15:09:44
Job time : 9.30012 secs

RESULT 2

US-09-745-032-1
Sequence 1, Application US/09745032
Patent No. US2001002719A1
GENERAL INFORMATION:
APPLICANT: Boone, Thomas C.
APPLICANT: Cheung, Ellen N.
APPLICANT: Herhenson, Susan I.
APPLICANT: Young, John D.
TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS
FILE REFERENCE: A-411A US Revised073100
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US/09/745,032
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 08/684,353
PRIOR FILING DATE: 1996-07-19
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 120
TYPE: PRT
ORGANISM: Human
US-09-745-032-1

Query Match 98.2% Score 641; DB 10; Length 120;
Best Local Similarity 99.2% Pred. No. 1,3e-63;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YAEKSHRGEYSVCSSESLMTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETCKEA 61
DB 2 YAEKSHRGEYSVCSSESLMTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETCKEA 61
QY 62 RPVKNCGRGIDDKHNSCKTSQTYVRALTSNNKLVGMRIIDTSCVLSRKIGRT 120
DB 62 RPVKNCGRGIDDKHNSCKTSQTYVRALTSNNKLVGMRIIDTSCVLSRKIGRT 120

RESULT 3

US-09-742-600-1
Sequence 1, Application US/09742600
Patent No. US20020010135A1
GENERAL INFORMATION:
APPLICANT: Boone, Thomas C.
APPLICANT: Cheung, Ellen N.
APPLICANT: Herhenson, Susan I.
APPLICANT: Young, John D.
TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS
FILE REFERENCE: A-411A US Revised073100
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US/09/742,600
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 08/684,353
PRIOR FILING DATE: 1996-07-19
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 120
TYPE: PRT
ORGANISM: Human
US-09-742-600-1

Query Match 98.2% Score 641; DB 10; Length 120;
Best Local Similarity 99.2% Pred. No. 1,3e-63;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YAEKSHRGEYSVCSSESLMTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETCKEA 61
DB 2 YAEKSHRGEYSVCSSESLMTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETCKEA 61
QY 62 RPVKNCGRGIDDKHNSCKTSQTYVRALTSNNKLVGMRIIDTSCVLSRKIGRT 120

DB 62 RPVKNCGRGIDDKHNSCKTSQTYVRALTSNNKLVGMRIIDTSCVLSRKIGRT 120

RESULT 4

US-09-872-090-1
Sequence 1, Application US/09872090
Patent No. US20020052488A1
GENERAL INFORMATION:
APPLICANT: Boone, Thomas C.
APPLICANT: Cheung, Ellen Ngol Yin
APPLICANT: Herhenson, Susan I.
APPLICANT: Young, John D.
TITLE OF INVENTION: ANALOGS OF NT-3 (As Amended)
FILE REFERENCE: A-411B
CURRENT FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 09/255,953
PRIOR FILING DATE: 1999-02-23
PRIOR APPLICATION NUMBER: 08/684,353
PRIOR FILING DATE: 1996-07-19
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 120
TYPE: PRT
ORGANISM: Homo sapiens
US-09-872-090-1

Query Match 98.2% Score 641; DB 10; Length 120;
Best Local Similarity 99.2% Pred. No. 1,3e-63;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YAEKSHRGEYSVCSSESLMTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETCKEA 61
DB 2 YAEKSHRGEYSVCSSESLMTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETCKEA 61
QY 62 RPVKNCGRGIDDKHNSCKTSQTYVRALTSNNKLVGMRIIDTSCVLSRKIGRT 120
DB 62 RPVKNCGRGIDDKHNSCKTSQTYVRALTSNNKLVGMRIIDTSCVLSRKIGRT 120

RESULT 5

US-08-450-842-4
Sequence 4, Application US/08450842
Patent No. US20020045576A1
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 Inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,842
FILING DATE: 514
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426419
FILING DATE: 19-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030013
FILING DATE: 22-MAR-1993

OY 62 RPYKNCGRGIDDKHNSCKTSQTYVRALTSNNKLVGMRIIDTSCVSLSRKIGRT 120
11
DB 61 APVDMCGRGIDDKHNSCKTSQTYVRALTSNNKLVGMRIIDTSCVSLSRKIGRT 119

RESULT 9
US-09-745-032-3
Sequence 3, Application US/09745032
Patent No. US20010027179A1
GENERAL INFORMATION:
APPLICANT: Boone, Thomas C.
APPLICANT: Cheung, Ellen N.
APPLICANT: Hersenson, Susan I.
APPLICANT: Young, John D.
TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS
FILE REFERENCE: A-411A US Revised073100
CURRENT APPLICATION NUMBER: US/09/745,032
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 09/214,214
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 08/684,353
PRIOR FILING DATE: 1996-07-19
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 120
TYPE: PRT
ORGANISM: Human
US-09-745-032-3

Query Match 96.3%: Score 629; DB 10; Length 120;
Best Local Similarity 97.5%: Pred. No. 2.7e-62;
Matches 116: Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 YAEKSHRGESVCDSESLWYTDKSSAIDIRGHQVTVLGEIKTGNSPVKOYFETRCKEA 61
11
DB 2 YAEKSHRGESVCDSESLWYTDKSSAIDIRGHQVTVLGEIKTGNSPVKOYFETRCKEA 61
OY 62 RPYKNCGRGIDDKHNSCKTSQTYVRALTSNNKLVGMRIIDTSCVSLSRKIGRT 120
11
DB 62 APVDMCGRGIDDKHNSCKTSQTYVRALTSNNKLVGMRIIDTSCVSLSRKIGRT 120

RESULT 10
US-09-742-600-3
Sequence 3, Application US/09742600
Patent No. US20020010135A1
GENERAL INFORMATION:
APPLICANT: Boone, Thomas C.
APPLICANT: Cheung, Ellen N.
APPLICANT: Hersenson, Susan I.
APPLICANT: Young, John D.
TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS
FILE REFERENCE: A-411A US Revised073100
CURRENT APPLICATION NUMBER: US/09/742,600
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 09/214,214
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 08/684,353
PRIOR FILING DATE: 1996-07-19
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 120
TYPE: PRT
ORGANISM: Human
US-09-742-600-3

Query Match 96.3%: Score 629; DB 10; Length 120;
Best Local Similarity 97.5%: Pred. No. 2.7e-62;
Matches 116: Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 YAEKSHRGESVCDSESLWYTDKSSAIDIRGHQVTVLGEIKTGNSPVKOYFETRCKEA 61

DB 2 YAEKSHRGESVCDSESLWYTDKSSAIDIRGHQVTVLGEIKTGNSPVKOYFETRCKEA 61
11
OY 62 RPYKNCGRGIDDKHNSCKTSQTYVRALTSNNKLVGMRIIDTSCVSLSRKIGRT 120
11
DB 62 APVDMCGRGIDDKHNSCKTSQTYVRALTSNNKLVGMRIIDTSCVSLSRKIGRT 120

RESULT 11
US-09-872-090-3
Sequence 3, Application US/09872090
Patent No. US20020052488A1
GENERAL INFORMATION:
APPLICANT: Boone, Thomas C.
APPLICANT: Cheung, Ellen Ngol Yin
APPLICANT: Hersenson, Susan I.
APPLICANT: Young, John D.
TITLE OF INVENTION: ANALOGS OF NT-3 (As Amended)
FILE REFERENCE: A-411B
CURRENT APPLICATION NUMBER: US/09/872,090
CURRENT FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 09/255,953
PRIOR FILING DATE: 1999-02-23
PRIOR APPLICATION NUMBER: 08/684,353
PRIOR FILING DATE: 1996-07-19
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 120
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Analog of
US-09-872-090-3

Query Match 96.3%: Score 629; DB 10; Length 120;
Best Local Similarity 97.5%: Pred. No. 2.7e-62;
Matches 116: Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 YAEKSHRGESVCDSESLWYTDKSSAIDIRGHQVTVLGEIKTGNSPVKOYFETRCKEA 61
11
DB 2 YAEKSHRGESVCDSESLWYTDKSSAIDIRGHQVTVLGEIKTGNSPVKOYFETRCKEA 61
OY 62 RPYKNCGRGIDDKHNSCKTSQTYVRALTSNNKLVGMRIIDTSCVSLSRKIGRT 120
11
DB 62 APVDMCGRGIDDKHNSCKTSQTYVRALTSNNKLVGMRIIDTSCVSLSRKIGRT 120

RESULT 12
US-09-745-032-7
Sequence 7, Application US/09745032
Patent No. US20010027179A1
GENERAL INFORMATION:
APPLICANT: Boone, Thomas C.
APPLICANT: Cheung, Ellen N.
APPLICANT: Hersenson, Susan I.
APPLICANT: Young, John D.
TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS
FILE REFERENCE: A-411A US Revised073100
CURRENT APPLICATION NUMBER: US/09/745,032
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 09/214,214
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 08/684,353
PRIOR FILING DATE: 1996-07-19
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 117
TYPE: PRT
ORGANISM: Human
US-09-745-032-7

Query Match 94.8% Score 619; DB 10; Length 117;
Best Local Similarity 97.4% Pred. No. 3.2e-61;
Matches 114: Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 YAEKSHRGEYSVCDSESLMTYDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 61
DB 1 YAEKSHRGEYSVCDSESLMTYDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 60

OY 62 RPYKNCRCGIDDKHNNKSOCKTSQTYVRALTSNNKLVGMWIRIDTSCVALSRKIG 118
DB 61 APVDNCGRGIDDKHNNKSOCKTSQTYVRALTSNNKLVGMWIRIDTSCVALSRKIG 117

RESULT 13
US-09-742-600-7
Sequence 7, Application US/09742600
Patent No. US20020010135A1
GENERAL INFORMATION:
APPLICANT: Boone, Thomas C.
APPLICANT: Cheung, Ellen N.
APPLICANT: Hershenson, Susan I.
APPLICANT: Young, John D.
TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS
FILE REFERENCE: A-411A US Revised073100
CURRENT APPLICATION NUMBER: US/09/742,600
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 09/214,214
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 08/684,353
PRIOR FILING DATE: 1996-07-19
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 117
TYPE: PRT
ORGANISM: Human
US-09-742-600-7

Query Match 94.8% Score 619; DB 10; Length 117;
Best Local Similarity 97.4% Pred. No. 3.2e-61;
Matches 114: Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 YAEKSHRGEYSVCDSESLMTYDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 61
DB 1 YAEKSHRGEYSVCDSESLMTYDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 60

OY 62 RPYKNCRCGIDDKHNNKSOCKTSQTYVRALTSNNKLVGMWIRIDTSCVALSRKIG 118
DB 61 APVDNCGRGIDDKHNNKSOCKTSQTYVRALTSNNKLVGMWIRIDTSCVALSRKIG 117

RESULT 14
US-09-872-090-7
Sequence 7, Application US/09872090
Patent No. US20020052488A1
GENERAL INFORMATION:
APPLICANT: Boone, Thomas C.
APPLICANT: Cheung, Ellen Ngai Yin
APPLICANT: Hershenson, Susan I.
APPLICANT: Young, John D.
TITLE OF INVENTION: Analogs of NT-3 (as Amended)
FILE REFERENCE: A-411B
CURRENT APPLICATION NUMBER: US/09/872,090
CURRENT FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 09/255,953
PRIOR FILING DATE: 1999-02-23
PRIOR APPLICATION NUMBER: 08/684,353
PRIOR FILING DATE: 1996-07-19
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 117

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Analog of
OTHER INFORMATION: human NT-3.
US-09-872-090-7

Query Match 94.8% Score 619; DB 10; Length 117;
Best Local Similarity 97.4% Pred. No. 3.2e-61;
Matches 114: Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 YAEKSHRGEYSVCDSESLMTYDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 61
DB 1 YAEKSHRGEYSVCDSESLMTYDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 60

OY 62 RPYKNCRCGIDDKHNNKSOCKTSQTYVRALTSNNKLVGMWIRIDTSCVALSRKIG 118
DB 61 APVDNCGRGIDDKHNNKSOCKTSQTYVRALTSNNKLVGMWIRIDTSCVALSRKIG 117

RESULT 15
US-09-745-032-5
Sequence 5, Application US/09745032
Patent No. US20010027179A1
GENERAL INFORMATION:
APPLICANT: Boone, Thomas C.
APPLICANT: Cheung, Ellen N.
APPLICANT: Hershenson, Susan I.
APPLICANT: Young, John D.
TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS
FILE REFERENCE: A-411A US Revised073100
CURRENT APPLICATION NUMBER: US/09/745,032
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 09/214,214
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 08/684,353
PRIOR FILING DATE: 1996-07-19
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 118
TYPE: PRT
ORGANISM: Human
US-09-745-032-5

Query Match 94.8% Score 619; DB 10; Length 118;
Best Local Similarity 97.4% Pred. No. 3.3e-61;
Matches 114: Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 YAEKSHRGEYSVCDSESLMTYDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 61
DB 2 YAEKSHRGEYSVCDSESLMTYDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 61

OY 62 RPYKNCRCGIDDKHNNKSOCKTSQTYVRALTSNNKLVGMWIRIDTSCVALSRKIG 118
DB 62 APVDNCGRGIDDKHNNKSOCKTSQTYVRALTSNNKLVGMWIRIDTSCVALSRKIG 118

Search completed: December 2, 2002, 15:14:35
Job time : 5.2204 secs

GenCore version 5.1.3
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OM protein - protein search, using SW model

Run on: December 2, 2002, 15:05:37 (Search time 25.9086 Seconds
(without alignments)
668.605 Million cell updates/sec

Title: US-10-072-681-6

Perfect score: 698

Sequence: 1 GVSETPAPASRCELAVCDAY.....RWIRIDPACVCTILSRGTA 130

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

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23: /SID52/gcgdata/geneseq/emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	698	100.0	130	AA048890	Human neurotrophin-4
2	698	100.0	130	AA029112	Human neurotrophin-4
3	698	100.0	210	AA022465	Neurotrophic facto
4	694	99.4	210	AA022482	Neurotrophic facto
5	689	98.7	130	AA092009	Human neurotrophin-4
6	689	98.7	215	AA030691	Human neurotrophin-4
7	689	98.7	215	AA047102	Human NT-4 encode
8	684	98.0	130	AA022477	Neurotrophic facto
9	684	98.0	130	AA022479	Neurotrophic facto
10	683	97.9	130	AA022471	Neurotrophic facto

11	683	97.9	130	13	AA022480	Neurotrophic facto
12	683	97.9	215	13	AA029735	Human NT-4 encode
13	682	97.7	130	13	AA022481	Neurotrophic facto
14	680	97.4	130	13	AA022470	Neurotrophic facto
15	678	97.1	130	13	AA022469	Neurotrophic facto
16	676	96.8	130	13	AA022478	Neurotrophic facto
17	650	93.1	126	13	AA022475	Neurotrophic facto
18	642	92.0	124	13	AA022473	Neurotrophic facto
19	586	84.0	114	13	AA022476	Neurotrophic facto
20	565	80.9	118	22	AA035947	NT-4 amino acid se
21	540	77.4	142	13	AA022472	Neurotrophic facto
22	535.5	76.7	107	13	AA022474	Neurotrophic facto
23	499.5	71.6	186	13	AA022468	Neurotrophic facto
24	494.5	70.8	216	13	AA022466	Neurotrophic facto
25	475.5	68.1	257	13	AA022467	Neurotrophic facto
26	415	59.5	236	15	AA047098	Xenopus NT-4 fragm
27	415	59.5	237	13	AA029491	NT-4, Xenopus Xe
28	415	59.5	239	15	AA047097	Xenopus mature NT-
29	367	52.6	132	13	AA047104	Human NT-4 encode
30	364	52.1	123	13	AA021859	Chimeric neurotrop
31	361	51.7	123	13	AA021857	Chimeric neurotrop
32	360	51.6	119	13	AA052302	Mutant hNNT-3-1-11
33	360	51.6	119	22	AA050871	Human NT-3(1-119)R
34	360	51.6	120	22	AA052300	Mutant met-hNNT-3
35	360	51.6	120	22	AA050869	Human r-metNNT-3
36	358	51.3	119	13	AA029495	NT-3, mouse, Mus
37	358	51.3	119	15	AA054086	Neurotrophin-3, R
38	358	51.3	119	20	AA061118	Neurotrophin-3, W11
39	358	51.3	119	22	AA064995	Nerve growth facto
40	358	51.3	119	22	AA035946	NT-3 amino acid se
41	358	51.3	120	17	AA029392	Conjugate of neuro
42	358	51.3	120	18	AA010014	Human neurotrophin
43	358	51.3	120	21	AA010455	Human R-metNNT pr
44	358	51.3	120	22	AA050868	Human R-metNNT pr
45	358	51.3	136	12	AA011306	Nerve Growth Facto

ALIGNMENTS

RESULT 1	AA048890	standard: Protein: 130 AA.
ID	AA048890	
XX	AA048890;	
AC		
XX		
XX		
DT	12-OCT-1998 (first entry)	
XX		
DE	Human neurotrophin-4/5.	
XX		
KW	Neurotrophin-4/5; NT-4/5; human; purification;	
KW	hydrophobic interaction chromatography.	
XX		
OS	Homo sapiens.	
XX		
XX		
FT	Key	Location/Qualifiers
FT	Region	61..78
FT		/note="conserved Cys-containing region involved in
FT		Cys knot motif"
FT	Region	119..121
FT		/note="conserved Cys-containing region involved in
FT		Cys knot motif"
XX		
PN	W09821234-A2.	
XX		
PD	22-MAY-1998.	
XX		
XX		
PF	14-NOV-1997;	97WO-US21068.
XX		
XX	28-MAY-1997;	97US-0047855.
PR	15-NOV-1996;	96US-0030838.
XX		
PA	(GETH) GENENTECH INC.	

```

XX PI Beck JT, Burton LE, Schmelzer CH;
DR WPI: 1998-32233/28.
XX Isolation of neurotrophin(s) from, e.g. mis-folded or glycosylated
PT variant(s) - using hydrophobic interaction chromatography.
PT optionally in combination with high performance cation exchange
XX chromatography
PS
XX Disclosure: page 38: 59pp: English.
XX
CC This polypeptide comprises human neurotrophin-4/5 (NT-4/5) mature
CC polypeptide. Methods are provided for large-scale purification of
CC neurotrophins, including NT-4/5, suitable for clinical use. A
CC claimed method comprises: (1) separating the neurotrophin from the
CC other proteins using a hydrophobic interaction chromatography resin
CC (HIC); and optionally (2) separating the neurotrophin from a
CC chemical variant by high performance cation exchange chromatography
CC (HCEC). The processes can also be used for purification of e.g.
CC human nerve growth factor (NGF) (see AAM48886), mouse NGF (see
CC AAM48887), brain-derived neurotrophic factor (see AAM4888) and
CC neurotrophin-3 (see AAM4889). The processes allow separation of
CC neurotrophins from various undesirable misprocessed, misfolded,
CC site, glycosylated or charge forms. They allow selective
CC separation from variants and other molecules, and from other
CC polypeptides with high PI. The processes are applicable to
CC starting materials from various sources, including fermentation
XX broths or lysed bacterial or mammalian cells.
XX
S0 Sequence 130 AA:
XX
XX Query Match 100.0%; Score 698; DB 19; Length 130;
XX Best Local Similarity 100.0%; Pred. No. 1,7e-71;
XX Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps
XX
XX QY 1 GVSETPAPSRGELAVCDANSGWTPRPAVDLRGEVGLGEPAPAGGSPLRQYFETR 60
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||
XX DB 1 GVSETPAPSRGELAVCDANSGWTPRPAVDLRGEVGLGEPAPAGGSPLRQYFETR 60
XX
XX QY 61 CKAADNAEKGCGPAGGCGCGVDRRHVSECKAKOSYVRLTAHAGRGWRMIRIDTACV 120
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||
XX DB 61 CKAADNAEKGCGPAGGCGCGVDRRHVSECKAKOSYVRLTAHAGRGWRMIRIDTACV 120
XX
XX QY 121 CTLLSRTGRA 130
XX ||||||||
XX DB 121 CTLLSRTGRA 130
XX
XX RESULT 2
XX AAB29112
XX ID AAB29112 standard; Protein; 130 AA.
XX
XX AA29112;
XX
XX DT 02-FEB-2001 (first entry)
XX
XX DE Human neutrophin-4/5.
XX
XX KW Neutrophin; trkb; trkc; ototoxicity-related balance impairment;
XX Meniere's syndrome; myringitis; otitis media;
XX acute vestibular neuronitis; herpes zoster oticus; labyrinthitis;
XX middle; labyrinthine tumour; petrositis; otosclerosis; bacteria.
XX
XX OS Homo sapiens.
XX
XX PN US6121235-A.
XX
XX PD 19-SEP-2000.
XX
XX PF 29-DEC-1995; 95US-0581662.
XX
XX PR 29-DEC-1995; 95US-0581662.

```

```

XX PA (GETH ) GENENTECH INC.
XX PI Gao W:
XX MP: 2000-618200/59.
XX DR
XX PT Treating ototoxin-induced neuronal-related balance impairment and
XX PR promoting vestibular ganglion neuron survival prior to, upon or after
XX exposure to an ototoxin, comprises administering a trkB or trkB agonist
PT _
XX PS Disclosure; Column 47-48; 40pp; English.
XX CC The present invention relates to treating ototoxin-induced
CC neuronal-related balance impairment in a mammal by administering a
CC trkB or trkB agonist, particularly neurotrophin-4/5 (NT-4/5).
CC CC Ototoxicity-related balance impairments include Meniere's syndrome,
CC myringitis, otitis media, acute vestibular neuritis, herpes zoster
CC oticus, labyrinthitis, middle or labyrinthine tumours, petrositis and
CC otosclerosis. NT-4/5 may also be used to treat diseases
CC induced by gram positive, gram negative and acid-fast bacteria. The
CC present sequence is a protein used in the invention.
XX CC
SQ Sequence 130 AA:
Query Match 100.0%; Score 698; DB 21; Length 130;
Best Local Similarity 100.0%; Pred. No. 1,7e-71;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY 1 GVSETAPASRRGELAVCDVSGWYTDRRTAYVDLRGREVEVLGEVPAAAGSPLRQFFETR 60
DB 1 GVSETAPASRRGELAVCDVSGWYTDRRTAYVDLRGREVEVLGEVPAAAGSPLRQFFETR 60
QY 61 CAAADAAEKGCGGAGGGCGRGVDRHHVSECKAKOSVTRALTAHAAGRGVMIRIDTACY 120
DB 61 CAADAAREGGCGAGCGGCGRGVDRHHVSECKAKOSVTRALTAHAAGRGVMIRIDTACY 120
QY 121 CTLLSRGTGRA 130
DB 121 CTLLSRGTGRA 130
RESULT 3
AAR22465
ID AAR22465 standard; Protein: 210 AA.
XX AC AAR22465;
XX DT 22-SEP-1992 (first entry)
XX DE Neurotrophic factor 4.
XX KM Huntington's chorea; ALS; NT-4; NGF; BDNF; NT-3; neuron.
XX OS Homo sapiens.
XX PN MOJ205254-A.
XX PD 02-APR-1992.
XX PF 24-SEP-1991; 91MO-US06950.
XX PR 25-SEP-1990; 90US-0587707.
XX RA 31-JAN-1991; 91US-0648482.
XX PA (GETH ) GENENTECH INC.
XX PI Rosenthal A;
XX DR WP: 1992-132123/16.
XX DR N-PADB; AAQ23663.
XX DR
```

PT Neurotrophic factor-4 - useful for treating neurodegenerative
 PT diseases e.g. Alzheimer's and Parkinson's diseases, nerve cells
 PT damaged by e.g. diabetes
 XX
 PS Disclosure; Fig 1: 84pp: English.

CC The sequence shows the entire amino acid sequence for the mature
 CC human neurotrophic factor-4 (NT-4) gene, (nucleotide sequence
 CC AA023653). This protein can be useful in treating damaged nerve cells
 CC or neurodegenerative diseases eg. Huntington's chorea, Alzheimer's
 CC disease, ALS and Parkinson's disease.
 CC NT-4 is a novel trophic factor with a broad tissue distribution.
 CC It complements NGF, BDNF, and NT-3, which are trophic factors for
 CC some peripheral neurons. This factor can act alone or with other
 CC trophic factors, or defined subsets of neurons to achieve the
 CC correct neuronal connections both in the peripheral and central
 CC nervous system.

XX Sequence 210 AA:

Query Match 100.0%; Score 698; DB 13; Length 210;
 Best Local Similarity 100.0%; Pred. No. 3, 1e-71;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYSETAPASRRGELAVCAVSGWTDRTAVDLRGREVEVLGEVPAAGSPKQYFEETR 60
 DB 81 GYSETAPASRRGELAVCAVSGWTDRTAVDLRGREVEVLGEVPAAGSPKQYFEETR 140
 OY 61 CKADNAEEGPGAGGCGRGVDRRHVSECKAKOSYRALTAAAGRCVGMWRIRIDTACV 120
 DB 141 CKADNAEEGPGAGGCGRGVDRRHVSECKAKOSYRALTAAAGRCVGMWRIRIDTACV 200
 OY 121 CTLLSRTGRA 130
 DB 201 CTLLSRTGRA 210

RESULT 4

ID AAR22482 standard; Protein: 210 AA.

AC AAR22482;

DT 22-SEP-1992 (first entry)

XX Neurotrophic factor 4 activity variants.

DE NT-4; NT-3; BDNF; NGF; mutagenesis; substitution.

KW NT-4; NT-3; BDNF; NGF; mutagenesis; substitution.

KW Homo sapiens.

OS Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Neurotrophic factor-4 - useful for treating neurodegenerative
 PT diseases e.g. Alzheimer's and Parkinson's diseases, nerve cells
 PT damaged by e.g. diabetes
 XX
 PS Disclosure; Page 9: 84pp: English.

CC The sequence shows a portion of the amino acid sequence of human
 CC neurotrophic factor-4 (NT-4), (full sequence AAR22465). Positions
 CC 70, 71 and 83 are positions of various amino acid substitutions.
 CC Substitutions at these positions can cause a marked differentiation
 CC in the activity of the trophic element.
 CC The sites of greatest interest for substitutional mutagenesis include
 CC sites where the amino acids found in BDNF, NGF, NT-3, and NT-4 are
 CC substantially different in terms of side chain bulk, charge, or
 CC hydrophobicity, but where there is also a high degree of homology at
 CC the selected site within various animal analogues of NGF, NT-3 and
 CC BDNF.

XX Sequence 210 AA:

Query Match 99.4%; Score 694; DB 13; Length 210;
 Best Local Similarity 99.2%; Pred. No. 8, 9e-71;
 Matches 129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYSETAPASRRGELAVCAVSGWTDRTAVDLRGREVEVLGEVPAAGSPKQYFEETR 60
 DB 81 GYSETAPASRRGELAVCAVSGWTDRTAVDLRGREVEVLGEVPAAGSPKQYFEETR 140
 OY 61 CKADNAEEGPGAGGCGRGVDRRHVSECKAKOSYRALTAAAGRCVGMWRIRIDTACV 120
 DB 141 CKADNAEEGPGAGGCGRGVDRRHVSECKAKOSYRALTAAAGRCVGMWRIRIDTACV 200
 OY 121 CTLLSRTGRA 130
 DB 201 CTLLSRTGRA 210

RESULT 5

ID AAY92009 standard; Protein: 130 AA.

AC AAY92009;

DT 19-JUL-2000 (first entry)

XX Human neurotrophin-4 monomer.

DE human neurotrophin-3 monomer; CKGF; mutant; cysteine knot growth factor;

KW human neurotrophin-3 monomer; CKGF; mutant; cysteine knot growth factor;

KW hairpin loop; neurodegenerative.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

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XX Homo sapiens.

XX Homo sapiens.

FT Key a receptor
 PN WO200017360-A1.
 XX 30-MAR-2000.
 XX 19-MAR-1999: 99MO-US05908.
 XX 22-SEP-1998: 98MO-US19772.
 XX (UYMA-) UNIV MARYLAND BALTIMORE.
 PA Weidtraub BD, Szklidlinski MW;
 PI WPI: 2000-283585/24.
 DR New mutant cysteine knot growth factor proteins comprising one or more
 XX mutant subunits, useful for treating or preventing diseases e.g.
 PT hypothyroidism and thyroid cancer
 PS Claim 177: Page 300: 320pp: English.
 XX This is the wild type human neurotrophin-4 monomer.
 CC Mutants comprise at least one electrostatic charge altering mutation in a
 CC beta hairpin loop, resulting in increased bioactivity.
 CC Mutant cysteine knot growth factor (CKGF) proteins comprising one or more
 CC mutant subunits and having novel properties or improved pharmacological
 CC properties, compared to wild type CKGFs, are claimed. The CKGF
 CC superfamily comprises at least four families of growth factors: the
 CC glycoprotein hormones, the platelet-derived growth factor (PDGF) family,
 CC the neurotrophins and the transforming growth factor-beta family; the
 CC families are known to be structurally similar (especially comprising the
 CC cysteine knot topology) and it was shown that mutations at certain
 CC positions in the CKGF hairpin loops of family members and other members
 CC of the CKGF superfamily could significantly alter the biological
 CC activities of the CKGF.
 CC Mutant neurotrophins are useful for diagnosis and treatment of
 CC neurodegenerative diseases.
 XX
 SO Sequence 130 AA:
 Query Match 98.7%; Score 689; DB 21; Length 130;
 Best Local Similarity 99.2%; Pred. No. 1.8e-70;
 Matches 129: Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GVSETAPASRRGELAVCDVSGWTDRTAVDLRGREVEVGEVPAAGSPLRQYFFETR 60
 DB 1 GVSETAPASRRGELAVCDVSGWTDRTAVDLRGREVEVGEVPAAGSPLRQYFFETR 60
 QY 61 CKADNAEEGGPGAGCGGCGVDRRHVSECKAKOSYVALTAHAGRGVGMIRIDTACV 120
 DB 61 CKADNAEEGGPGAGCGGCGVDRRHVSECKAKOSYVALTAHAGRGVGMIRIDTACV 120
 QY 121 CTLSRTGRA 130
 DB 121 CTLSRTGRA 130
 XX
 RESULT 6
 AAR30691
 ID AAR30691 standard; Protein: 215 AA.
 XX
 AC AAR30691:
 XX
 DT 18-MAY-1993 (first entry)
 XX
 DE Human neurotrophin-4.
 XX
 KW stress protector protein; protection; toxic shock; stress;
 KW stress susceptibility.
 XX
 OS Homo sapiens.
 XX

FN Key Location/Qualifiers
 FT Region 81..83
 FT /Label- N-glycosylation consensus sequence.
 FT Cleavage-site 84..85
 FT /Label- predicted preproteins cleavage site
 XX
 PN WO9222665-A.
 XX
 XX 23-DEC-1992.
 XX
 PD 11-JUN-1992: 92MO-US05006.
 XX
 PF 12-JUN-1991: 91US-0715185.
 PR 21-NOV-1991: 91US-0796106.
 XX
 XX (REGG-) REGENERON PHARM INC.
 PA Fendli JP, Panayiotatos N;
 PI WPI: 1993-018148/02.
 DR P-PSDB: AAR30690.
 DR
 XX Recovery of recombinant biologically active neurotrophin(s) -
 PT comprises solidifying protein in soln. contg. strong denaturing
 PT agent and free of reducing agent
 PS Claim 83: Fig 11: 164pp: English.
 XX
 CC This sequence represents human neurotrophin 4. The coding sequence
 CC is fused to lamb signal sequences to enable its recombinant production.
 CC The protein is newly discovered and its biological role under
 CC investigation.
 CC
 SO Sequence 215 AA:
 Query Match 98.7%; Score 689; DB 14; Length 215;
 Best Local Similarity 99.2%; Pred. No. 3.4e-70;
 Matches 129: Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GVSETAPASRRGELAVCDVSGWTDRTAVDLRGREVEVGEVPAAGSPLRQYFFETR 60
 DB 86 GVSETAPASRRGELAVCDVSGWTDRTAVDLRGREVEVGEVPAAGSPLRQYFFETR 145
 QY 61 CKADNAEEGGPGAGCGGCGVDRRHVSECKAKOSYVALTAHAGRGVGMIRIDTACV 120
 DB 146 CKADNAEEGGPGAGCGGCGVDRRHVSECKAKOSYVALTAHAGRGVGMIRIDTACV 205
 QY 121 CTLSRTGRA 130
 DB 206 CTLSRTGRA 215
 XX
 RESULT 7
 AAR47102
 ID AAR47102 standard; Protein: 215 AA.
 XX
 AC AAR47102:
 XX
 DT 21-JUN-1994 (first entry)
 XX
 DE Human NT-4 encode by genomic phage clone 7-2.
 XX
 KW Neurotrophin-4; NT-4; Viper; Xenopus; fat; human; nerve growth factor;
 KW brain-derived neurotrophin factor; BDNF; NGF; acute neuropraxia; NT-3;
 KW gene family; survival; growth; differentiation; neuron; cholinergic;
 KW basal forebrain; cholinergic neuron; dopaminergic; neuron disease;
 KW peripheral neuropathy; hippocampus; striatum; neurotmesis; atoxmesis;
 KW diabetic neuropathy; amyotrophic lateral sclerosis; compression;
 KW tumour; abscess; trauma; Alzheimer's disease; Parkinson's disease;
 KW retina; retinal ganglion cell degeneration; antibody; diagnosis.
 XX
 OS Homo sapiens.
 XX

XX MO9325684-A.
 XX 23-DEC-1993.
 XX 11-JUN-1993: 93MO-US05672.
 XX 12-JUN-1992: 92US-0898194.
 XX (REGC-) REGENERON PHARM INC.
 XX Altar CA, Distefano P, Ip N, Ventimiglia R, Wiegand S;
 XX Wong V, Yancopoulos GD;
 XX WPI: 1994-007541/01.
 XX N-PSDB: AA054715.
 XX Neurotrophin-4-proteins which support survival, growth and
 XX differentiation of motor neurons - used to treat motor neuron
 XX disorders e.g. dopaminergic and cholinergic neuron diseases
 XX
 XX Disclosure: Page 145; 181pp; English.
 XX
 XX The sequences given in AAR47095-104 represent neurotrophin-4 (NT-4),
 XX fragments and derivatives of NT-4, and were derived from viper,
 XX xenopus, rat and human. NT-4 is a member of the brain-derived
 XX neurotrophin factor (BDNF)/nerve growth factor (NGF)/NT-3 gene family.
 XX NT-4 proteins can promote the survival, growth and differentiation
 XX of neurons, such as basal forebrain cholinergic neurons. NT-4
 XX proteins can be used to treat dopaminergic or cholinergic neuron
 XX diseases and disorders. NT-4 related proteins may be used to treat
 XX peripheral neuropathy and diseases of the hippocampus and striatum.
 XX Disorders which may be treated in this way, include acute neuropathia,
 XX neuromuscular atonias, diabetic neuropathy, amyotrophic lateral
 XX sclerosis or compression, a tumour, abscess, trauma, Alzheimer's
 XX disease, Parkinson's disease or a disorder of the retina, especially
 XX involving retinal ganglion cell degeneration. Anti-NT-4 antibodies
 XX may be used for diagnostic or therapeutic purposes, eg. to monitor the
 XX progression of diseases associated with alterations in the pattern of
 XX NT-4 expression.
 XX
 XX Sequence 215 AA:
 XX
 XX Query Match 98.7%: Score 689; DB 15; Length 215;
 XX Best Local Similarity 99.2%: Pred. No. 3,4e-70;
 XX Matches 129: Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX 1 GVSETAPASRRGELAVCAVSGWTDRTAVDLRGREVEVLGEVPAAGSPLRQYFFETR 60
 XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 XX DB 86 GVSETAPASRRGELAVCAVSGWTDRTAVDLRGREVEVLGEVPAAGSPLRQYFFETR 145
 XX
 XX 61 CKADNAEEGGPGAGCGCGVDRHRHVSCKAKOSYVRLTAHAQGRVGRWIRIDTACV 120
 XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 XX DB 146 CKADNAEEGGPGAGCGCGVDRHRHVSCKAKOSYVRLTAHAQGRVGRWIRIDTACV 205
 XX
 XX 121 CTLLSRTGRA 130
 XX ||||||||||||
 XX DB 206 CTLLSRTGRA 215
 XX
 XX RESULT 8
 XX AAR22477
 XX ID AAR22477 standard; Protein: 130 AA.
 XX
 XX AAR22477:
 XX
 XX 22-SEP-1992 (first entry)
 XX
 XX Neurotrophic factor 4 activity variants.
 XX
 XX NT-4; NGF; NT-3; BDNF; variant; deletion; tertiary structure;
 XX homology; activity.
 XX
 XX Synthetic.
 XX
 XX OS

XX Key Location/Qualifiers
 XX FT Misc-difference 53.53
 XX FT Label- HIS
 XX
 XX MO9205254-A.
 XX 02-APR-1992.
 XX
 XX 24-SEP-1991: 91MO-US06950.
 XX
 XX 25-SEP-1990: 90US-0587707.
 XX 31-JAN-1991: 91US-0648482.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Rosenthal A;
 XX WPI: 1992-132123/16.
 XX
 XX Neurotrophic factor-4 - useful for treating neurodegenerative
 XX diseases e.g. Alzheimer's and Parkinson's diseases, nerve cells
 XX damaged by e.g. diabetes
 XX
 XX Disclosure: Seq 59; 84pp; English.
 XX
 XX The sequence shows an NT-4 variant protein, in which the Arg
 XX residue at position 133 of NT-4 (sequence given in AAR22465), is
 XX replaced by a His residue. This corresponds to position 53 of the
 XX mature NT-4 protein. This substitution renders the NT-4 resistant to
 XX proteolysis, thereby creating a variant of NT-4 that is more stable.
 XX The sites of greatest interest for substitutional mutagenesis include
 XX sites where the amino acids found in BDNF, NGF, NT-3, and NT-4 are
 XX substantially different in terms of side chain bulk, charge or
 XX hydrophobicity, but where there is also a high degree of homology at
 XX the selected site within various animal analogues of BDNF, NGF and
 XX NT-3.
 XX
 XX Sequence 130 AA:
 XX
 XX Query Match 98.0%: Score 684; DB 13; Length 130;
 XX Best Local Similarity 98.5%: Pred. No. 6,8e-70;
 XX Matches 128: Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 XX 1 GVSETAPASRRGELAVCAVSGWTDRTAVDLRGREVEVLGEVPAAGSPLRQYFFETR 60
 XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 XX DB 61 CKADNAEEGGPGAGCGCGVDRHRHVSCKAKOSYVRLTAHAQGRVGRWIRIDTACV 120
 XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 XX DB 61 CKADNAEEGGPGAGCGCGVDRHRHVSCKAKOSYVRLTAHAQGRVGRWIRIDTACV 120
 XX
 XX 121 CTLLSRTGRA 130
 XX ||||||||||||
 XX DB 121 CTLLSRTGRA 130
 XX
 XX RESULT 9
 XX AAR22479
 XX ID AAR22479 standard; Protein: 130 AA.
 XX
 XX AAR22479:
 XX
 XX 22-SEP-1992 (first entry)
 XX
 XX Neurotrophic factor 4 activity variants.
 XX
 XX NT-4; NGF; NT-3; BDNF; variant; deletion; tertiary structure;
 XX homology; activity.
 XX
 XX Synthetic.
 XX
 XX Key Location/Qualifiers

FT Misc-difference 108..108
 XX /label- PHE
 XX WO9205254-A.
 XX
 XX 02-APR-1992.
 XX
 XX 24-SEP-1991; 91MO-US06950.
 XX
 XX 25-SEP-1990; 90US-0587707.
 XX 31-JAN-1991; 91US-0648482.
 XX
 XX (GERTH) GENENTECH INC.
 XX
 XX Rosenthal A;
 XX
 XX WPI: 1992-132123/16.
 XX
 XX Neurotrophic factor-4 - useful for treating neurodegenerative
 XX diseases e.g. Alzheimer's and Parkinson's diseases, nerve cells
 XX damaged by e.g. diabetes
 XX
 XX Disclosure: Seq 61; 84pp: English.
 XX
 XX The sequence shows an NT-4 variant protein, in which the phe
 XX residue at position 108 of NT-4 (sequence given in AAR22465), is
 XX replaced by a His residue. This corresponds to position 108 of the
 XX mature NT-4 protein. The sites of greatest interest for
 XX CC in BDNF, NGF, NT-3, and NT-4 are substantially different in terms of
 XX CC substitutional mutagenesis include sites where the amino acids found
 XX CC in BDNF, NGF, NT-3, and NT-4 are substantially different in terms of
 XX CC side chain bulk, charge or hydrophobicity, but where there is also a
 XX CC high degree of homology at the selected site within various animal
 XX CC analogues of BDNF, NGF and NT-3.
 XX
 XX Sequence 130 AA:
 XX
 XX Query Match 98.0%; Score 684; DB 13; Length 130;
 XX Best Local Similarity 98.5%; Pred. No. 6.8e-70;
 XX Matches 128; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 XX 1 GVSETAPASRGELAVCDVAVSGWTDRTAVDLRGREVEVLGEVPAAGSPRLROYFEETR 60
 XX DB 1 GVSETAPASRGELAVCDVAVSGWTDRTAVDLRGREVEVLGEVPAAGSPRLROYFEETR 60
 XX
 XX 61 CKADNAEEGPGAGGGCGVDRRHVSECKAKOSYVRLTAHOGRGVGRMIRIDTACV 120
 XX DB 61 CKADNAEEGPGAGGGCGVDRRHVSECKAKOSYVRLTAHOGRGVGRMIRIDTACV 120
 XX
 XX 121 CTLLSRTGRA 130
 XX DB 121 CTLLSRTGRA 130
 XX
 XX RESULT 10
 XX AAR22471
 XX ID AAR22471 standard; Protein; 130 AA.
 XX
 XX AAR22471;
 XX
 XX 22-SEP-1992 (first entry)
 XX
 XX Neurotrophic factor 4 variants (E67).
 XX
 XX NT-4; NT-3; BDNF; NGF; mutagenesis; substitution; non-conservative.
 XX
 XX Homo sapiens.
 XX
 XX Key location/Qualifiers
 XX FT Misc-difference 67..67
 XX FT /label- SER, THR
 XX
 XX WO9205254-A.
 XX
 XX

PD 02-APR-1992.
 XX
 XX 24-SEP-1991; 91MO-US06950.
 XX
 XX 25-SEP-1990; 90US-0587707.
 XX 31-JAN-1991; 91US-0648482.
 XX
 XX (GERTH) GENENTECH INC.
 XX
 XX Rosenthal A;
 XX
 XX WPI: 1992-132123/16.
 XX
 XX Neurotrophic factor-4 - useful for treating neurodegenerative
 XX diseases e.g. Alzheimer's and Parkinson's diseases, nerve cells
 XX damaged by e.g. diabetes
 XX
 XX Disclosure: Page 45-46; 84pp: English.
 XX
 XX The sequence shows a portion of the amino acid sequence of human
 XX neurotrophic factor-4 (NT-4), (full sequence AAR22465). Position 67
 XX is a point of a non-conservative substitution which can cause a
 XX marked differentiation in the activity of the trophic element.
 XX Either Ser or Thr may be included at this point. This substitution
 XX changes an acidic amino acid for a hydrophilicity neutral one. The
 XX sites of greatest interest for substitutional mutagenesis include
 XX sites where the amino acids found in BDNF, NGF, NT-3, and NT-4 are
 XX substantially different in terms of side chain bulk, charge, or
 XX hydrophobicity, but where there is also a high degree of homology at
 XX the selected site within various animal analogues of NGF, NT-3 and
 XX BDNF.
 XX
 XX Sequence 130 AA:
 XX
 XX Query Match 97.9%; Score 683; DB 13; Length 130;
 XX Best Local Similarity 98.5%; Pred. No. 8.9e-70;
 XX Matches 128; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 XX 1 GVSETAPASRGELAVCDVAVSGWTDRTAVDLRGREVEVLGEVPAAGSPRLROYFEETR 60
 XX DB 1 GVSETAPASRGELAVCDVAVSGWTDRTAVDLRGREVEVLGEVPAAGSPRLROYFEETR 60
 XX
 XX 61 CKADNAEEGPGAGGGCGVDRRHVSECKAKOSYVRLTAHOGRGVGRMIRIDTACV 120
 XX DB 61 CKADNAEEGPGAGGGCGVDRRHVSECKAKOSYVRLTAHOGRGVGRMIRIDTACV 120
 XX
 XX 121 CTLLSRTGRA 130
 XX DB 121 CTLLSRTGRA 130
 XX
 XX RESULT 11
 XX AAR22480
 XX ID AAR22480 standard; Protein; 130 AA.
 XX
 XX AAR22480;
 XX
 XX 22-SEP-1992 (first entry)
 XX
 XX Neurotrophic factor 4 activity variants.
 XX
 XX NT-4; NT-3; BDNF; NGF; mutagenesis; substitution.
 XX
 XX Homo sapiens.
 XX
 XX Key location/Qualifiers
 XX FT Misc-difference 84..84
 XX FT /label- GLN, HIS, ASN, THR, TYR, TRP
 XX
 XX WO9205254-A.
 XX
 XX 02-APR-1992.
 XX
 XX

PF 24-SEP-1991; 91WO-US06950.
 XX 25-SEP-1990; 90US-0587707.
 PR 31-JAN-1991; 91US-0648482.
 XX (GETH) GENENTECH INC.
 PA Rosenthal A;
 PI MPI; 1992-132123/16.
 DR
 XX
 XX Neurotrophic factor-4 - useful for treating neurodegenerative
 PT diseases e.g. Alzheimer's and Parkinson's diseases, nerve cells
 PT damaged by e.g. diabetes
 XX
 XX
 PS Disclosure; Seq 62-67; 84pp; English.
 XX
 XX The sequence shows a portion of the amino acid sequence of human
 CC neurotrophic factor-4 (NT-4), (full sequence AAR22465). Position 84
 CC is a point at which substitution mutation causes a marked
 CC differentiation in the activity of the trophic element. Either Gln,
 CC His, Asp, Thr, Tyr or Trp may be included at this point. The sites
 CC of greatest interest for substitutional mutagenesis include sites
 CC where the amino acids found in BDNF, NGF, NT-3, and NT-4 are
 CC substantially different in terms of side chain bulk, charge, or
 CC hydrophobicity, but where there is also a high degree of homology at
 CC the selected site within various animal analogues of NGF, NT-3 and
 CC BDNF.
 XX
 XX Sequence 130 AA:
 SQ
 Query Match 97.9%; Score 683; DB 13; Length 130;
 Best Local Similarity 98.5%; Pred. No. 8.9e-70;
 Matches 128; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 GVSETAPASRRGELAVCDVSGWYTDRTAVDLRGREVEVLGEVPAAGSPPLROYFFETR 60
 DB 1 GVSSETAPASRRGELAVCDVSGWYTDRTAVDLRGREVEVLGEVPAAGSPPLROYFFETR 60
 OY 61 CKADNAEEGGPGAGGGCGRGVDRRHMYSECKAKOSYVRALTAHAGRGVGRWIRIDTACY 120
 DB 61 CKADNAEEGGPGAGGGCGRGVDRRHMYSECKAKOSYVRALTAHAGRGVGRWIRIDTACY 120
 OY 121 CTLSRTGRA 130
 DB 121 CTLSRTGRA 130
 DE Human NT-4, encoded by clone 7-2.
 XX
 XX Neurotrophin; NT; nerve growth factor; NGF;
 KW brain-derived neurotrophic factor; BDNF; probe; primer.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT MISC-difference 2 /note- "conserved residue in presequence"
 FT MISC-difference 6 /note- "conserved residue in presequence"
 FT MISC-difference 9 /note- "conserved residue in presequence"
 FT MISC-difference 48..51 /note- "conserved residues in presequence"
 FT MISC-difference 54 /note- "conserved residues in presequence"

FT MISC-difference 62 /note- "conserved residue in presequence"
 FT Modified-site 81..83 /note- "conserved residue in presequence"
 FT Cleavage-site 84..85 /label- N-glycosylation_site
 XX
 XX MO9220365-A.
 XX
 XX 26-NOV-1992.
 PD
 XX
 XX 20-MAY-1992; 92NO-US04266.
 PF
 XX
 XX 21-MAY-1991; 91US-0703450.
 PR 12-JUL-1991; 91US-0729253.
 PR 23-JUL-1991; 91US-0734422.
 PR 28-AUG-1991; 91US-0751356.
 PR 20-SEP-1991; 91US-0762674.
 PR 14-NOV-1991; 91US-0791924.
 XX
 XX (REG-) REGENERON PHARM INC.
 PA
 XX Hallbook F, Ibaner Moliner CF, Persson HB, Yancopoulos GD;
 PI MPI; 1992-415468/50.
 DR N-PSDB; AMO32230.
 XX
 XX Use of neurotrophin-4 for promoting growth and survival of nerve
 PT cells - useful in treating neurological, fertility and
 PT immunological disorders and in diagnosis
 XX
 XX Disclosure; Page 117-119 + fig 18; 180pp; English.
 PS
 CC Oligonucleotide probes and primers were synthesised based on the NT
 CC family including NGF, BDNF and NT-3. These were used to isolate DNA
 CC encoding NT-4 from nucleic acid from xenopus ovaries. This DNA was
 CC then used to isolate other mammalian DNA encoding NT-4, including
 CC human NT-4 DNA.
 XX
 XX Sequence 215 AA:
 SQ
 Query Match 97.9%; Score 683; DB 13; Length 215;
 Best Local Similarity 98.5%; Pred. No. 1.6e-69;
 Matches 128; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 GVSETAPASRRGELAVCDVSGWYTDRTAVDLRGREVEVLGEVPAAGSPPLROYFFETR 60
 DB 86 GVSETAPASRRGELAVCDVSGWYTDRTAVDLRGREVEVLGEVPAAGSPPLROYFFETR 145
 OY 61 CKADNAEEGGPGAGGGCGRGVDRRHMYSECKAKOSYVRALTAHAGRGVGRWIRIDTACY 120
 DB 146 CKADNAEEGGPGAGGGCGRGVDRRHMYSECKAKOSYVRALTAHAGRGVGRWIRIDTACY 205
 OY 121 CTLSRTGRA 130
 DB 206 CTLSRTGRA 215
 DE Human NT-4, encoded by clone 7-2.
 XX
 XX Neurotrophin; NT; nerve growth factor; NGF;
 KW brain-derived neurotrophic factor; BDNF; probe; primer.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT MISC-difference 2 /note- "conserved residue in presequence"
 FT MISC-difference 6 /note- "conserved residue in presequence"
 FT MISC-difference 9 /note- "conserved residue in presequence"
 FT MISC-difference 48..51 /note- "conserved residues in presequence"
 FT MISC-difference 54 /note- "conserved residues in presequence"

FT Misc-difference 116..116
 FT /note- "GLU, ASN, GLN, TYR, SER, THR"
 XX
 XX WO9205254-A.
 XX
 XX 02-APR-1992.
 XX
 XX 24-SEP-1991; 91WO-US06950.
 XX
 XX 25-SEP-1990; 90US-0587707.
 XX 31-JAN-1991; 91US-0648482.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Rosenthal A;
 XX
 XX WPI: 1992-132123/16.
 XX
 XX Neurotrophic factor-4 - useful for treating neurodegenerative
 PT diseases e.g. Alzheimer's and Parkinson's diseases, nerve cells
 PT damaged by e.g. diabetes
 PT
 PS Disclosure: Seq 68-73; 84pp: English.
 PS
 XX The sequence shows a portion of the amino acid sequence of human
 CC neurotrophic factor-4 (NT-4), (full sequence AAR22465). Position 116
 CC is a point at which substitution mutation causes a marked
 CC differentiation in the activity of the trophic element. Either Glu,
 CC Asn, Gln, Tyr, Ser or Thr may be included at this point. The sites
 CC of greatest interest for substitutional mutagenesis include sites
 CC where the amino acids found in BDNF, NGF, NT-3, and NT-4 are
 CC substantially different in terms of side chain bulk, charge, or
 CC hydrophobicity, but where there is also a high degree of homology at
 CC the selected site within various animal analogues of NGF, NT-3 and
 CC BDNF.
 CC
 SQ Sequence 130 AA:
 Query Match 97.7%; Score 682; DB 13; Length 130;
 Best Local Similarity 98.5%; Pred. No. 1,2e-69;
 Matches 128; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GVSETAPASRGELAVCDVSGWYTDRTTAVDLRGREVEVLGEVPAAGSPLRQYFEETR 60
 DB 1 GVSETAPASRGELAVCDVSGWYTDRTTAVDLRGREVEVLGEVPAAGSPLRQYFEETR 60
 QY 61 CKADNAEEGGPGAGGGCGVDRRHVSECKAKOSYVRLTAHAGRGVGMIRIDTACY 120
 DB 61 CKADNAEEGGPGAGGGCGVDRRHVSECKAKOSYVRLTAHAGRGVGMIRIDTACY 120
 QY 121 CTLLSRTGRA 130
 DB 121 CTLLSRTGRA 130
 RESULT 14
 AAR22470
 ID AAR22470 standard; Protein: 130 AA.
 XX
 XX AAR22470:
 XX
 XX 22-SEP-1992 (first entry)
 XX
 XX Neurotrophic factor 4 variants (R85).
 XX
 XX NT-4; NT-3; BDNF; NGF; mutagenesis; substitution.
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 85..85
 FT /Label= GLU, PHE, PRO, TYR, TRP
 XX

PN WO9205254-A.
 XX
 XX 02-APR-1992.
 XX
 XX 24-SEP-1991; 91WO-US06950.
 XX
 XX 25-SEP-1990; 90US-0587707.
 XX 31-JAN-1991; 91US-0648482.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Rosenthal A;
 XX
 XX WPI: 1992-132123/16.
 XX
 XX Neurotrophic factor-4 - useful for treating neurodegenerative
 PT diseases e.g. Alzheimer's and Parkinson's diseases, nerve cells
 PT damaged by e.g. diabetes
 PT
 PS Disclosure: Page 43; 84pp: English.
 PS
 XX The sequence shows a portion of the amino acid sequence of human
 CC neurotrophic factor-4 (NT-4), (full sequence AAR22465). Position 85
 CC is a point at which substitution mutation causes a marked
 CC differentiation in the activity of the trophic element. Either Glu,
 CC Phe, Pro, Tyr or Trp may be included at this point. The sites of
 CC greatest interest for substitutional mutagenesis include sites where
 CC the amino acids found in BDNF, NGF, NT-3, and NT-4 are substantially
 CC different in terms of side chain bulk, charge, or hydrophobicity, but
 CC where there is also a high degree of homology at the selected site
 CC within various animal analogues of NGF, NT-3 and BDNF.
 CC
 SQ Sequence 130 AA:
 Query Match 97.4%; Score 680; DB 13; Length 130;
 Best Local Similarity 98.5%; Pred. No. 2e-69;
 Matches 128; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GVSETAPASRGELAVCDVSGWYTDRTTAVDLRGREVEVLGEVPAAGSPLRQYFEETR 60
 DB 1 GVSETAPASRGELAVCDVSGWYTDRTTAVDLRGREVEVLGEVPAAGSPLRQYFEETR 60
 QY 61 CKADNAEEGGPGAGGGCGVDRRHVSECKAKOSYVRLTAHAGRGVGMIRIDTACY 120
 DB 61 CKADNAEEGGPGAGGGCGVDRRHVSECKAKOSYVRLTAHAGRGVGMIRIDTACY 120
 QY 121 CTLLSRTGRA 130
 DB 121 CTLLSRTGRA 130
 RESULT 15
 AAR22469
 ID AAR22469 standard; Protein: 130 AA.
 XX
 XX AAR22469:
 XX
 XX 22-SEP-1992 (first entry)
 XX
 XX Neurotrophic factor 4 variants (G78).
 XX
 XX NT-4; NT-3; BDNF; NGF; mutagenesis; substitution.
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 78..78
 FT /Label= LYS, HIS, GLN, ARG
 XX
 XX WO9205254-A.
 XX
 XX 02-APR-1992.
 XX

```

PF 24-SEP-1991; 91WO-US06950.
XX
PR 25-SEP-1990; 90US-0587707.
PR 31-JAN-1991; 91US-0648482.
XX
PA (GETH ) GENENTECH INC.
XX
PI Rosenthal A;
XX
DR WPI: 1992-132123/16.
XX
XX Neurotrophic factor-4 - useful for treating neurodegenerative
PT diseases e.g. Alzheimer's and Parkinson's diseases, nerve cells
PT damaged by e.g. diabetes
XX
XX Disclosure; page 40-41; 84pp; English.
XX
XX The sequence shows a portion of the amino acid sequence of human
CC neurotrophic factor-4 (NT-4), (full sequence AAK22465). Position 78
CC is a point at which substitution mutation causes a marked
CC differentiation in the activity of the trophic element. Either Lys,
CC His, Gln, or Arg may be included at this point. The sites of greatest
CC interest for substitutional mutagenesis include sites where the amino
CC acids found in BDNF, NGF, NT-3, and NT-4 are substantially different
CC in terms of side chain bulk, charge, or hydrophobicity, but where
CC there is also a high degree of homology at the selected site within
CC various animal analogues of NGF, NT-3 and BDNF.
XX
SO Sequence 130 AA;

Query Match 97.1%; Score 678; DB 13; Length 130;
Best Local Similarity 98.5%; Pred. No. 3,3e-69;
Matches 128; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GYSETPAPASRRGELAVCDANSGWYTDRTTRAVDLRGREVEYLGEVPAGGSPLRQYFFETR 60
DB 1 GYSETPAPASRRGELAVCDANSGWYTDRTTRAVDLRGREVEYLGEVPAGGSPLRQYFFETR 60
OY 61 CKADNAEEGSGPGAGGCGRCVDRRHMYSECKAKOSYVRLTAHAGRGVGNRWIRIDTACY 120
DB 61 CKADNAEEGSGPGAGGCGRCVDRRHMYSECKAKOSYVRLTAHAGRGVGNRWIRIDTACY 120
OY 121 CTLLSRTGRA 130
DB 121 CTLLSRTGRA 130

```

Search completed: December 2, 2002, 15:08:40
 Job time : 25.9086 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 2, 2002, 15:05:43 ; Search time 10.3634 Seconds
(without alignments)
1205.921 Million cell updates/sec

Title: US-10-072-681-6

Perfect score: 698

Sequence: 1 GVSETAPASRGEIACVDAV.....RWIIDPACVCTLSRTGRA 130

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	689	98.7	210	2 A42687	neurotrophin-4 pre
2	663	95.0	209	2 B42687	neurotrophin-4 pre
3	415	59.5	236	2 JH0400	neurotrophin-3 pre
4	358	51.3	257	2 C40304	neurotrophin-3 pre
5	358	51.3	257	2 I50400	neurotrophin-3 pre
6	358	51.3	258	2 S09155	neurotrophin-3 pre
7	358	51.3	258	2 A35781	hippocampus-derive
8	345	49.4	247	2 A40304	brain-derived neur
9	345	49.4	249	2 S12555	brain-derived neur
10	345	49.4	249	2 B40304	brain-derived neur
11	345	49.4	252	2 A30361	brain-derived neur
12	342	49.0	248	2 J50188	brain-derived neur
13	340	48.7	259	2 I51708	brain-derived neur
14	336	48.1	114	2 I84765	brain-derived neur
15	327	46.8	114	2 I50606	brain-derived neur
16	315	45.1	114	2 I51599	brain-derived neur
17	308.5	44.2	245	2 I56570	beta-nerve growth
18	307.5	44.1	125	2 A26312	nerve growth facto
19	307.5	44.1	329	2 I46614	nerve growth facto
20	305.5	43.8	303	1 NGRTBA	nerve growth facto
21	305.5	43.8	307	1 NGMSG	nerve growth facto
22	302.5	43.3	243	2 A26311	nerve growth facto
23	297.5	42.6	286	1 NGHUBM	nerve growth facto
24	295.5	42.3	241	2 J14097	nerve growth facto
25	290	41.5	235	2 I14481	nerve growth facto
26	269.5	38.6	243	2 I51193	nerve growth facto
27	265	38.0	116	1 NGKXJI	nerve growth facto
28	264.5	37.9	117	2 S28161	nerve growth facto
29	255	36.5	116	2 A58566	nerve growth facto

30	255	36.5	246	2 A59218	nerve growth facto
31	241.5	34.6	194	2 I51709	nerve growth facto
32	228.5	32.7	286	2 S50855	neurotrophin-6 - s
33	90	12.9	992	2 T08772	hypothetical prote
34	83	11.9	949	2 J07802	urp protein - mous
35	80.5	11.5	1070	2 T31332	nuclease - Aeromon
36	80.5	11.5	1507	2 A40328	neurexin I-alpha p
37	80	11.5	622	2 J05425	transcription init
38	79.5	11.4	372	2 H70595	probable entc prot
39	76.5	11.0	860	1 EAMS	elastin precursor
40	76.5	11.0	1530	2 I45944	neurexin I-alpha -
41	74.5	10.7	577	2 B87010	probable isochoris
42	73.5	10.5	6260	2 T30228	polyketide synthas
43	72.5	10.4	625	2 S13919	potassium channel
44	72.5	10.4	940	2 T01854	hypothetical prote
45	72	10.3	894	2 C85756	prophage p12 prote

ALIGNMENTS

Result 1

A42687
neurotrophin-4 precursor - human
M:Alternate names: neurotrophin-5
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C:Accession: A42687; JH0503

R:ID, N.Y.; Ibanez, C.F.; Nye, S.H.; McClain, J.; Jones, P.F.; Giles, D.R.; Belluscio,
Proc. Natl. Acad. Sci. U.S.A. 89, 3060-3064, 1992

A:Title: Mammalian neurotrophin-4: structure, chromosomal localization, tissue distri
A:Reference number: A42687; MUID:9221967; PMID:1113578

A:Accession: A42687

A:Molecule type: DNA

A:Residues: 1-210 <1P1>

A:Cross-references: GB:M86528; NID:q190264; PIDN:AAA60154.1; PID:q190265
A:Note: sequence extracted from NCBI backbone (NCBIN:93810, NCBI:P:93811)

R:Berremeter, L.R.; Winslow, J.W.; Kaplan, D.R.; Nikolic, K.; Goeddel, D.V.; Rosenb
Neuron 7, 857-866, 1991

A:Title: Neurotrophin-5: a novel neurotrophic factor that activates trk and trkB.
A:Reference number: JH0503; MUID:92075279; PMID:1742028

A:Accession: JH0503

A>Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-210 <BER>

C:Comment: The neurotrophins stimulate autophosphorylation and transduce signals thro
C:Gene: GDB:NTF5

A:Cross-references: GDB:134723; OMIM:162662

A:Map position: 19pter-19qter

C:Superfamily: nerve growth factor beta chain

C:Keywords: glycoprotein

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-80/Domain: propeptide #status predicted <PRO>

F:81-210/Product: neurotrophin-4 #status predicted <NEU>

F:76/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 98.7% Score 689; DB 2; Length 210;

Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVSETAPASRGEIACVDAVSGMVTDRRTAVDLRGRREVYLGVEVPAAGSPRLQYFEETR 60
DB 81 GVSETAPASRGEIACVDAVSGMVTDRRTAVDLRGRREVYLGVEVPAAGSPRLQYFEETR 140
QY 61 CKADNABEGGPGAGGCGVRBRHNVSECRKOSVYALTAHOGVGGRHRTITQACV 120
DB 141 CKADNABEGGPGAGGCGVRBRHNVSECRKOSVYALTAHOGVGGRHRTITQACV 200
QY 121 CTTLSRTGRA 130
DB 201 CTTLSRTGRA 210

RESULT 2

842687 neurotrophin-4 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Dec-1993 #sequence, revision 31-Dec-1993 #text_change 16-Jul-1999
C:Accession: 842687; JH0504; JH0505
R:Proc. Natl. Acad. Sci. U.S.A. 89, 3060-3064, 1992
Proc. Natl. Acad. Sci. U.S.A. 89, 3060-3064, 1992
A:Title: Mammalian neurotrophin-4: structure, chromosomal localization, tissue distribution
A:Reference number: A42687; MUID:92212967; PMID:1313578
A:Accession: 842687
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-209 <TRP>
A:Cross-references: GB:M6742; NID:9205775; PIDN:AAA1728.1; PID:9205776
R:Berkemeier, L.R.; Winslow, J.M.; Kaplan, D.R.; Nikolic, K.; Goeddel, D.V.; Rosenthal,
Neuron 7, 857-866, 1991
A:Title: Neurotrophin-5: a novel neurotrophic factor that activates trk and trkB.
A:Reference number: JH0503; MUID:92075279; PMID:1742028
A:Accession: JH0504
A:Molecule type: DNA
A:Residues: 1-209 <BER>
A:Accession: JH0505
A:Molecule type: mRNA
A:Residues: 1-176, 'P', 178-209 <BER>
A:Cross-references: GB:S69323; NID:9240025; PIDN:AAB20548.1; PID:9240026
C:Comment: This protein is a targeted-derived, diffusible neurotrophic factor.
C:Comment: The neurotrophin stimulate autophosphorylation and transduce signals through
C:Superfamily: nerve growth factor beta chain
C:Keywords: glycoprotein
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-79/Domain: propeptide #status predicted <PRO>
F:80-209/Product: neurotrophin-5 #status predicted <PRO>
F:75/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 95.0% Score 663; DB 2; Length 209;
Best Local Similarity 94.6% Pred. No. 3; Se-57;
Matches 123; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 GVSTAPASRRCGLAVCAVSGWTDRTAVDLRGREVEVLGEVPAAGSPKRYFFETR 60
|||||
DB 80 GVSTAPASRRCGLAVCAVSGWTDRTAVDLRGREVEVLGEVPAAGSPKRYFFETR 139
|||||
QY 61 CKADNAEGGRCAGCGCGVDRHNVSECKAKOSYVALLTAHOGVGRVIRIDTACV 120
|||||
DB 140 CKASAGEGPGVGGCGKGVDRHNVSECKAKOSYVALLTAHOGVGRVIRIDTACV 199
|||||
QY 121 CTLLSRTGRA 130
|||||
DB 200 CTLLSRTGRA 209
|||||

RESULT 3
JH0400 neurotrophin-4 precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 31-Dec-1991 #sequence, revision 31-Dec-1991 #text_change 16-Jul-1999
C:Accession: JH0400
R:Hallboeck, F.; Idenez, C.F.; Persson, H.
Neuron 6, 845-858, 1991
A:Title: Evolutionary studies of the nerve growth factor family reveal a novel member at
A:Reference number: JH0400; MUID:91222573; PMID:2022430
A:Accession: JH0400
A:Molecule type: DNA
A:Residues: 1-236 <HAL>
A:Cross-references: GB:Z30090; NID:9455533; PIDN:CAA82906.1; PID:9455534
C:Comment: This protein belongs to the nerve growth factor family.
C:Superfamily: nerve growth factor beta chain
C:Keywords: glycoprotein
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-113/Domain: propeptide #status predicted <PRO>
F:114-236/Product: neurotrophin-4 #status predicted <MAT>

F:106/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 59.5% Score 415; DB 2; Length 236;
Best Local Similarity 63.0% Pred. No. 5; Se-33;
Matches 80; Conservative 15; Mismatches 24; Indels 8; Gaps 2;

QY 3 SEVAPASRRCGLAVCAVSGWTDRTAVDLRGREVEVLGEVPAAGSPKRYFFETR 62
|||||

DB 117 SDVSLSRRCGLAVCAVSGWTDRTAVDLRGREVEVLGEVPAAGSPKRYFFETR 175
|||||

QY 63 ADNAEGGRCAGCGCGVDRHNVSECKAKOSYVALLTAHOGVGRVIRIDTACV 122
|||||

DB 176 PS-----GSTRRCGCGVDRHNVSECKAKOSYVALLTAHOGVGRVIRIDTACV 228
|||||

QY 123 LLSRTGR 129
|||||

DB 229 LLSRTGR 235
|||||

RESULT 4

C40304 neurotrophin-3 precursor - human

N:Alternate names: nerve growth factor 2; NGF-2

C:Species: Homo sapiens (man)

C:Date: 03-Apr-1992 #sequence, revision 30-Sep-1993 #text_change 16-Jul-1999
C:Accession: A36208; JH0141; C40304; S10719; C60536

R:Jones, K.R.; Reichardt, L.F. 87, 8060-8064, 1990
Proc. Natl. Acad. Sci. U.S.A. 87, 8060-8064, 1990

A:Title: Molecular cloning of a human gene that is a member of the nerve growth facto

A:Reference number: A36208; MUID:91045937; PMID:2236018
A:Accession: A36208

A:Molecule type: DNA

A:Residues: 1-257 <ROS>

A:Cross-references: GB:M37763; NID:9189300; PIDN:AAA59953.1; PID:9189301

R:Rosenthal, A.; Goeddel, D.V.; Nguyen, T.; Lewis, M.; Shih, A.; Lammeg, G.R.; Nikol

Neuron 4, 767-773, 1990

A:Title: Primary structure and biological activity of a novel human neurotrophic fact

A:Reference number: JH0141; MUID:90262727; PMID:2344409
A:Accession: JH0141

A:Molecule type: DNA

A:Residues: 1-257 <ROS>

R:Malosonier, P.C.; Le Beau, M.M.; Espinosa III, R.; Ip, N.Y.; Belluscio, L.; de la

Genomics 10, 558-568, 1991

A:Title: Human and rat brain-derived neurotrophic factor and neurotrophin-3: gene str

A:Reference number: A40304; MUID:91365361; PMID:1885806
A:Accession: C40304

A:Molecule type: DNA

A:Residues: 1-257 <NAI>

A:Cross-references: GB:M61180; NID:9189302; PIDN:AAA63231.1; PID:9189303

R:Kishino, Y.; Yoshimura, K.; Nakahama, K.

FEBS Lett. 266, 187-191, 1990

A:Title: Cloning and expression of a cDNA encoding a novel human neurotrophic factor.

A:Reference number: S10719; MUID:90306351; PMID:2365067
A:Accession: S10719

A:Molecule type: DNA

A:Residues: 1-257 <NAI>

A:Cross-references: GB:X53655; NID:9287794; PIDN:CAA37703.1; PID:9287795

R:Yancopoulos, G.D.; Malosonier, P.C.; Ip, N.Y.; Aldrich, T.H.; Belluscio, L.; Boul

Cold Spring Harb. Symp. Quant. Biol. 55, 371-379, 1990

A:Title: Neurotrophic factors, their receptors, and the signal transduction pathways

A:Accession: C60536
A:Status: not compared with conceptual translation
A:Molecule type: DNA

A:Residues: 1-73, 'Q', '75-77', 'R', '79-108', 'T', '110-257' <VAN>
C:Genetics: GDB:NTF3
A:Gene: GDB:NTF3
A:Cross-references: GDB:125917; OMIM:162660
A:Map position: 12p13-12p13
C:Superfamily: nerve growth factor beta chain
C:Keywords: glycoprotein
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-138/Domain: propeptide #status predicted <PRO>

A:Title: Brain-derived neurotrophic factor is more highly conserved in structure and function
 A:Reference number: 151708; MUID:92333301; PMID:1629719
 A:Accession: 151708
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-269 <GOT>
 A:Cross-references: EMBL:X5942; NID:965275; PIDN:CAA42567.1; PID:965276
 C:Genetics:
 A:Gene: BDNF
 C:Superfamily: nerve growth factor beta chain
 C:Keywords: 91ycoprotein
 F:1-16/Domain: signal sequence #status predicted <SIG>
 F:19-150/Domain: propeptide #status predicted <PRO>
 F:151-269/Product: brain-derived neurotrophic factor #status predicted <MAT>
 F:143/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:163-230,208-259,218-261/Disulfide bonds: #status predicted

Query Match 48.7%; Score 340; DB 2; Length 269;
 Best Local Similarity 51.2%; Pred. No. 1,1e-25;
 Matches 63; Conservative 23; Mismatches 25; Indels 10; Gaps 3;

OY 9 SRGELAVCAVSGWT--DRRTAVDLRGREVEVLGEVPAAGSPLRQYFETRCADNA 66
 DB 155 SRGELSVCDISQWTAADKTAIDMSQGTVMEXVVPVPMGQ-LKQYFETRCNP--- 210
 OY 67 EEGPGAGGGCGRVDRRHVSSECKAKOSYVRLTAHAGRGVGRMIRIDTACVCTL 126
 DB 211 ----KGYTKGCGRGIDKRMHNSOCRTTOSYVRLTMDNKKRIGRFIRIDTSCVCTL 266
 OY 127 TGR 129
 DB 267 RGR 269

RESULT 14

184765
 brain-derived neurotrophic factor - rhesus macaque (fragment)
 C:Species: Macaca mulatta (rhesus macaque)
 C:Date: 04-Sep-1997 #sequence_revision 13-Mar-1998 #text_change 16-Jul-1999
 C:Accession: 184765
 R:Jackson, P.J.; Towne, M.D.; Huntsman, M.M.
 FEBS Lett. 265, 260-264, 1991
 A:Title: Comparison of mammalian, chicken and Xenopus brain-derived neurotrophic factor
 A:Reference number: 150606; MUID:91309745; PMID:1906813
 A:Accession: 184765
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-114 <ISA>
 A:Cross-references: EMBL:X61475; NID:9288317; PIDN:CAA43703.1; PID:9288318
 C:Superfamily: nerve growth factor beta chain
 C:Keywords: brain; growth factor

Query Match 48.1%; Score 336; DB 2; Length 114;
 Best Local Similarity 54.7%; Pred. No. 1,2e-25;
 Matches 64; Conservative 21; Mismatches 22; Indels 10; Gaps 3;

OY 9 SRGELAVCAVSGWT--DRRTAVDLRGREVEVLGEVPAAGSPLRQYFETRCADNA 66
 DB 6 ARGELSVCDISQWTAADKTAIDMSQGTVMEXVVPVPMGQ-LKQYFETRCNP--- 61
 OY 67 EEGPGAGGGCGRVDRRHVSSECKAKOSYVRLTAHAGRGVGRMIRIDTACVCTL 123
 DB 62 ----KGYTKGCGRGIDKRMHNSOCRTTOSYVRLTMDNKKRIGRFIRIDTSCVCTL 114

RESULT 15

150606
 brain-derived neurotrophic factor - chicken (fragment)
 C:Species: Gallus gallus (chicken)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
 C:Accession: 150606
 R:Jackson, P.J.; Towne, M.D.; Huntsman, M.M.
 FEBS Lett. 285, 260-264, 1991

A:Title: Comparison of mammalian, chicken and Xenopus brain-derived neurotrophic factor
 A:Reference number: 150606; MUID:91309745; PMID:1906813
 A:Accession: 150606
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-114 <ISA>
 A:Cross-references: EMBL:X61476; NID:9288305; PIDN:CAA43704.1; PID:9288306
 C:Superfamily: nerve growth factor beta chain

Query Match 46.8%; Score 327; DB 2; Length 114;
 Best Local Similarity 54.7%; Pred. No. 8,9e-25;
 Matches 64; Conservative 18; Mismatches 25; Indels 10; Gaps 3;

OY 9 SRGELAVCAVSGWT--DRRTAVDLRGREVEVLGEVPAAGSPLRQYFETRCADNA 66
 DB 6 ARGELSVCDISQWTAADKTAIDMSQGTVMEXVVPVPMGQ-LKQYFETRCNP--- 61
 OY 67 EEGPGAGGGCGRVDRRHVSSECKAKOSYVRLTAHAGRGVGRMIRIDTACVCTL 123
 DB 62 ----KGYTKGCGRGIDKRMHNSOCRTTOSYVRLTMDNKKRIGRFIRIDTSCVCTL 114

Search completed: December 2, 2002, 15:14:01
 Job time: 11.3634 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 2, 2002, 15:05:43 : Search time 5.33411 Seconds
(without alignments)
1010.837 Million cell updates/sec

Title: US-10-072-681-6

Perfect score: 698
Sequence: 1 GVSETPAPSRGELAVCDAY.....RWIRIDTACVCTILSTRGNA 130

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SwissProt_40.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	689	98.7	210 1	NT5_HUMAN P34130 homo sapien
2	663	95.0	209 1	NT5_RAT P34131 rattus norv
3	501.5	71.8	186 1	NT6G_HUMAN P34134 homo sapien
4	494.5	70.8	257 1	NT6A_HUMAN P34132 homo sapien
5	478.5	68.6	257 1	NT6B_HUMAN P34133 homo sapien
6	415	59.5	236 1	NT4_XENLA P24727 xenopus lae
7	358	51.3	257 1	NT3_CHICK P24733 gallus gall
8	358	51.3	257 1	NT3_HUMAN P20783 homo sapien
9	358	51.3	258 1	NT3_MOUSE P20181 mus musculu
10	358	51.3	258 1	NT3_RAT P18280 rattus norv
11	356	51.0	257 1	NT3_FELCA O95832 felis silve
12	355	50.9	260 1	NT3_XENLA O70183 xenopus lae
13	346	49.6	255 1	BDNF_CAVPO P23560 homo sapien
14	345	49.4	247 1	BDNF_HUMAN P23560 homo sapien
15	345	49.4	247 1	BDNF_PROLO O18752 procyon lot
16	345	49.4	247 1	BDNF_URSAR O18752 ursus arcto
17	345	49.4	247 1	BDNF_URSML O18753 ursus malay
18	345	49.4	249 1	BDNF_MOUSE P23137 rattus norv
19	345	49.4	249 1	BDNF_MOUSE P23137 rattus norv
20	345	49.4	252 1	BDNF_RAT P14082 sus scrofa
21	344	49.3	247 1	BDNF_FELCA O95832 felis silve
22	342	49.0	248 1	BDNF_BOVIN O95106 bos taurus
23	340	48.7	269 1	BDNF_XIPHA O06225 xiphophorus
24	336	48.1	114 1	BDNF_XIPMA O06225 macaca mula
25	336	48.1	270 1	BDNF_CHICK P25429 gallus gall
26	335	48.0	245 1	BDNF_CYPICA O90322 cyprinus ca
27	315	45.1	114 1	BDNF_XENLA P25432 xenopus lae
28	314.5	45.1	231 1	NGF_BOVIN P13600 bos taurus
29	308.5	44.2	241 1	NGF_RAT P25427 rattus norv
30	307.5	44.1	229 1	NGF_PIG O29074 sus scrofa
31	305.5	43.8	241 1	NGF_MOUSE P01139 mus musculu
32	305.5	43.8	241 1	NGF_PRANA P20675 pronomys nat
33	302.5	43.3	243 1	NGF_CHICK P05200 gallus gall

ALIGNMENTS

RESULT 1	ID	NT5_HUMAN	STANDARD:	PRT:	210 AA.
AC	P34130:				
DT	01-FEB-1994 (Rel. 28, Created)				
DT	01-FEB-1994 (Rel. 28, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Neurotrophin-5 precursor (NT-5) (Neurotrophin-4)				
DE	(NT-4) (Neurotrophic factor 4).				
GN	NTF5 OR NTF4.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID:9606;				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Prostate;				
RX	MEDLINE=92212967; PubMed=1313578;				
RA	IP N.Y., Ibanez C.F., Nye S.H., McClellan J., Jones P.F., Gies D.R.,				
RA	Belluscio L., le Beau M.M., Esplanosa R. II, Squitino S.P., Persson H.,				
RA	Yancopoulos G.D.;				
RT	"Mammalian neurotrophin-4: structure, chromosomal localization,				
RT	tissue distribution, and receptor specificity."				
RT	Proc. Natl. Acad. Sci. U.S.A. 89:3060-3064(1992).				
RL	(2)				
RN	SEQUENCE FROM N.A.				
RP	X-RAY CRYSTALLOGRAPHY (2.75 ANGSTROMS).				
RX	MEDLINE=20095835; PubMed=10631974;				
RA	Robinson R.C., Radzilewski C., Spraggon G., Greenwald J.,				
RA	Kostura M.R., Butnick L.D., Stuart D.I., Choe S., Jones E.Y.;				
RT	"The structure of the neurotrophin 4 homodimer and the brain-derived				
RT	neurotrophic factor/neurotrophin 4 heterodimer reveal a common Trk-				
RT	binding site."				
RL	Protein Sci. 8:2589-2597(1999).				
RC	- FUNCTION: TARGET-DERIVED SURVIVAL FACTOR FOR PERIPHERAL SENSORY				
CC	SYMPATHETIC NEURONS.				
CC	- TISSUE SPECIFICITY: HIGHEST LEVELS IN PROSTATE, LOWER LEVELS				
CC	IN THYMUS, PLACENTA, AND SKELETAL MUSCLE. EXPRESSED IN EMBRYONIC				
CC	AND ADULT TISSUES.				
CC	- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.				
CC	-----				
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib-sib.ch).				
CC	-----				

DR EMBL: M86528; AAA60154.1; -.
 DR PIR: JH0503; JH0503.
 DR PIR: A42687; A42687.
 DR PDB: 1B8M; 03-FEB-99.
 DR PDB: 1B8M; 26-FEB-99.
 DR Genew: HGNC:8024; NTF5.
 DR MIM: 162662; -.
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF_1.
 DR PRINTS: PR00268; NGF.
 DR PRODOM: PD002052; NGF_1.
 DR SMART: SM00140; NGF_1.
 DR PROSITE: PS00248; NGF_1; 1.
 DR PROSITE: PS0270; NGF_2; 1.
 DR Growth factor; Signal; 3D-structure.
 DR SIGNAL: 1 24 POTENTIAL.
 FT PROPEP 25 80
 FT CHAIN 81 210 NEUROTROPHIN-5.
 FT DISULFID 97 170
 FT DISULFID 141 199
 FT DISULFID 158 201
 FT CARBOHYD 76 76
 FT SEQUENCE 210 AA; 22426 MW; DBC6A30195E139AD CRC64; (POTENTIAL).

Query Match 98.7%; Score 689; DB 1; Length 210;
 Best Local Similarity 99.2%; Pred. No. 5.5e-60;
 Matches 129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GVSETAPASRRCGLAVCAVSGWTDRTTAVDLRGREVEVLGEVPAAGSPRLQYFEETR 60
 DB 81 GVSETAPASRRCGLAVCAVSGWTDRTTAVDLRGREVEVLGEVPAAGSPRLQYFEETR 140
 OY 61 CKADNAEEGCGAGCGGCGVDRRHVSECKAKOSYVALTLAHAGRGWRIRIDTACV 120
 DB 141 CKADNAEEGCGAGCGGCGVDRRHVSECKAKOSYVALTLADSGRGWRIRIDTACV 200
 OY 121 CTLLSRGTA 130
 DB 201 CTLLSRGTA 210

RESULT 2

ID NT5_RAT STANDARD: PRT: 209 AA.
 AC P34131;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Neurotrophin-5 precursor (NT-5) (Neurotrophin-4)
 DE (NT-4) (Neurotrophic factor 4).
 DE NTF5 OR NTF4 OR NT4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 OX 11
 RN SEQUENCE FROM N.A.
 RP MEDLINE-92212967; Pubmed-1313578;
 RA IP N.Y., Ibanez C.F., Nye S.H., McClain J., Jones P.F., Giles D.R.,
 RA Belluscio L., Le Beau M.N., Espinosa R. III, Squinto S.P., Persson R.,
 RA Vancopoulos G.D.;
 RA "Mammalian neurotrophin-4: structure, chromosomal localization,
 RA tissue distribution, and receptor specificity";
 RA Proc. Natl. Acad. Sci. U.S.A. 89:3060-3064(1992).
 RN 12
 RP SEQUENCE FROM N.A.
 RP MEDLINE-92075279; Pubmed-1742028;
 RA Berkemeier L.R., Wlanslow J.W., Kaplan D.R., Nikolic K., Goeddel D.V.,
 RA Rosenthal A.;
 RA "Neurotrophin-5: a novel neurotrophic factor that activates trk and
 RA cFos";
 RA Neuron 7:857-866(1991).
 CC -!- FUNCTION: COULD SERVE AS A TARGET-DERIVED TROPHIC FACTOR FOR

SENSOR AND SYMPATHETIC NEURONS.
 -!- TISSUE SPECIFICITY: EXPRESSED IN THYMUS, MUSCLE, OVARY, BRAIN,
 HEART, STOMACH AND KIDNEY. EXPRESSED IN BOTH EMBRIO AND ADULT
 TISSUES.

-!- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.

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DR EMBL: M86742; AAA11728.1; -.
 DR PIR: S59323; AAB20548.1; -.
 DR PIR: JH0504; JH0504.
 DR PIR: B42687; B42687.
 DR HSSP: P34130; 1B8M.
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF_1.
 DR PRINTS: PR00268; NGF.
 DR PRODOM: PD002052; NGF_1.
 DR SMART: SM00140; NGF_1.
 DR PROSITE: PS00248; NGF_1; 1.
 DR PROSITE: PS0270; NGF_2; 1.
 DR Growth factor; Signal; 21
 DR SIGNAL: 1 21 POTENTIAL.
 FT PROPEP 22 79
 FT CHAIN 80 209 NEUROTROPHIN-5.
 FT DISULFID 96 169 BY SIMILARITY.
 FT DISULFID 140 198 BY SIMILARITY.
 FT DISULFID 157 200 BY SIMILARITY.
 FT CARBOHYD 75 75
 FT CONFLICT 177 177 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT SEQUENCE 209 AA; 22332 MW; DF5112C0C5D5B85 CRC64;

Query Match 95.0%; Score 663; DB 1; Length 209;
 Best Local Similarity 94.6%; Pred. No. 1.8e-57;
 Matches 123; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 GVSETAPASRRCGLAVCAVSGWTDRTTAVDLRGREVEVLGEVPAAGSPRLQYFEETR 60
 DB 80 GVSETAPASRRCGLAVCAVSGWTDRTTAVDLRGREVEVLGEVPAAGSPRLQYFEETR 139
 OY 61 CKADNAEEGCGAGCGGCGVDRRHVSECKAKOSYVALTLAHAGRGWRIRIDTACV 120
 DB 140 CKADNAEEGCGAGCGGCGVDRRHVSECKAKOSYVALTLADSGRGWRIRIDTACV 199
 OY 121 CTLLSRGTA 130
 DB 200 CTLLSRGTA 209

RESULT 3

ID NT6G_HUMAN STANDARD: PRT: 186 AA.
 AC P34134;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-OCT-2001 (Rel. 41, Last annotation update)
 DE Neurotrophin-6 gamma (NT-6 gamma) (Fragment).
 DE NT6G.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 OX 11
 RN SEQUENCE FROM N.A.
 RP TISSUE-Fetal;
 RC MEDLINE-92158359; Pubmed-1496419;
 RA Berkemeier L.R., Ozelcalk T., Francke U., Rosenthal A.;
 RA "Human chromosome 19 contains the neurotrophin-5 gene locus and three

related genes that may encode novel acidic neurotrophins.*;
RT Somet, Cell Mol. Genet. 18:233-245(1992).
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: S41541; AAB22781.1; -
DR HSSP: P34130; 1B98.
DR Genew: HGNC:8027; NTF6G.
DR MIM: 604023; -
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF; 1.
DR ProDom: PD002052; NGF; 1.
DR SMART: SM00140; NGF; 1.
DR PROSITE: PS00248; NGF_1; PARTIAL.
DR PROSITE: PS50270; NGF_2; 1.
DR Growth factor; 1.
KM NON_TER 1 1
FT DISULFID 72 146 BY SIMILARITY.
FT CARBOHYD 51 51 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 186 AA; 19553 MW; B584396F5AA4981C CRC64;
Query Match 71.8%; Score 501.5; DB 1; Length 186;
Best Local Similarity 77.1%; Pred. No. 7.5e-42;
Matches 101; Conservative 6; Mismatches 23; Indels 1; Gaps 1;
OY 1 GVSETAPASRKGELAVCDVAGVWTDRTTAVDLRGREVEVLGEVPAAGSPURGYFFETR 60
DB 56 GVSTSPASHQCELVCDVAVWTDRTTAVDLVLEVEVLGEVPAAGSSLRHGFVTC 115
OY 61 CKADNAEEGPGAGGCGRGV-DRRHVSECKAKOSYVRLTAHAGRGVNRIRIDTAC 119
DB 116 FKADNSEEGRGVGGAGAAAGVWGTGHWSECKAKOSYVRLTAHAGRGVNRIRIDTAC 175
OY 120 VCTLLSRGTGA 130
DB 176 VCTLLSRGTGA 186
RESULT 4
NT6A_HUMAN STANDARD: PRT; 257 AA.
ID NT6A_HUMAN
AC P34132;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neurotrophin-6 alpha (NT-6 alpha) (Fragment).
GN NTF6A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal;
RX MEDLINE=92358359; PubMed=1496419;
RA Berlemeter L.R., Oezcelik T., Francke U., Rosenthal A.;
RT Human chromosome 19 contains the neurotrophin-5 gene locus and three
RT related genes that may encode novel acidic neurotrophins.*;
RL Somet, Cell Mol. Genet. 18:233-245(1992).
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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CC -----
DR EMBL: S41522; AAB22779.1; -
DR HSSP: P34130; 1B98.
DR Genew: HGNC:8025; NTF6A.
DR MIM: 604021; -
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF; 1.
DR ProDom: PD002052; NGF; 1.
DR SMART: SM00140; NGF; 1.
DR PROSITE: PS00248; NGF_1; PARTIAL.
DR PROSITE: PS50270; NGF_2; 1.
DR Growth factor; Polymorphism.
KM NON_TER 1 1
FT DISULFID 143 217 BY SIMILARITY.
FT CARBOHYD 122 122 N-LINKED (GLCNAC...) (POTENTIAL).
FT VARIANT 186 186 R -> H.
FT VARIANT 186 186 /FTID-VAR_004627.
FT VARIANT 242 242 I -> T.
SQ SEQUENCE 257 AA; 27246 MW; 74AB6C03BD78A3BB CRC64;
Query Match 70.8%; Score 494.5; DB 1; Length 257;
Best Local Similarity 76.3%; Pred. No. 5e-41; 23; Indels 1; Gaps 1;
Matches 100; Conservative 7; Mismatches 23; Indels 1; Gaps 1;
OY 1 GVSETAPASRKGELAVCDVAGVWTDRTTAVDLRGREVEVLGEVPAAGSPURGYFFETR 60
DB 127 GVSTSPASHQCELVCDVAVWTDRTTAVDLVLEVEVLGEVPAAGSSLRHGFVTC 186
OY 61 CKADNAEEGPGAGGCGRGV-DRRHVSECKAKOSYVRLTAHAGRGVNRIRIDTAC 119
DB 187 FKADNSEEGRGVGGAGAAAGVWGTGHWSECKAKOSYVRLTAHAGRGVNRIRIDTAC 246
OY 120 VCTLLSRGTGA 130
DB 247 VCTLLSRGTGA 257
RESULT 5
NT6B_HUMAN STANDARD: PRT; 257 AA.
ID NT6B_HUMAN
AC P34133;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neurotrophin-6 beta (NT-6 beta) (Fragment).
GN NTF6B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal;
RX MEDLINE=92358359; PubMed=1496419;
RA Berlemeter L.R., Oezcelik T., Francke U., Rosenthal A.;
RT Human chromosome 19 contains the neurotrophin-5 gene locus and three
RT related genes that may encode novel acidic neurotrophins.*;
RL Somet, Cell Mol. Genet. 18:233-245(1992).
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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 CC -----
 DR EMBL: M83378; AAA68880.1; -
 DR HSP: P20783; 188K;
 DR InterPro: IPR002400; GF_cytknot.
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF; 1.
 DR PRINTS: PR00438; GFCYSKNOT.
 DR PRINTS: PR00268; NGF.
 DR ProDom: PD002052; NGF; 1.
 DR SMART: SM00140; NGF; 1.
 DR PROSITE: PS00248; NGF_1; 1.
 DR PROSITE: PS0270; NGF_2; 1.
 DR Growth factor; Signal.
 RM SIGNAL 1 16 POTENTIAL.
 FT PROPEP 17 138
 FT CHAIN 139 257 NEUROTROPHIN-3.
 FT DISULFID 152 217 BY SIMILARITY.
 FT DISULFID 195 246 BY SIMILARITY.
 FT DISULFID 205 248 BY SIMILARITY.
 FT CARBOHYD 131 131 N-LINKED (GLCNAC...) (POTENTIAL).
 SO SEQUENCE 257 AA; 29701 MW; E043BA2A005C1E7 CRC64;
 Query Match 51.3%; Score 358; DB 1; Length 257;
 Best Local Similarity 55.4%; Pred. No. 8, 6e-28;
 Matches 67; Conservative 18; Mismatches 28; Indels 8; Gaps 3;
 Oy 9 SRRELAVCAVSGWTDRATVDLNGREVEVGEVPAAGSGPLNGPFFETCKADNME 68
 Db 144 SHRGYSVCSESLMTDKASLIDIRHOVTGEL-KTGNSPVQOYFETCK-----E 197
 Oy 69 GGPAGGGGCGRVDNRHVSSECKAKOSYVALTAHAQNGVNRMRIDTACVCTLLSTRG 128
 Db 198 AKPVK--NGCRGIDDKHMSCKXTSQYVALTSENNKLVGWRMRIDTSCVALSRIG 255
 Oy 129 R 129
 Db 256 R 256
 RESULT 8
 NT3_HUMAN STANDARD; PRT; 257 AA.
 AC P20783;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neutrophin-3 precursor (NT-3) (Neutrophilic factor) (HNF)
 DE (Nerve growth factor 2) (NGF-2).
 GN NT3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90262727; PubMed=2344409;
 RA Roseman A., Goeddel D.V., Nguyen T., Lewis M., Shih A.,
 RA Larmee G.R., Nikolic K., Winslow J.W.;
 RT "Primary structure and biological activity of a novel human
 RT neurotrophic factor.";
 RL Neuron 4:767-773(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91045937; PubMed=2236018;
 RA Jones K.R., Reichardt L.F.;
 RT "Molecular cloning of a human gene that is a member of the nerve
 RT growth factor family.";

RL Proc. Natl. Acad. Sci. U.S.A. 87:8060-8064(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90306351; PubMed=2365067;
 RA Kishino Y., Yoshimura K., Nakahama K.;
 RT "Cloning and expression of a cDNA encoding a novel human neurotrophic
 RT factor.";
 RL FEBS Lett. 266:187-191(1990).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91365361; PubMed=189806;
 RA Maisongier P.C., Le Beau M.M., Espinosa R. III, Ip N.Y.,
 RA Belluscio L., de la Monte S.M., Squinto S., Furch M.E.,
 RA Yancopoulos G.D.;
 RT "Human and rat brain-derived neurotrophic factor and neurotrophin-3:
 RT gene structures, distributions, and chromosomal localizations.";
 RL Genomics 10:558-568(1991).
 RN [5]
 RP SEQUENCE OF 194-236 FROM N.A.
 RC TISSUE=Leukocyte;
 RX MEDLINE=9122573; PubMed=2025430;
 RA Halboeck F., Ibanez C.F., Persson H.;
 RT "Evolutionary studies of the nerve growth factor family reveal a
 RT novel member abundantly expressed in Xenopus ovary.";
 RL Neuron 6:845-858(1991).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE=95217877; PubMed=7703225;
 RA Robinson R.C., Radziejewski C., Stuart D.I., Jones E.Y.;
 RT "Structure of the brain-derived neurotrophic factor/neurotrophin 3
 RT heterodimer.";
 RL Biochemistry 34:4139-4146(1995).
 RN [7]
 RP VARIANT GLU-76.
 RX MEDLINE=95251647; PubMed=7733919;
 RA Hattori M., Nanko S.;
 RT "Association of neurotrophin-3 gene variant with severe forms of
 RT schizophrenia.";
 RL Biochem. Biophys. Res. Commun. 209:513-518(1995).
 RN [8]
 RP VARIANT GLU-76.
 RX MEDLINE=96253892; PubMed=8925252;
 RA Arinami T., Takekoshi K., Itokawa M., Hamaguchi H., Toru M.;
 RT "Failure to find associations of the CA repeat polymorphism in the
 RT first intron and the Gly-63/Glu-63 polymorphism of the neurotrophin-3
 RT gene with schizophrenia.";
 RL Psychiatr. Genet. 6:113-15(1996).
 CC -1- FUNCTION: SEEMS TO PROMOTES THE SURVIVAL OF VISCERAL AND
 CC PROPRIOCEPTIVE SENSORY NEURONS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: BRAIN AND PERIPHERAL TISSUES.
 CC -1- POLYMORPHISM: Variant Glu-76 (frequently reported as Glu-63) was
 CC thought to be associated with severe forms of schizophrenia. This
 CC does not seem to be the case.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
 CC -----
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 CC -----
 DR EMBL: X53655; CAA37703.1; -
 DR EMBL: M37763; AAA59953.1; -
 DR EMBL: M61180; AAA63231.1; -
 DR PIR: JH0141; JH0141.
 DR PIR: A36208; A36208.
 DR PIR: S10719; S10719.
 DR PIR: C40304; C40304.
 DR PDB: 1BND; 04-APR-96.
 DR PDB: 1B8K; 09-FEB-99.

```

DR Genev: HGNC:8023: NTF3.
DR MIM: 162660: -.
DR InterPro: IPR002400: GF_cysknct.
DR InterPro: IPR002072: NGF.
DR Pfam: PF00243: NGF.1.
DR PRINTS: PR00438: GFCYSKNCT.
DR PRINTS: PR00268: NGF.
DR ProDom: PD002052: NGF.1.
DR SMART: SM00140: NGF.1.
DR PROSITE: PS00248: NGF_1; 1.
DR PROSITE: PS50270: NGF_2; 1.
DR Growth factor: Signal; Polymorphism: 3D-structure.
KW SIGNAL.
FT SIGNAL 1 16
FT PROPEP 17 138
FT CHAIN 139 257
FT DISULFID 152 217
FT DISULFID 195 246
FT DISULFID 205 248
FT CARBOHD 131 131
FT VARIANT 76 76
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT G->E.
FT /FTID-VAR.012084.
SQ SEQUENCE 257 AA: 29354 MW: 394583B3B25E03 CRC64:
Query Match 51.3%; Score 358; DB 1; Length 257;
Best Local Similarity 55.4%; Pred. No. 8.6e-28;
Matches 67; Conservative 18; Mismatches 28; Indels 8; Gaps 3;
OY 9 SRRGELAVCDVAGVTRRTAVDLRGREVEVLGEVPAAGSPPLRYOFFETRCKADNAEE 68
DB 144 SHRGELVCDSESLVMTWTKSSAIDIRGHQVTLGEI-KTNSPVPKQVETTRCK-----E 197
OY 69 GGGPAGGCGRGVDRRHVWSECKAKSYVRLTAAGRGVGMWRIRIDTACVCTLLSRFG 128
DB 198 ARPVK--NGCRIDDKHNNKSOCKTSQTVYRALTSNNKLVGMWRIRIDTSCVCLSRKIG 255
OY 129 R 129
DB 256 R 256

RESULT 9
NT3_MOUSE STANDARD: PRT: 258 AA.
ID NT3_MOUSE
AC P20181:
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (HDNF)
DE (Nerve growth factor 2) (NGF-2).
DE NTF3 OR NTF-3.
GN NTF3 OR NTF-3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90190865; PubMed=2314473;
RA Hohn A., Leebrock J., Bailey K., Barde Y.-A.;
RT Identification and characterization of a novel member of the nerve
RT growth factor/brain-derived neurotrophic factor family.*;
RL Nature 344:339-341(1990).
CC -1- FUNCTION: SEEMS TO PROMOTES THE SURVIVAL OF VISCERAL AND
CC PROPHODERPTIVE SENSOR NEURONS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: BRAIN AND PERIPHERAL TISSUES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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CC -----
CC EMBL: X53257; CA37348.1; -.
CC DR PIR: S09155; S09155.
CC DR HSSP: P20783; 1B8K.
CC DR MGd: MG1:97380; NTF3.
CC DR InterPro: IPR002400: GF_cysknct.
CC DR InterPro: IPR002072: NGF.
CC Pfam: PF00243: NGF.1.
CC PRINTS: PR00438: GFCYSKNCT.
CC PRINTS: PR00268: NGF.
CC ProDom: PD002052: NGF.1.
CC SMART: SM00140: NGF.1.
CC PROSITE: PS00248: NGF_1; 1.
CC PROSITE: PS50270: NGF_2; 1.
CC Growth factor: Signal.
KW SIGNAL.
FT SIGNAL 1 16
FT PROPEP 17 139
FT CHAIN 140 258
FT DISULFID 153 218
FT DISULFID 196 247
FT DISULFID 206 249
FT CARBOHD 131 131
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 258 AA: 29587 MW: 7180064E8A6E042 CRC64:
Query Match 51.3%; Score 358; DB 1; Length 258;
Best Local Similarity 55.4%; Pred. No. 8.6e-28;
Matches 67; Conservative 18; Mismatches 28; Indels 8; Gaps 3;
OY 9 SRRGELAVCDVAGVTRRTAVDLRGREVEVLGEVPAAGSPPLRYOFFETRCKADNAEE 68
DB 145 SHRGELVCDSESLVMTWTKSSAIDIRGHQVTLGEI-KTNSPVPKQVETTRCK-----E 198
OY 69 GGGPAGGCGRGVDRRHVWSECKAKSYVRLTAAGRGVGMWRIRIDTACVCTLLSRFG 128
DB 199 ARPVK--NGCRIDDKHNNKSOCKTSQTVYRALTSNNKLVGMWRIRIDTSCVCLSRKIG 256
OY 129 R 129
DB 257 R 257

RESULT 10
NT3_RAT STANDARD: PRT: 258 AA.
ID NT3_RAT
AC P18280:
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (HDNF)
DE (Nerve growth factor 2) (NGF-2).
DE NTF3 OR NTF-3.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90319130; PubMed=2164684;
RA Ernfors P., Ibanez C.F., Ebendal T., Olson L., Persson H.;
RT Molecular cloning and neurotrophic activities of a protein with
RT structural similarities to nerve growth factor: developmental and
RT topographical expression in the brain.*;
RL Proc. Natl. Acad. Sci. U.S.A. 87:5454-5458(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90208301; PubMed=2321006;
RA Maisonneville P.C., Belluscio L., Squinto S., Ip N.Y., Furch M.E.,
RA Lindsay R.M., Yancopoulos G.D.;
RT "Neurotrophin-3: a neurotrophic factor related to NGF and BDNF.*";
RL Science 247:1446-1451(1990).
RN [3]
RP SEQUENCE FROM N.A.

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RX MEDLINE-91365361: PubMed-1889806;
RA Maisompierre P.C., Le Beau M.M., Esplinoza R. III, IP N.Y.,
RA Belluscio L., de la Monte S.M., Squinto S., Furch M.E.,
RA Yancopoulos G.D.,
RA "Human and rat brain-derived neurotrophic factor and neurotrophin-3:
RT gene structures, distributions, and chromosomal localizations.",
RL Genomics 10:558-568(1991).
RN
RP [4]
RP SEQUENCE OF 195-237 FROM N.A.
RC STRAIN-Sprague-Dawley: TISSUE-liver;
RX MEDLINE-9122573: PubMed-205430;
RA Hallboeck F., Ibanez C.F., Persson H.,
RA "Evolutionary studies of the nerve growth factor family reveal a
RT novel member abundantly expressed in xenopus ovary.",
RL Neuron 6:845-858(1991).
CC -1- FUNCTION: SEEMS TO PROMOTES THE SURVIVAL OF VISCERAL AND
CC PROPRIOCEPTIVE SENSORY NEURONS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: BRAIN AND PERIPHERAL TISSUES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL: M34643; AAA4313.1; -
DR EMBL: M3368; AAA4172.1; -
DR EMBL: M61179; AAA63497.1; -
DR PIR: A35781; A35781.
DR PIR: A40094; A40094.
DR HSSP: P20783; 1B8K.
DR InterPro: IPR002400; GE_cysknot.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRODOM: PD00268; NGF.
DR PRODOM: PD002052; NGF; 1.
DR SMART: SM00140; NGF; 1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS50270; NGF_2; 1.
KM Growth factor: Signal.
KT Growth factor: Signal.
FT SIGNAL 1 16 POTENTIAL.
FT PROPEP 17 139
FT CHAIN 140 258 NEUROTROPHIN-3.
FT DISULFID 153 218 BY SIMILARITY.
FT DISULFID 195 247 BY SIMILARITY.
FT DISULFID 206 249 BY SIMILARITY.
FT CARBOHYD 131 131 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 258 AA; 29644 MW; 74D557CF8518A1CE CRC64;

Query Match 51.3%; Score 358; DB 1; Length 258;
Best Local Similarity 55.4%; Pred. No. 8.6e-28;
Matches 67; Conservative 18; Mismatches 28; Indels 8; Gaps 3;

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ID NT3_FELCA STANDARD: PRT; 257 AA.
AC 091512;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (HDMF)
DE (Nerve growth factor 2) (NGF-2).
GN NTFS.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxId=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20211727: PubMed-10745216;
RA Lein E.S., Hohn A., Shatz C.J.;
RT "Dynamic regulation of BDNF and NT-3 expression during visual system
RT development.";
RL J. Comp. Neurol. 420:1-18(2000).
CC -1- FUNCTION: SEEMS TO PROMOTES THE SURVIVAL OF VISCERAL AND
CC PROPRIOCEPTIVE SENSORY NEURONS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC -----
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CC or send an email to license@sdb-sdb.ch).
CC -----
DR EMBL: AF192538; AAF03424.1; -
DR HSSP: P20783; 1B8K.
DR InterPro: IPR002400; NGF.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF; 1.
DR PRINTS: PR00268; NGF.
DR PRODOM: PD002052; NGF; 1.
DR SMART: SM00140; NGF; 1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS50270; NGF_2; 1.
KM Growth factor: Signal.
FT SIGNAL 1 16 POTENTIAL.
FT PROPEP 17 138
FT CHAIN 139 257 NEUROTROPHIN-3.
FT DISULFID 152 217 BY SIMILARITY.
FT DISULFID 195 246 BY SIMILARITY.
FT DISULFID 205 248 BY SIMILARITY.
FT CARBOHYD 131 131 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 257 AA; 29403 MW; EB53FE59C5113E4 CRC64;

Query Match 51.0%; Score 356; DB 1; Length 257;
Best Local Similarity 54.5%; Pred. No. 1.3e-27;
Matches 66; Conservative 20; Mismatches 27; Indels 8; Gaps 3;

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01-NOV-1997 (Rel. 35, last sequence update)
 30-MAY-2000 (Rel. 39, last annotation update)
 Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (HNF) (Nerve growth factor 3) (NGF-2)
 Xenopus laevis (African clawed frog).
 Eukaryote; Metazoa; Chordata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodidae; Xenopus.
 NCBI_Taxid=8355;
 [1]
 SEQUENCE FROM N.A.
 TISSUE=Brain;
 MEDLINE=97252639; PubMed=9096131;
 Xie K., Wang T., Olafsson P., Mizuno K., Lu B.;
 "Activity-dependent expression of NT-3 in muscle cells in culture: implications in the development of neuromuscular junctions.";
 J. Neurosci. 17:2947-2958(1997).
 [2]
 SEQUENCE OF 197-217 FROM N.A.
 TISSUE=Liver;
 MEDLINE=9122573; PubMed=2035430;
 Hallboeck F., Ibanez C.F., Petsson H.;
 "Evolutionary studies of the nerve growth factor family reveal a novel member abundantly expressed in Xenopus ovary.";
 Neuron 6:845-858(1991).
 -1- FUNCTION: SEEMS TO PROMOTE THE SURVIVAL OF VISCERAL AND PROPRIOCEPTIVE SENSOR NEURONS.
 -1- SUBCELLULAR LOCATION: Secreted.
 -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.

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 EMBL: U27576; AB017723.1; -
 HSP: P20783; 188K.
 DR InterPro: IPR002400; GF_cysknoc.
 DR Pfam: PF00243; NGF. 1.
 DR PRINTS: PR00438; GFCSKNOT.
 DR PRODOM: PD002052; NGF. 1.
 DR SMART: SM00140; NGF. 1.
 DR PROSITE: PS00248; NGF_1; 1.
 DR PROSITE: PS0270; NGF_2; 1.
 KW Growth factor; Signal.
 FT SIGNAL 1 16 POTENTIAL.
 FT PROPEP 17 141 NEUROTROPHIN-3.
 FT CHAIN 142 260 BY SIMILARITY.
 FT DISULFID 155 220 BY SIMILARITY.
 FT DISULFID 198 249 BY SIMILARITY.
 FT DISULFID 208 251 BY SIMILARITY.
 FT CARBOHYD 114 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 260 AA; 30022 MW; FFB8507A5E8A93C5 CRC64;
 Query Match 50.9%; Score 355; DB 1; Length 260;
 Best Local Similarity 55.0%; Pred. No. 1,7e-27;
 Matches 66; Conservative 18; Mismatches 28; Indels 8; Gaps 3;
 Oy 11 RGEAVCDVAGSGVDRRTAVDLRGREVEVGEVPAAGSPLRQYFFETRCADNAEEGG 70
 Db 149 RGEISVDSSESLMTDKMAIDIRGHVTVLGEI-KTGNSPVKQYFFETRCCK-----EAR 202
 Oy 71 PGAGGGCGRCVDRRHVYSECKAKOSYVRLTAHAGRGVGMIRIDTACVCTLIISRTGRA 130
 Db 203 PVK--NGCRGIDDKHNSQCKTSQTVYRALTSENNKAVGMIRIDISCVCAISRKIGRS 260
 RESULT 13

BDNF_CAVPO STANDARD; PRT; 255 AA.
 ID BDNF_CAVPO
 AC 070183;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, last sequence update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE Brain-derived neurotrophic factor precursor (BDNF).
 GN BDNF.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryote; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hysticognathi; Cavidae; Cavia.
 OX NCBI_Taxid=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Hartley white; TISSUE=Liver;
 RA Inoue N., Nakayama C., Nozuchi H.;
 Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RL FUNCTION: PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS THAT ARE ALL LOCATED EITHER IN THE CENTRAL NERVOUS SYSTEM OR DIRECTLY CONNECTED TO IT (BY SIMILARITY).
 CC -1- LOCATED TO IT (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.

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 EMBL: AB012097; BAA25176.1; -
 HSP: P23560; 188M.
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF. 1.
 DR PRINTS: PR00268; NGF. 1.
 DR PRODOM: PD002052; NGF. 1.
 DR SMART: SM00140; NGF. 1.
 DR PROSITE: PS00248; NGF_1; 1.
 DR PROSITE: PS0270; NGF_2; 1.
 KW Growth factor; Signal.
 FT SIGNAL 1 18 POTENTIAL.
 FT PROPEP 19 135 BY SIMILARITY.
 FT CHAIN 137 255 BRAIN-DERIVED NEUROTROPHIC FACTOR.
 FT SITE 57 58 CLEAVAGE (BY SIP) (BY SIMILARITY).
 FT DISULFID 149 216 BY SIMILARITY.
 FT DISULFID 194 245 BY SIMILARITY.
 FT DISULFID 204 247 BY SIMILARITY.
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 255 AA; 28308 MW; BA95BA3EBB88FA04 CRC64;
 Query Match 49.6%; Score 346; DB 1; Length 255;
 Best Local Similarity 54.5%; Pred. No. 1,2e-26;
 Matches 67; Conservative 21; Mismatches 25; Indels 10; Gaps 3;
 Oy 9 SRRGELAVCDVAGSGVDRRTAVDLRGREVEVGEVPAAGSPLRQYFFETRCADNA 66
 Db 141 ARRGELSVCDVSSESLMTDKMAIDIRGHVTVLGEI-KTGNSPVKQYFFETRCCK--- 196
 Oy 67 EBGPGAGGCGRCVDRRHVYSECKAKOSYVRLTAHAGRGVGMIRIDTACVCTLIIS 126
 Db 197 ---MGTRGRCGRIDKRNHNSQCKTSQTVYRALTSENNKAVGMIRIDISCVCTLI 252
 Oy 127 TGR 129
 Db 253 RGR 255
 RESULT 14
 BDNF_HUMAN STANDARD; PRT; 247 AA.
 ID BDNF_HUMAN
 AC P23560; Q9UC24; Q9BY17;
 DT 01-NOV-1991 (Rel. 20, Created)

Db 245 RGR 247

Job time : 5.33411 secs

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RESULT 15
ID BDNF_PROLO STANDARD: PRT: 247 AA.
AC 018735;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Brain-derived neurotrophic factor precursor (BDNF).
OS BDNF.
OS Precyon 10tor (Raccoon).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Procyonidae; Procyon.
OX NCBI_TaxID=9654;
RN 11
RP SEQUENCE FROM N.A.
RA Lm F.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS THAT ARE
CC ALL LOCATED EITHER IN THE CENTRAL NERVOUS SYSTEM OR DIRECTLY
CC CONNECTED TO IT (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL: AF003188; AAB71654.1; -.
DR HSSP: P23560; 188M.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF; 1.
DR PRINTS: PR00268; NGF.
DR PRODOM: PD002052; NGF; 1.
DR SMART: SM00140; NGF; 1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS50270; NGF_2; 1.
KW Growth factor; Signal.
FT SIGNAL 1 18
FT PROPEP 19 128 POTENTIAL.
FT CHAIN 129 247 BY SIMILARITY.
FT SITE 57 58 BRAIN-DERIVED NEUROTROPHIC FACTOR.
FT DISULFID 141 208 CLEAVAGE (BY SLP) (BY SIMILARITY).
FT DISULFID 186 237 BY SIMILARITY.
FT DISULFID 196 239 BY SIMILARITY.
FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SQUENCE 247 AA: 27834 MW: 58377E4FE1F52A0 CRC64;

Query Match 49.4%; Score 345; DB 1; Length 247;
Best Local Similarity 53.7%; Pred. No. 1.5e-26;
Matches 66; Conservative 22; Mismatches 25; Indels 10; Gaps 3;

OY 9 SRGELAVCDVAGVWT--DRRTAVDLGRREVVLGEVPAAGSPLRQYFEETCKADNA 66
Db 133 ARRGELSTVCSISEMTADKKTAVDMGSGVTVLEKVPVSKGQ-LKQYFEETKCNP--- 188
OY 67 EEGGPAAGGCGCGVDRRHVWSECKAKOSYVRLTAHAGRGVGRKIRIDTACVCTILSR 126
Db 189 ---MGYTEGCGKIDKRMNSQCRSTOSYVRALTMDSKRIGKRIIDTSCVCTILTK 244
OY 127 TGR 129
Db 245 RGR 247
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Search completed: December 2, 2002, 15:12:44

GenCore version 5.1.3
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OM protein - protein search, using SW model

Run on: December 2, 2002, 15:05:42 : Search time 20.1172 seconds
(without alignments)
1331.501 Million cell updates/sec

Title: US-10-072-681-6
Perfect score: 698
Sequence: 1 GVSEFAPASRNGELAVCDV.....RWIRDPACVCTILSRGTA 130

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL.21:*
1: SP_Archaea:*
2: SP_Bacteria:*
3: SP_Fungi:*
4: SP_Human:*
5: SP_Invertebrate:*
6: SP_Mammal:*
7: SP_mhc:*
8: SP_Organelle:*
9: SP_Phage:*
10: SP_Plant:*
11: SP_Protozoa:*
12: SP_Virus:*
13: SP_Vertebrate:*
14: SP_Unclassified:*
15: SP_Virus:*
16: SP_Bacteriophage:*
17: SP_Archaea:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	345	49.4	153	11	09CYL3 mus musculus
2	345	49.4	247	6	097759 allurus ful
3	345	49.4	249	11	09VH14 mus musculus
4	336	48.1	177	13	0918L2 poephila gu
5	334	47.9	246	13	080674 cyclophlops
6	332	47.6	246	13	080675 phrynosoma
7	328	47.0	246	13	080676 leptaia sp
8	327	46.8	270	13	09VH42 brachydania
9	323.5	46.3	324	13	09VH95 lampetra fl
10	322	46.1	241	6	09N182 macaca fusc
11	317.5	45.5	247	13	080677 cytotriclo
12	297.5	42.6	241	4	09P208 homo sapien
13	297.5	42.6	241	4	09P208 homo sapien
14	297.5	42.6	241	4	09P208 homo sapien
15	297.5	42.6	241	6	09N2P1 pan troglod
16	297.5	42.6	241	6	09N2P0 gorilla gor

17	297.5	42.6	241	6	09N2E9	09n2e9 pongo pygma
18	296	42.4	101	6	09T222	09t222 macaca fusc
19	277.5	39.8	294	11	091XB4	091xb4 mus musculu
20	266.5	38.2	217	6	09N1B3	09n1b3 macaca fusc
21	265.5	38.0	241	13	090W38	090w38 bothrops ja
22	262.5	37.6	241	13	090E29	090e29 croceatus du
23	228.5	32.7	286	13	091988	091988 xiphophorus
24	216	30.9	85	6	002792	002792 notoryctes
25	215	30.9	87	4	09P224	09p224 homo sapien
26	213	30.2	85	6	013114	013114 leiodon mac
27	213	30.5	85	6	013122	013122 latipus ro
28	213	30.5	85	6	002795	002795 ornithorhyn
29	213	30.5	85	6	002798	002798 pelaeus br
30	213	30.5	85	6	013104	013104 cercartacus
31	213	30.5	85	6	002790	002790 macropus fu
32	213	30.5	85	6	013105	013105 daayuroides
33	213	30.5	85	6	002801	002801 techylosasu
34	212.5	30.4	87	6	09TMC3	09tmc3 cervus elap
35	212	30.4	85	6	002803	002803 trichosurus
36	178	25.5	186	12	09J5D9	09j5d9 fowlipox vir
37	162	23.2	185	6	09BFK7	09bfk7 erinaceus c
38	162	23.2	185	6	09BFK0	09bfk0 chetophrac
39	160	22.9	185	11	099WV9	099wv9 pedetes cap
40	159	22.8	184	6	09BRJ5	09brj5 tupia alai
41	159	22.8	185	6	09BRK5	09brk5 condylura c
42	159	22.8	185	6	09BRK5	09brk5 condylura c
43	159	22.8	186	6	09BFJ3	09bfj3 choleopus d
44	159	22.8	186	6	09BFJ2	09bfj2 choleopus d
45	159	22.8	186	6	09BFK9	09bfk9 tamandua te

ALIGNMENTS

RESULT 1
ID 09CYL3 PRELIMINARY: PRT; 153 AA.
AC 09CYL3;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Brain derived neurotrophic factor.
GN BDNF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid-10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRIO;
RX MEDLINE=21083660; PUBMED=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochila H.,
RA Ruch P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quakebush J.,
RA Schirai L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Kono H., Baldarelli R., Barch G.,
RA Blake J., Boileil D., Bojunga N., Carninci P., de Bonaldo K.F.,
RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch R.-F.,
RA Suzuki H., Toyo-oka K., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK017559; BAB30805.1; -
HSSP; P23560; 1B8M.

OY 127 TGR 129
DB 244 RGR 246

RESULT 8

OYH42 PRELIMINARY; PRT: 270 AA.

AC OYH42: 01-MAY-1999 (TREMblrel. 10, Created)

DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)

DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)

DE Brain-derived neurotrophic factor.

OS Brachydanio rerio (zebrafish) (zebra danio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

NCBI_TaxID=7955;

SEQUENCE FROM N.A.

RA Hashimoto H., Heinrich G.;

RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.

DR HSSP: U42489; AAD00016.1; -

DR HSSP: P23560; 188M.

DR 2FIN: 2DB-GENE-000412-1; bdnf.

DR InterPro: IPR002072; NGF.

DR Pfam: PF00243; NGF.1.

DR PRINTS: PR00268; NGF.

DR PRODOM: PD002052; NGF.1.

DR SMART: SM00248; NGF_1; 1.

DR PROSITE: PS00270; NGF_2; 1.

SEQUENCE 270 AA; 29482 MW; 6BF136101B4E45C0 CRC64;

Query Match

Best Local Similarity 46.8%; Score 327; DB 13; Length 270;

Matches 62; Conservative 25; Mismatches 26; Indels 10; Gaps 3;

OY 9 SRGELAVCDVAVSGVT--DRTAVDLGRREVVLGEVPAAGSSPLRQFFETRCADNA 66

DB 156 ARWGEISVCDISISOMVTAVDKRTAIDMSGOTVLEKVPYVNGO-LKQYETKCRNP--- 211

OY 67 EEGCGAGGCGRGVDRHWHVSECKAKOSYVRALTAAGCRWRIRDTACVLTSLR 126

DB 212 ----LGYTEGCGKIDKRNHNSGCTTTSYVRALTNKSKRIGRIRITDSCVLTITK 267

OY 127 TGR 129

DB 268 RGR 270

RESULT 9

OYH95 PRELIMINARY; PRT: 324 AA.

AC OYH95: 01-NOV-1999 (TREMblrel. 12, Created)

DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)

DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)

DE Neurotrophin.

GN NTL.

OS Lampetra fluviatilis (River lamprey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;

OC Petromyzontiformes; Petromyzontidae; Lampetra.

NCBI_TaxID=7748;

SEQUENCE FROM N.A.

RA TISSUE=LIVER;

RX MEDLINE=99003404; PubMed=9786977;

RT "Lampetra fluviatilis neurotrophin homolog, descendant of a

neurotrophin ancestor, discloses the early molecular evolution of

neurotrophins in the vertebrate subphylum."

RL J. Neurosci. 18:8700-8711(1998).

DR EMBL: AF071432; AAD22744.1; -.

DR HSSP: P20783; 188K.

DR InterPro: IPR002072; NGF.

DR Pfam: PF00243; NGF.1.

DR PRODOM: PD002052; NGF.1.

DR SMART: SM00140; NGF.1.

DR PROSITE: PS50270; NGF_2; 1.

CHAIN 141 324

SEQUENCE 324 AA; 35267 MW; 9D6B56C1978F8485 CRC64;

Query Match

Best Local Similarity 46.3%; Score 323.5; DB 13; Length 324;

Matches 69; Conservative 14; Mismatches 41; Indels 31; Gaps 4;

OY 7 PASR--RGELAVCDVAVSGVTRTAVDLGRREVVLGEVPAAGS----- 50

DB 170 PSRRPRHGEVPAAGSSRRVSDRDYAFDTGWRVRLGELSLSSSSSSSSSSSQS 229

OY 51 --PLRQFFETRCADNAEEG-----GCGAG-CGCGRGVDRHWHVSECKAKOS 95

DB 230 STSVKQFFETRCADNAEEG-----GCGAG-CGCGRGVDRHWHVSECKAKOS 289

OY 96 YVRALTAAGCRWRIRDTACVLTSLRGA 130

DB 290 FVRALTEADAGRILAWRMIRLDTACVLTSLRGGCA 324

RESULT 10

OYH82 PRELIMINARY; PRT: 241 AA.

AC OYH82: 01-OCT-2000 (TREMblrel. 15, Created)

DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)

DE Neurotrophin-3 (Fragment).

OS Macaca fasciata (Japanese macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecoidea; Macaca.

NCBI_TaxID=9542;

SEQUENCE FROM N.A.

RA TISSUE=BLOOD;

RX MEDLINE=99270338; PubMed=10340513;

RA Okuno H., Tokuyama W., Li Y.X., Hashimoto T., Miyashita Y.;

RT "Quantitative evaluation of neurotrophin and trk mRNA expression in

visual and limbic areas along the occipito-temporo-hippocampal pathway

in adult macaque monkeys."

RT J. Comp. Neurol. 408:378-398(1999).

GN [2]

OS TISSUE=BLOOD;

RA Hashimoto T., Okuno H., Tokuyama W., Li Y.X., Miyashita Y.;

RT "Expression of brain-derived neurotrophic factor, neurotrophin-3 and

their receptor messenger RNAs in monkey rhinal cortex."

RL Neurosci. 0:0-0(2000)

DR EMBL: AF22683; AAF33791.1; -.

DR HSSP: P20783; 188K.

DR InterPro: IPR002072; NGF.

DR Pfam: PF00243; NGF.1.

DR PRINTS: PR00268; NGF.

DR PRODOM: PD002052; NGF.1.

DR SMART: SM00248; NGF.1.

DR PROSITE: PS50270; NGF_2; 1.

FT NON_TER 1 1

FT TER 241 241

SEQUENCE 241 AA; 27803 MW; AB95E457C7B07113 CRC64;

Query Match

Best Local Similarity 46.1%; Score 322; DB 6; Length 241;

Matches 61; Conservative 16; Mismatches 24; Indels 8; Gaps 3;

OY 9 SRBELAYCDVAGWTDRTAVDLRGREVEVLGEVPAAGSPLRQYFEETRCKADNAEE 68
 DB 141 SRBELAYCDVAGWTDRTAVDLRGREVEVLGEVPAAGSPLRQYFEETRCKADNAEE 194
 OY 69 GGRGAGGCGGCGVDRRRHMYSECKAKOSYVALTAHAGRGVNRIRIDT 117
 DB 195 ARPK--NGCRGIDDKHNSOCTKTSOTYVALTSENKLVGMRIRIDT 241

RESULT 11

OY 08G677 PRELIMINARY: PRT: 247 AA.
 AC 08G677: 01-JUN-2002 (TREMblrel. 21, Created)
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
 DE 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DB Brain derived neurotrophic factor.
 OS Tylocotilion taliaensis.
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Caudata; Salamandridae; Salamandridae;
 CC Tylocotilion.
 CC NCBI_TaxID=129885;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cao M., Yang Y.H., Zhang Y.Z.:
 RT Cloning and sequence analysis of brain derived neurotrophic factor
 RT (BDNF) gene from Sichuan Newt (Tylocotilion taliaensis).
 RL Yang Yung Yu Huan Ching Sheng Wu Hsueh Pao 8:0-012002).
 DR EMBL: AF97712; AAM18078.1;
 SO SEQUENCE 247 AA; 27841 MW; FFCB5F28A7620DED CRC64;

Query Match 45.58; Score 317.5; DB 13; Length 247;
 Best Local Similarity 51.28; Pred. No. 1.2e-23;
 Matches 63; Conservative 23; Mismatches 23; Indels 11; Gaps 4;

OY 5 TAPASRGLAYCDVAGWTDRTAVDLRGREVEVLGEVPAAGSPLRQYFEETRCK 62
 DB 130 SGPA-RBELAYCDVAGWTDRTAVDLRGREVEVLGEVPAAGSPLRQYFEETRCK 185
 OY 63 ADNAEEGCGGCGVDRRRHMYSECKAKOSYVALTAHAGRGVNRIRIDTACT 122
 DB 186 -----RRPMGIMKDGCKIDKRTMSOCTKTSOTYVALTSENKLVGMRIRIDTACT 240
 OY 123 LLSRTGR 129
 DB 241 LTKRGR 247

RESULT 12

OY 09P208 PRELIMINARY: PRT: 241 AA.
 AC 09P208: 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DB Beta-nerve growth factor (Fragment).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kilano T., Kobayakawa H., Saltou N.:
 RT "Silver Project."
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBD databases.
 DR EMBL: AB017517; BA090437.1;
 DR HSSP: P01135; 1BET.
 DR InterPro: IPR02072; NCF.
 DR Pfam: PF00243; NCF. 1.
 DR PRINTS: PR00268; NCF.
 DR ProDom: PD002052; NCF. 1.

DR SMART: SM00140; NCF. 1.
 DR PROSITE: PS00248; NCF_1; 1.
 DR PROSITE: PS0270; NCF_2; 1.
 FT MONTER 241 241
 SO SEQUENCE 241 AA; 26998 MW; D531ED825D96C14 CRC64;

Query Match 42.68; Score 297.5; DB 4; Length 241;
 Best Local Similarity 46.58; Pred. No. 1.1e-21;
 Matches 59; Conservative 20; Mismatches 39; Indels 9; Gaps 3;

OY 3 SETAPASRGLAYCDVAGWTDRTAVDLRGREVEVLGEVPAAGSPLRQYFEETRCK 62
 DB 122 SSSHPFIRHGEFVCDVSVVGGDKTATDICKREYVNLGEV-NINVSFKQYFEETRCK 180
 OY 63 ADNAEEGCGGCGVDRRRHMYSECKAKOSYVALTAHAGRGVNRIRIDTACT 122
 DB 181 DPNPVD-----SGCRGIDSKHNSICTTTHFVALTMCK-QAAMFIRIDTACTV 232
 OY 123 LLSRTGR 129
 DB 233 LSKAVR 239

RESULT 13

OY 09P60 PRELIMINARY: PRT: 241 AA.
 AC 09P60: 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DB Nerve growth factor beta.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Zhang B., Zhou Y., Peng X., Yuan J., Qiang B.:
 RT Submitted (AUG-2001) to the EMBL/GenBank/DBD databases.
 RL EMBL: AF411526; AA05874.1;
 DR InterPro: IPR02072; NCF.
 DR Pfam: PF00243; NCF. 1.
 DR ProDom: PD002052; NCF. 1.
 DR PROSITE: PS00248; NCF_1; UNKNOWN_1.
 DR PROSITE: PS0270; NCF_2; 1.
 SO SEQUENCE 241 AA; 26964 MW; 745216485C21E558 CRC64;

Query Match 42.68; Score 297.5; DB 4; Length 241;
 Best Local Similarity 45.78; Pred. No. 1.1e-21;
 Matches 58; Conservative 22; Mismatches 38; Indels 9; Gaps 3;

OY 3 SETAPASRGLAYCDVAGWTDRTAVDLRGREVEVLGEVPAAGSPLRQYFEETRCK 62
 DB 122 SSSHPFIRHGEFVCDVSVVGGDKTATDICKREYVNLGEV-SINVSFKQYFEETRCK 180
 OY 63 ADNAEEGCGGCGVDRRRHMYSECKAKOSYVALTAHAGRGVNRIRIDTACT 122
 DB 181 DPNPVD-----SGCRGIDSKHNSICTTTHFVALTMCK-QAAMFIRIDTACTV 232
 OY 123 LLSRTGR 129
 DB 233 LSKAVR 239

RESULT 14

OY 09UKL8 PRELIMINARY: PRT: 241 AA.
 AC 09UKL8: 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DB Nerve growth factor B.

GN NGFB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9256269; PubMed=10322959;
RA Tong Y., Wang H., Chen M.;
RT cloning and sequencing of the gene for premature beta nerve growth
RL factor. J
RN Chung Kuo Ying Yung Sheng Li Hsueh Tsa Chih 13:316-318(1997).
[2]
RP SEQUENCE FROM N.A.
RA Tong Y., Wang H.;
RL Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF150960; AAD55975.1; -.
DR HSSP: P01139; 1BET.
DR InterPro: IPR002072; NGF.
DR Pfam: PFD0243; NGF_1.
DR PRINTS: PR00268; NGF.
DR PRODom: PDD02052; NGF_1.
DR SMART: SM00140; NGF_1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS02070; NGF_2; 1.
SO SEQUENCE 241 AA: 26959 MW: 6190FC65B3BD671 CRC64;

[illegible]

SQ	SEQUENCE	241 AA:	26868 MW:	B39FAA8912C0A0B CRC64:
Oy	Query Match Best Local Similarity	42.6% 46.5%	Score 297.5: Pred. No.	DB 6: 1.1e-21:
	Matches	59;	Conservative	20; Mismatches 39; Indels 9; Gaps 3.
Oy	3	SETPASRGRELAVCDVAGSMWTDRTAYDLDLGREVEYLCEVPAGSGSPLEPoyFEETRCK	62	
Dd	122	SSSHPIHRIREFSVSDSYVMGDKTTADTKIDIKGEYMLGVEF-NINNSVFQFFETFKR	160	
Oy	63	ADNAEEGGPGAGGGCGCYDRRRHYEBCANOSYSRYALTAHGCRGRMYIRITACTCT	122	
Dd	181	DPNPVD-----SCKGIDISKHMINSYCITTTFVALTMOCK-QAAARFTRIDTACVCY	232	
Oy	123	LLSRTGR	129	
Dd	233	LSRKAVR	239	

Search completed: December 2, 2002, 15:12:03
Job time : 21.1172 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 2, 2002, 15:05:42 : Search time 8.99179 Seconds
(without alignments)
425.386 Million cell updates/sec

Title: US-10-072-681-6

Perfect score: 698

Sequence: 1 GVSETAPASRGELAVCAV.....RMIRIDPACVCTLSRTGRA 130

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued: Patents_AA:*
1: /cgn2_6/prodata1/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata1/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata1/1aa/6A.COMB.pep:*
4: /cgn2_6/prodata1/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/prodata1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	698	100.0	130	3	US-08-970-865-6
2	698	100.0	130	3	US-08-581-662-1
3	698	100.0	130	4	US-09-363-573-6
4	698	100.0	130	4	US-09-675-503-6
5	698	100.0	130	4	US-09-664-293-1
6	689	98.7	130	1	US-08-440-049-5
7	689	98.7	130	2	US-08-441-513A-5
8	689	98.7	130	5	PCT-US95-06918-6
9	689	98.7	130	5	PCT-US91-06950-2
10	689	98.7	168	2	US-08-424-826A-6
11	689	98.7	168	3	US-08-928-694-6
12	689	98.7	168	5	PCT-US91-06950-6
13	689	98.7	210	1	US-08-451-947-2
14	689	98.7	210	2	US-08-424-826A-2
15	689	98.7	210	3	US-08-928-694-2
16	689	98.7	210	5	PCT-US91-06950-2
17	689	98.7	215	1	US-07-796-106-23
18	689	98.7	130	1	US-08-451-947-62
19	689	98.7	130	1	US-08-451-947-68
20	689	98.7	130	2	US-08-424-826A-62
21	689	98.7	130	2	US-08-424-826A-68
22	689	98.7	130	3	US-08-928-694-62
23	689	98.7	130	3	US-08-928-694-68
24	689	98.7	130	5	PCT-US91-06950-62
25	689	98.7	130	5	PCT-US91-06950-68
26	689	98.0	130	1	US-08-451-947-22
27	689	98.0	130	1	US-08-451-947-59

28	684	98.0	130	1	US-08-451-947-61	Sequence 61, Appl
29	684	98.0	130	1	US-08-451-947-63	Sequence 63, Appl
30	684	98.0	130	1	US-08-451-947-64	Sequence 64, Appl
31	684	98.0	130	1	US-08-451-947-69	Sequence 69, Appl
32	684	98.0	130	2	US-08-424-826A-22	Sequence 22, Appl
33	684	98.0	130	2	US-08-424-826A-59	Sequence 59, Appl
34	684	98.0	130	2	US-08-424-826A-61	Sequence 61, Appl
35	684	98.0	130	2	US-08-424-826A-63	Sequence 63, Appl
36	684	98.0	130	2	US-08-424-826A-64	Sequence 64, Appl
37	684	98.0	130	2	US-08-424-826A-69	Sequence 69, Appl
38	684	98.0	130	3	US-08-928-694-22	Sequence 22, Appl
39	684	98.0	130	3	US-08-928-694-59	Sequence 59, Appl
40	684	98.0	130	3	US-08-928-694-61	Sequence 61, Appl
41	684	98.0	130	3	US-08-928-694-63	Sequence 63, Appl
42	684	98.0	130	3	US-08-928-694-64	Sequence 64, Appl
43	684	98.0	130	3	US-08-928-694-69	Sequence 69, Appl
44	684	98.0	130	5	PCT-US91-06950-22	Sequence 22, Appl
45	684	98.0	130	5	PCT-US91-06950-59	Sequence 59, Appl

ALIGNMENTS

RESULT 1
US-08-970-865-6
Sequence 6, Application US/08970865
Patent No. 6005081
GENERAL INFORMATION:
APPLICANT: Louis E. Burton, Charles H. Schmelzer, Joanne T. Beck
TITLE OF INVENTION: Purification of NGR
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/970, 865
FILING DATE: 14-NO. 6005081-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030838
FILING DATE: 11/15/1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047855
FILING DATE: 5/29/1997
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P106362
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-970-865-6
Query Match 100.0%, Score 698, DB 3, Length 130:
Best Local Similarity 100.0%, Pred. No. 5, 2e-73:
Matches 130, Conservative 0, Mismatches 0, Indels 0, Gaps 0:
1 GVSETAPASRGELAVCAVDRRAVDLRGVEVGEVPAAGSPFLROYFEETR 60
|||||

Db 1 GVSETAPASRGEALVCDVAVSGWYTDRTAVDLRGREVEVLGEVPAAGSPLRQYFFETR 60
QY 61 CKADNAEEGPGAGGGCGVDRRHVSECKAKOSYVALTAHACRGVGMIRIDTACY 120
Db 61 CKADNAEEGPGAGGGCGVDRRHVSECKAKOSYVALTAHACRGVGMIRIDTACY 120
QY 121 CTLISRTGRA 130
Db 121 CTLISRTGRA 130

RESULT 2

US-08-581-662-1
Sequence 1, Application US/08581662
Patent No. 6121235
GENERAL INFORMATION:
APPLICANT: Geo. Wei-Qiang
TITLE OF INVENTION: Treatment of Balance Impairments
FILE REFERENCE: P0981
CURRENT APPLICATION NUMBER: US/08/581,662
CURRENT FILING DATE: 1995-12-29
NUMBER OF SEQ ID NOS: 36
SEQ ID NO 1
LENGTH: 130
TYPE: PRT
ORGANISM: Homo sapiens
US-08-581-662-1

Query Match

100.0%; Score 698; DB 3; Length 130;
Best Local Similarity 100.0%; Pred. No. 5,2e-73;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVSETAPASRGEALVCDVAVSGWYTDRTAVDLRGREVEVLGEVPAAGSPLRQYFFETR 60
Db 1 GVSETAPASRGEALVCDVAVSGWYTDRTAVDLRGREVEVLGEVPAAGSPLRQYFFETR 60
QY 61 CKADNAEEGPGAGGGCGVDRRHVSECKAKOSYVALTAHACRGVGMIRIDTACY 120
Db 61 CKADNAEEGPGAGGGCGVDRRHVSECKAKOSYVALTAHACRGVGMIRIDTACY 120
QY 121 CTLISRTGRA 130
Db 121 CTLISRTGRA 130

RESULT 3

US-09-363-573-6
Sequence 6, Application US/09363573
Patent No. 6184360

GENERAL INFORMATION:
APPLICANT: Louis E. Burton, Charles H. Schmelzer, Joanne T. Beck

TITLE OF INVENTION: Purification of NCF

NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: WinPatln (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/363,573

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/970,865

FILING DATE: 14-NO. 6184360-1997

APPLICATION NUMBER: 60/030838

FILING DATE: 11/15/1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047855
FILING DATE: 5/29/1997
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1063R2
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-363-573-6

Query Match

100.0%; Score 698; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 5,2e-73;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVSETAPASRGEALVCDVAVSGWYTDRTAVDLRGREVEVLGEVPAAGSPLRQYFFETR 60
Db 1 GVSETAPASRGEALVCDVAVSGWYTDRTAVDLRGREVEVLGEVPAAGSPLRQYFFETR 60
QY 61 CKADNAEEGPGAGGGCGVDRRHVSECKAKOSYVALTAHACRGVGMIRIDTACY 120
Db 61 CKADNAEEGPGAGGGCGVDRRHVSECKAKOSYVALTAHACRGVGMIRIDTACY 120
QY 121 CTLISRTGRA 130
Db 121 CTLISRTGRA 130

RESULT 4

US-09-675-503-6
Sequence 6, Application US/09675503
Patent No. 6423831

GENERAL INFORMATION:

APPLICANT: Burton, Louis E.

APPLICANT: Beck, Joanne T.

TITLE OF INVENTION: ISOLATION OF NEUROTROPHINS FROM A

TITLE OF INVENTION: MIXTURE CONTAINING OTHER PROTEINS AND NEUROTROPHIN VARIANTS

FILE REFERENCE: GENENT 03/02

CURRENT APPLICATION NUMBER: US/09/675,503

PRIOR FILING DATE: 2000-09-29

PRIOR APPLICATION NUMBER: 60/030838

PRIOR FILING DATE: 1996-11-15

PRIOR APPLICATION NUMBER: 60/047855

PRIOR FILING DATE: 1997-05-29

PRIOR APPLICATION NUMBER: 08/970865

PRIOR FILING DATE: 1997-11-14

PRIOR APPLICATION NUMBER: 09/363573

PRIOR FILING DATE: 1999-07-29

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 6

LENGTH: 130

TYPE: PRT

ORGANISM: Homo sapien

US-09-675-503-6

Query Match

100.0%; Score 698; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 5,2e-73;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVSETAPASRGEALVCDVAVSGWYTDRTAVDLRGREVEVLGEVPAAGSPLRQYFFETR 60
Db 1 GVSETAPASRGEALVCDVAVSGWYTDRTAVDLRGREVEVLGEVPAAGSPLRQYFFETR 60

OY 61 CKADNAEBCGPGAGCGCGVDRRHVSECKAKOSYVRLTAHAOGVGRMIRIDTACY 120
|||||
DB 61 CKADNAEBCGPGAGCGCGVDRRHVSECKAKOSYVRLTAHAOGVGRMIRIDTACY 120
OY 121 CTLISRTGRA 130
|||||
DB 121 CTLISRTGRA 130

RESULT 5

US-09-664-295-1
; Sequence 1, Application US/09664295
; Patent No. 6429196
; GENERAL INFORMATION:
; APPLICANT: Gao, Wei-Oiang
; TITLE OF INVENTION: Treatment of Balance Impairments
; FILE REFERENCE: GENENT.051C1
; CURRENT APPLICATION NUMBER: US/09/664,295
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 08/581,662
; PRIOR FILING DATE: 1995-12-29
; NUMBER OF SEQ ID NOS: 37
; SEQ ID NO 1
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-664-295-1

Query Match 100.0%; Score 698; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 5.2e-73;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GVSETAPASRGELAVCDVSGWTDRTAVDLRGREVLGEPVPAAGSPLRQFFETR 60
|||||
DB 1 GVSETAPASRGELAVCDVSGWTDRTAVDLRGREVLGEPVPAAGSPLRQFFETR 60
OY 61 CKADNAEBCGPGAGCGCGVDRRHVSECKAKOSYVRLTAHAOGVGRMIRIDTACY 120
|||||
DB 61 CKADNAEBCGPGAGCGCGVDRRHVSECKAKOSYVRLTAHAOGVGRMIRIDTACY 120
OY 121 CTLISRTGRA 130
|||||
DB 121 CTLISRTGRA 130

RESULT 6

US-08-440-049-5
; Sequence 5, Application US/08440049
; Patent No. 5728803
; GENERAL INFORMATION:

; APPLICANT: Uffer, Roman
; APPLICANT: Presta, Leonard G.
; APPLICANT: Winslow, John W.
; TITLE OF INVENTION: PANROTROPIC NEUROTROPIC FACTORS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,049
; FILING DATE: 12-May-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/253937

; FILING DATE: 03-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P0905C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8674
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-440-049-5

Query Match 98.7%; Score 689; DB 1; Length 130;
Best Local Similarity 99.2%; Pred. No. 5.7e-72;
Matches 129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GVSETAPASRGELAVCDVSGWTDRTAVDLRGREVLGEPVPAAGSPLRQFFETR 60
|||||
DB 1 GVSETAPASRGELAVCDVSGWTDRTAVDLRGREVLGEPVPAAGSPLRQFFETR 60
OY 61 CKADNAEBCGPGAGCGCGVDRRHVSECKAKOSYVRLTAHAOGVGRMIRIDTACY 120
|||||
DB 61 CKADNAEBCGPGAGCGCGVDRRHVSECKAKOSYVRLTAHAOGVGRMIRIDTACY 120
OY 121 CTLISRTGRA 130
|||||
DB 121 CTLISRTGRA 130

RESULT 7

US-08-441-513A-5
; Sequence 5, Application US/08441513A
; Patent No. 5981480
; GENERAL INFORMATION:

; APPLICANT: Uffer, Roman
; APPLICANT: Presta, Leonard G.
; APPLICANT: Winslow, John W.
; TITLE OF INVENTION: Panrotropic Neurotrophic Factors
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,513A
; FILING DATE: 15-May-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/253937
; FILING DATE: 03-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, P.D., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P0905C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: Amino Acid

TOPOLOGY: Linear
US-08-441-513A-5

Query Match 98.7%: Score 689; DB 2; Length 130;
Best Local Similarity 99.2%: Pred. No. 5.7e-72;
Matches 129: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVSETAPASRRGELAVCDVSGWYTDRTAVDLRGREVEVLGEVPAAGSPLROYFEETR 60
DB 1 GVSETAPASRRGELAVCDVSGWYTDRTAVDLRGREVEVLGEVPAAGSPLROYFEETR 60
QY 61 CADNAEEGGPGAGGCGRGVDRRHMYSECKAKOSYVRALTAAHAGRVGMWRIRIDTACV 120
DB 61 CADNAEEGGPGAGGCGRGVDRRHMYSECKAKOSYVRALTAAHAGRVGMWRIRIDTACV 120
QY 121 CTLLSRTGRA 130
DB 121 CTLLSRTGRA 130

RESULT 8

PCT-US95-06918-6
Sequence 6, Application PC/TUS9506918
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: PANTROPIC NEUTROTROPHIC FACTORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: peltin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06918
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 905PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US95-06918-6

Query Match 98.7%: Score 689; DB 5; Length 130;
Best Local Similarity 99.2%: Pred. No. 5.7e-72;
Matches 129: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVSETAPASRRGELAVCDVSGWYTDRTAVDLRGREVEVLGEVPAAGSPLROYFEETR 60
DB 1 GVSETAPASRRGELAVCDVSGWYTDRTAVDLRGREVEVLGEVPAAGSPLROYFEETR 60
QY 61 CADNAEEGGPGAGGCGRGVDRRHMYSECKAKOSYVRALTAAHAGRVGMWRIRIDTACV 120
DB 61 CADNAEEGGPGAGGCGRGVDRRHMYSECKAKOSYVRALTAAHAGRVGMWRIRIDTACV 120

QY 121 CTLLSRTGRA 130
DB 121 CTLLSRTGRA 130

RESULT 9

US-08-451-947-6
Sequence 6, Application US/08451947
Patent No. 5702906
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUTROTROPHIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: peltin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,947
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426419
FILING DATE: 19-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030013
FILING DATE: 22-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 1991
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 666P2C1D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-451-947-6

Query Match 98.7%: Score 689; DB 1; Length 168;
Best Local Similarity 99.2%: Pred. No. 7.3e-72;
Matches 129: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVSETAPASRRGELAVCDVSGWYTDRTAVDLRGREVEVLGEVPAAGSPLROYFEETR 60
DB 39 GVSETAPASRRGELAVCDVSGWYTDRTAVDLRGREVEVLGEVPAAGSPLROYFEETR 98
QY 61 CADNAEEGGPGAGGCGRGVDRRHMYSECKAKOSYVRALTAAHAGRVGMWRIRIDTACV 120
DB 99 CADNAEEGGPGAGGCGRGVDRRHMYSECKAKOSYVRALTAAHAGRVGMWRIRIDTACV 158
QY 121 CTLLSRTGRA 130
DB 159 CTLLSRTGRA 168

RESULT 10
US-08-424-826A-6
Sequence 6, Application US/08424826A
Patent No. 5830858
GENERAL INFORMATION:
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,826A
FILING DATE: 19-Apr-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240387
FILING DATE: 10-May-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 25-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0666P1C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-424-826A-6

Query Match 98.7%: Score 689; DB 2; Length 168;
Best Local Similarity 99.2%: Pred. No. 7.9e-72;
Matches 129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSETAPASRGEGLAVCAVSGWYDRTTAVDLRGREVEVLGEVPAAGSPLEQYFFETR 60
DB 39 GSETAPASRGEGLAVCAVSGWYDRTTAVDLRGREVEVLGEVPAAGSPLEQYFFETR 98
QY 61 CKADNAEEGPGAGGGCGRGVDRRHVSECKAKOSYVRLTAHQGVGWRIRITDTCY 120
DB 99 CKADNAEEGPGAGGGCGRGVDRRHVSECKAKOSYVRLTAHQGVGWRIRITDTCY 158
QY 121 CTLLSRTGRA 130
DB 159 CTLLSRTGRA 168

RESULT 11
US-08-928-694-6
Sequence 6, Application US/08928694
Patent No. 6037320
GENERAL INFORMATION:
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR

NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,694
FILING DATE: 12-Sep-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/451947
FILING DATE: 26-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426419
FILING DATE: 19-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030013
FILING DATE: 22-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 1991
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0666P2C1D2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-928-694-6

Query Match 98.7%: Score 689; DB 3; Length 168;
Best Local Similarity 99.2%: Pred. No. 7.9e-72;
Matches 129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSETAPASRGEGLAVCAVSGWYDRTTAVDLRGREVEVLGEVPAAGSPLEQYFFETR 60
DB 39 GSETAPASRGEGLAVCAVSGWYDRTTAVDLRGREVEVLGEVPAAGSPLEQYFFETR 98
QY 61 CKADNAEEGPGAGGGCGRGVDRRHVSECKAKOSYVRLTAHQGVGWRIRITDTCY 120
DB 99 CKADNAEEGPGAGGGCGRGVDRRHVSECKAKOSYVRLTAHQGVGWRIRITDTCY 158
QY 121 CTLLSRTGRA 130
DB 159 CTLLSRTGRA 168

RESULT 12
PCT-us91-06950-6
Sequence 6, Application PC/TUS9106950
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/06950
FILING DATE: 19910924
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
ATTORNEY/AGENT INFORMATION:
NAME: Hensley, Max D.
REGISTRATION NUMBER: 27,043
REFERENCE/DOCKET NUMBER: 666P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/266-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
PCT-US91-06950-6

Query Match 98.7%; Score 689; DB 5; Length 168;
Best Local Similarity 99.2%; Pred. No. 7,9e-72;
Matches 129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVSETPASRRGELAVCDVSGWYDRTAVDLRGREVEVGEVPAAAGSFLRQYFEETR 60
DB 39 GVSETPASRRGELAVCDVSGWYDRTAVDLRGREVEVGEVPAAAGSFLRQYFEETR 96
QY 61 CKADNAEEGGPGAGGGCGRGVDRRHVSECKAKOSYVALTAHOGRGVGMIRIDTACY 120
DB 99 CKADNAEEGGPGAGGGCGRGVDRRHVSECKAKOSYVALTAHOGRGVGMIRIDTACY 158
QY 121 CTLISRTGRA 130
DB 159 CTLISRTGRA 168

RESULT 13
US-08-451-947-2
Sequence 2, Application US/08451947
Patent No. 5702906
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,947

FILING DATE: 514
CLASSIFICATION: 514
PRIOR APPLICATION DATA: 08/426419
APPLICATION NUMBER: 19-APR-1995
FILING DATE: 19-APR-1995
PRIOR APPLICATION DATA: 08/030013
APPLICATION NUMBER: 22-MAR-1993
FILING DATE: 22-MAR-1993
PRIOR APPLICATION DATA: 07/648482
APPLICATION NUMBER: 31-JAN
FILING DATE: 31-JAN
PRIOR APPLICATION DATA: 07/587707
APPLICATION NUMBER: 1991
FILING DATE: 1991
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 666P2C1D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 210 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-451-947-2

Query Match 98.7%; Score 689; DB 1; Length 210;
Best Local Similarity 99.2%; Pred. No. 1e-71;
Matches 129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVSETPASRRGELAVCDVSGWYDRTAVDLRGREVEVGEVPAAAGSFLRQYFEETR 60
DB 81 GVSETPASRRGELAVCDVSGWYDRTAVDLRGREVEVGEVPAAAGSFLRQYFEETR 140
QY 61 CKADNAEEGGPGAGGGCGRGVDRRHVSECKAKOSYVALTAHOGRGVGMIRIDTACY 120
DB 141 CKADNAEEGGPGAGGGCGRGVDRRHVSECKAKOSYVALTAHOGRGVGMIRIDTACY 200
QY 121 CTLISRTGRA 130
DB 201 CTLISRTGRA 210

RESULT 14
US-08-424-826A-2
Sequence 2, Application US/08424826A
Patent No. 5830858
GENERAL INFORMATION:
APPLICANT: ROSENTHAL, ARNON
APPLICANT: GENENTECH, INC.
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,826A
FILING DATE: 19-APR-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240387
FILING DATE: 10-May-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 25-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Torchla, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0666PIC2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 210 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-424-826A-2

Query Match
Best Local Similarity 98.7%; Score 689; DB 2; Length 210;
Matches 129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVSETAPASRSGELAYCDVAVSGWTDRTAVDLRGREVEVLGEVPAAGSPRLROYFFETR 60
DB 81 GVSETAPASRSGELAYCDVAVSGWTDRTAVDLRGREVEVLGEVPAAGSPRLROYFFETR 140
QY 61 CKADNAEEGGPGAGGGCGGVDRRHVSECKAKQSYVRLTAHAGRGVGMIRIDTACY 120
DB 141 CKADNAEEGGPGAGGGCGGVDRRHVSECKAKQSYVRLTAHAGRGVGMIRIDTACY 200
QY 121 CTLLSRTGRA 130
DB 201 CTLLSRTGRA 210

RESULT 15
US-08-928-694-2
Sequence 2, Application US/08928694
Patent No. 6037320
GENERAL INFORMATION:
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Minipalin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,694
FILING DATE: 12-SEP-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/451947
FILING DATE: 26-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426419
FILING DATE: 19-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030013
FILING DATE: 22-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482

FILING DATE: 31-JAN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 1991
ATTORNEY/AGENT INFORMATION:
NAME: Torchla, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0666P2C1D2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 210 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-928-694-2

Query Match
Best Local Similarity 98.7%; Score 689; DB 3; Length 210;
Matches 129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVSETAPASRSGELAYCDVAVSGWTDRTAVDLRGREVEVLGEVPAAGSPRLROYFFETR 60
DB 81 GVSETAPASRSGELAYCDVAVSGWTDRTAVDLRGREVEVLGEVPAAGSPRLROYFFETR 140
QY 61 CKADNAEEGGPGAGGGCGGVDRRHVSECKAKQSYVRLTAHAGRGVGMIRIDTACY 120
DB 141 CKADNAEEGGPGAGGGCGGVDRRHVSECKAKQSYVRLTAHAGRGVGMIRIDTACY 200
QY 121 CTLLSRTGRA 130
DB 201 CTLLSRTGRA 210

Search completed: December 2, 2002, 15:09:45
Job time : 9.99179 secs

; Sequence 60, Application US/08450842
; Patent No. US20020045576A1
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; APPLICANT: ROSENTHAL, ARNON
; TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 Inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,842
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/426419
; FILING DATE: 19-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/030013
; FILING DATE: 22-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/648482
; FILING DATE: 31-JAN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/587707
; FILING DATE: 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: 666P2C1D3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8674
; TELEFAX: 415/952-9881
; TELERX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-450-842-60

Query Match 97.9%; Score 683; DB 8; Length 130;
Best Local Similarity 98.5%; Pred. No. 2.3e-60;
Matches 128; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYSETPAPSRBGLAVCAVSGMTDRTAVDLRGREYVIGEPAAAGSPRLQYFFETR 60
|||||
Db 1 GYSETPAPSRBGLAVCAVSGMTDRTAVDLRGREYVIGEPAAAGSPRLQYFFETR 60
|||||

QY 61 CKADNAEEGCGPAGCGGCGVDRRHVYSECKAKOSYVRLTAHAQGRVGRMIRIDTACV 120
|||||
Db 61 CKADNAEEGCGPAGCGGCGVDRRHVYSECKAKOSYVRLTAHAQGRVGRMIRIDTACV 120
|||||

QY 121 CTLLSTGRA 130
|||||
Db 121 CTLLSTGRA 130
|||||

Search completed: December 2, 2002, 15:14:35
Job time : 4.5721 secs

QY 121 CTLSTRGRA 130
DB 121 CTLSTRGRA 130

RESULT 13
US-08-450-842-20

Sequence 20, Application US/08450842
Patent No. US20020045576A1
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 Inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,842
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426419
FILING DATE: 19-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030013
FILING DATE: 22-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 1991
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 666P2C1D3
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-450-842-20

Query Match 97.9%; Score 683; DB 8; Length 130;
Best Local Similarity 98.5%; Pred. No. 2.3e-60;

Matches 128; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVSSTAPASRRGELAVCDVAVSGWTDRTAVDLRGREVEVLGEVPAAGSPLRQYFEETR 60
DB 1 GVSSTAPASRRGELAVCDVAVSGWTDRTAVDLRGREVEVLGEVPAAGSPLRQYFEETR 60
QY 61 CKADNAEEGGPGAGGCGCGVDRRHVNSECKAKOSYVRALTAHAGRVGMIRITDACY 120
DB 61 CKADNAEEGGPGAGGCGCGVDRRHVNSECKAKOSYVRALTAHAGRVGMIRITDACY 120
QY 121 CTLSTRGRA 130
DB 121 CTLSTRGRA 130

RESULT 14
US-08-450-842-23

Sequence 23, Application US/08450842
Patent No. US20020045576A1
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 Inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,842
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426419
FILING DATE: 19-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030013
FILING DATE: 22-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 1991
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 666P2C1D3
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-450-842-23

Query Match 97.9%; Score 683; DB 8; Length 130;
Best Local Similarity 98.5%; Pred. No. 2.3e-60;

Matches 128; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVSSTAPASRRGELAVCDVAVSGWTDRTAVDLRGREVEVLGEVPAAGSPLRQYFEETR 60
DB 1 GVSSTAPASRRGELAVCDVAVSGWTDRTAVDLRGREVEVLGEVPAAGSPLRQYFEETR 60
QY 61 CKADNAEEGGPGAGGCGCGVDRRHVNSECKAKOSYVRALTAHAGRVGMIRITDACY 120
DB 61 CKADNAEEGGPGAGGCGCGVDRRHVNSECKAKOSYVRALTAHAGRVGMIRITDACY 120
QY 121 CTLSTRGRA 130
DB 121 CTLSTRGRA 130

RESULT 15
US-08-450-842-60

OY 1 GVSFTAPASRRGELAVCDVAVSGWTDRTAVDLRGREVEVLGEVPAAGSPPLRQYFFETR 60
DB 1 GVSFTAPASRRGELAVCDVAVSGWTDRTAVDLRGREVEVLGEVPAAGSPPLRQYFFETR 60
OY 61 CKADNAEEGCGPAGGCGCGVDRRRHWVSECKAKOSYVRLTAHAGCGVGRWIRIDTACV 120
DB 61 CKADNAEEGCGPAGGCGCGVDRRRHWVSECKAKOSYVRLTAHAGCGVGRWIRIDTACV 120
OY 121 CTLISRTGRA 130
DB 121 CTLISRTGRA 130

RESULT 11

US-08-450-842-64
Sequence 64, Application US/08450842
Patent No. US20020045576A1
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patln (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,842
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426419
FILING DATE: 19-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030013
FILING DATE: 22-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 07/587707
FILING DATE: 1991
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 666P2C1D3
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-450-842-64

Query Match 98.0%; Score 684; DB 8; Length 130;
Best Local Similarity 98.5%; Pred. No. 1.8e-60;
Matches 128; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GVSFTAPASRRGELAVCDVAVSGWTDRTAVDLRGREVEVLGEVPAAGSPPLRQYFFETR 60
DB 1 GVSFTAPASRRGELAVCDVAVSGWTDRTAVDLRGREVEVLGEVPAAGSPPLRQYFFETR 60

OY 61 CKADNAEEGCGPAGGCGCGVDRRRHWVSECKAKOSYVRLTAHAGCGVGRWIRIDTACV 120
DB 61 CKADNAEEGCGPAGGCGCGVDRRRHWVSECKAKOSYVRLTAHAGCGVGRWIRIDTACV 120
OY 121 CTLISRTGRA 130
DB 121 CTLISRTGRA 130

RESULT 12

US-08-450-842-69
Sequence 69, Application US/08450842
Patent No. US20020045576A1
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patln (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,842
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426419
FILING DATE: 19-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030013
FILING DATE: 22-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 07/587707
FILING DATE: 1991
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 666P2C1D3
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-450-842-69

Query Match 98.0%; Score 684; DB 8; Length 130;
Best Local Similarity 98.5%; Pred. No. 1.8e-60;
Matches 128; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 GVSFTAPASRRGELAVCDVAVSGWTDRTAVDLRGREVEVLGEVPAAGSPPLRQYFFETR 60
DB 1 GVSFTAPASRRGELAVCDVAVSGWTDRTAVDLRGREVEVLGEVPAAGSPPLRQYFFETR 60
OY 61 CKADNAEEGCGPAGGCGCGVDRRRHWVSECKAKOSYVRLTAHAGCGVGRWIRIDTACV 120
DB 61 CKADNAEEGCGPAGGCGCGVDRRRHWVSECKAKOSYVRLTAHAGCGVGRWIRIDTACV 120

LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-450-842-59

Query Match 98.0%; Score 684; DB 8; Length 130;
Best Local Similarity 98.5%; Pred. No. 1.8e-60;
Matches 128; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVSETAPASRGEIACVAVSGWYTDRTAVDLRGREVEVLGEVPAAGSPLROYFEETR 60
DB 1 GVSETAPASRGEIACVAVSGWYTDRTAVDLRGREVEVLGEVPAAGSPLROYFEETR 60
OY 61 CKADNAEKGPGAGGGCGVDRHRHWSCKAKOSYVRLTAHAGRGVWRIRIDTACY 120
DB 61 CKADNAEKGPGAGGGCGVDRHRHWSCKAKOSYVRLTAHAGRGVWRIRIDTACY 120
OY 121 CTLSRTGRA 130
DB 121 CTLSRTGRA 130

RESULT 9

US-08-450-842-61
Sequence 61, Application US/08450842
Patent No. US20020045576A1
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: palin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,842
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426419
FILING DATE: 19-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030013
FILING DATE: 22-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 1991
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 666P2C1D3
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-450-842-61

Query Match 98.0%; Score 684; DB 8; Length 130;
Best Local Similarity 98.5%; Pred. No. 1.8e-60;
Matches 128; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVSETAPASRGEIACVAVSGWYTDRTAVDLRGREVEVLGEVPAAGSPLROYFEETR 60
DB 1 GVSETAPASRGEIACVAVSGWYTDRTAVDLRGREVEVLGEVPAAGSPLROYFEETR 60
OY 61 CKADNAEKGPGAGGGCGVDRHRHWSCKAKOSYVRLTAHAGRGVWRIRIDTACY 120
DB 61 CKADNAEKGPGAGGGCGVDRHRHWSCKAKOSYVRLTAHAGRGVWRIRIDTACY 120
OY 121 CTLSRTGRA 130
DB 121 CTLSRTGRA 130

RESULT 10

US-08-450-842-63
Sequence 63, Application US/08450842
Patent No. US20020045576A1
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: palin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,842
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426419
FILING DATE: 19-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030013
FILING DATE: 22-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 1991
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 666P2C1D3
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-450-842-63

Query Match 98.0%; Score 684; DB 8; Length 130;
Best Local Similarity 98.5%; Pred. No. 1.8e-60;
Matches 128; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 666P2C1D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-450-842-68

Query Match 98.1%; Score 685; DB 8; Length 130;
Best Local Similarity 98.5%; Pred. No. 1.4e-60;
Matches 128; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVSETAPASRGEIACVDAVSGVTDRTAVDLRGREVEVLGEVPAAGSPLRQYFEETR 60
DB 1 GVSETAPASRGEIACVDAVSGVTDRTAVDLRGREVEVLGEVPAAGSPLRQYFEETR 60
QY 61 CKADNAEEGPGAGGCGCGVDRRHMYSECKAKOSYVRLTAAGRGVGRWIRIDTACY 120
DB 61 CKADNAEEGPGAGGCGCGVDRRHMYSECKAKOSYVRLTAAGRGVGRWIRIDTACY 120
QY 121 CTLLSRTGRA 130
DB 121 CTLLSRTGRA 130

RESULT 7
US-08-450-842-22
Sequence 22, Application US/08450842
Patent No. US20020045576A1
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,842
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426419
FILING DATE: 19-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030013
FILING DATE: 22-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 1991
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 666P2C1D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674

TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-450-842-22

Query Match 98.0%; Score 684; DB 8; Length 130;
Best Local Similarity 98.5%; Pred. No. 1.4e-60;
Matches 128; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVSETAPASRGEIACVDAVSGVTDRTAVDLRGREVEVLGEVPAAGSPLRQYFEETR 60
DB 1 GVSETAPASRGEIACVDAVSGVTDRTAVDLRGREVEVLGEVPAAGSPLRQYFEETR 60
QY 61 CKADNAEEGPGAGGCGCGVDRRHMYSECKAKOSYVRLTAAGRGVGRWIRIDTACY 120
DB 61 CKADNAEEGPGAGGCGCGVDRRHMYSECKAKOSYVRLTAAGRGVGRWIRIDTACY 120
QY 121 CTLLSRTGRA 130
DB 121 CTLLSRTGRA 130

RESULT 8
US-08-450-842-59
Sequence 59, Application US/08450842
Patent No. US20020045576A1
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,842
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426419
FILING DATE: 19-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030013
FILING DATE: 22-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 1991
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 666P2C1D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 1991
ATTORNEY/AGENT INFORMATION:
NAME: TORCHIA, TIMOTHY E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 666P2C1D3
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 210 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-450-842-2

Query Match
Best Local Similarity 98.7%; Score 689; DB 8; Length 210;
Matches 129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVSETAPASRRGELAVCDVSGWYDRTAVDLRGREVEVLGEVPAAGSPLRQYFFETR 60
DB 81 GVSETAPASRRGELAVCDVSGWYDRTAVDLRGREVEVLGEVPAAGSPLRQYFFETR 140
QY 61 CKADNAEEGPGAGCGGCGVDRRHVSECKAKOSYVRLTAHAGRVGRWIRIDTACV 120
DB 141 CKADNAEEGPGAGCGGCGVDRRHVSECKAKOSYVRLTAHAGRVGRWIRIDTACV 200
QY 121 CTLSTRGRA 130
DB 201 CTLSTRGRA 210

RESULT 5
US-08-450-842-62
Sequence 62, Application US/08450842
Patent No. US20020045576A1
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,842
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426419
FILING DATE: 19-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030013
FILING DATE: 22-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/587707
FILING DATE: 1991
ATTORNEY/AGENT INFORMATION:
NAME: TORCHIA, TIMOTHY E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 666P2C1D3
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-450-842-62

Query Match
Best Local Similarity 98.1%; Score 685; DB 8; Length 130;
Matches 128; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVSETAPASRRGELAVCDVSGWYDRTAVDLRGREVEVLGEVPAAGSPLRQYFFETR 60
DB 1 GVSETAPASRRGELAVCDVSGWYDRTAVDLRGREVEVLGEVPAAGSPLRQYFFETR 60
QY 61 CKADNAEEGPGAGCGGCGVDRRHVSECKAKOSYVRLTAHAGRVGRWIRIDTACV 120
DB 61 CKADNAEEGPGAGCGGCGVDRRHVSECKAKOSYVRLTAHAGRVGRWIRIDTACV 120
QY 121 CTLSTRGRA 130
DB 121 CTLSTRGRA 130

RESULT 6
US-08-450-842-68
Sequence 68, Application US/08450842
Patent No. US20020045576A1
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,842
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426419
FILING DATE: 19-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030013
FILING DATE: 22-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 1991
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.

OY 121 CTLSTRGRA 130
|||
Db 121 CTLSTRGRA 130

RESULT 2

US-09-813-398-12
Sequence 12, Application US/09813398
Patent No. US20020169292A1
GENERAL INFORMATION:
APPLICANT: Bruce D. Weintraub
APPLICANT: Mariusz W. Szudlinski
TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
FILE REFERENCE: UOPMD.003C1
CURRENT APPLICATION NUMBER: US/09/813,398
PRIOR FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: PCT/US99/05908
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: PCT/US98/19772
PRIOR FILING DATE: 1998-09-22
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 131
TYPE: PRT
ORGANISM: HOMO SAPIEN
US-09-813-398-12

Query Match

98.7%: Score 689; DB 9; Length 131;
Best Local Similarity 99.2%: Pred. No. 5.3e-61;
Matches 129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GVSETAPASRRCGLAVCDVSGWYDRTAVDLRGREVEVLGEVPAAGGSLRQYFEETR 60
|||
Db 2 GVSETAPASRRCGLAVCDVSGWYDRTAVDLRGREVEVLGEVPAAGGSLRQYFEETR 61

OY 61 CKADNAEEGGPGAGGGCGVDRRHVSECKAKOSYVRLTAHAGRGVGMIRIDTACY 120
|||
Db 62 CKADNAEEGGPGAGGGCGVDRRHVSECKAKOSYVRLTAHAGRGVGMIRIDTACY 121

OY 121 CTLSTRGRA 130
|||
Db 122 CTLSTRGRA 131

RESULT 3

US-08-450-842-6
Sequence 6, Application US/08450842
Patent No. US20020045576A1
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: palin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,842
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426419

FILING DATE: 19-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/030013

FILING DATE: 22-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/648482

FILING DATE: 31-JAN

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/587707

FILING DATE: 1991

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: 666P2C1D3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-8674

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 168 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-450-842-6

Query Match

98.7%: Score 689; DB 8; Length 168;
Best Local Similarity 99.2%: Pred. No. 7.6e-61;
Matches 129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GVSETAPASRRCGLAVCDVSGWYDRTAVDLRGREVEVLGEVPAAGGSLRQYFEETR 60
|||
Db 39 GVSETAPASRRCGLAVCDVSGWYDRTAVDLRGREVEVLGEVPAAGGSLRQYFEETR 98

OY 61 CKADNAEEGGPGAGGGCGVDRRHVSECKAKOSYVRLTAHAGRGVGMIRIDTACY 120
|||
Db 99 CKADNAEEGGPGAGGGCGVDRRHVSECKAKOSYVRLTAHAGRGVGMIRIDTACY 158

OY 121 CTLSTRGRA 130
|||
Db 159 CTLSTRGRA 168

RESULT 4

US-08-450-842-2
Sequence 2, Application US/08450842
Patent No. US20020045576A1
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: palin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,842
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426419
FILING DATE: 19-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030013
FILING DATE: 22-MAR-1993

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OM protein - protein search, using sw model

Run on: December 2, 2002, 15:08:47 ; Search time 4.5721 Seconds
(without alignments)
452.778 Million cell updates/sec

Title: US-10-072-681-6
Perfect score: 698
Sequence: 1 GVSTFAPASRGLAVCDVAV.....RWIRIDYACVLTSLRTGTA 130

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 102317 seqs, 15924203 residues

Total number of hits satisfying chosen parameters: 102317

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
2: /cgn2_6/ptodata/1/pubpaa/PTCT_NEW_PUB pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB pep.*
7: /cgn2_6/ptodata/1/pubpaa/PTCTUS_PUBCOMB pep.*
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9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep.*
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13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	688	100.0	130	12	US-10-072-681-6
2	688	98.7	131	9	US-03-813-398-12
3	688	98.7	168	8	US-08-450-842-6
4	689	98.7	210	8	US-08-450-842-2
5	685	98.1	130	8	US-08-450-842-62
6	685	98.1	130	8	US-08-450-842-68
7	684	98.0	130	8	US-08-450-842-22
8	684	98.0	130	8	US-08-450-842-59
9	684	98.0	130	8	US-08-450-842-61
10	684	98.0	130	8	US-08-450-842-63
11	684	98.0	130	8	US-08-450-842-64
12	684	98.0	130	8	US-08-450-842-69
13	683	97.9	130	8	US-08-450-842-20
14	683	97.9	130	8	US-08-450-842-23
15	683	97.9	130	8	US-08-450-842-60
16	683	97.9	130	8	US-08-450-842-65
17	683	97.9	130	8	US-08-450-842-70
18	683	97.9	130	8	US-08-450-842-72
19	682	97.7	130	8	US-08-450-842-66

20	682	97.7	130	8	US-08-450-842-73	Sequence 73, Appl
21	681	97.6	130	8	US-08-450-842-17	Sequence 17, Appl
22	681	97.6	130	8	US-08-450-842-67	Sequence 67, Appl
23	680	97.4	130	8	US-08-450-842-18	Sequence 18, Appl
24	680	97.4	130	8	US-08-450-842-71	Sequence 71, Appl
25	679	97.3	130	8	US-08-450-842-19	Sequence 19, Appl
26	679	97.3	130	8	US-08-450-842-21	Sequence 21, Appl
27	677	97.0	130	8	US-08-450-842-13	Sequence 13, Appl
28	677	97.0	130	8	US-08-450-842-14	Sequence 14, Appl
29	677	97.0	130	8	US-08-450-842-15	Sequence 15, Appl
30	677	97.0	130	8	US-08-450-842-16	Sequence 16, Appl
31	669.5	95.9	129	8	US-08-450-842-53	Sequence 53, Appl
32	669.5	95.9	129	8	US-08-450-842-54	Sequence 54, Appl
33	651	93.3	130	8	US-08-450-842-47	Sequence 47, Appl
34	650	93.1	126	8	US-08-450-842-57	Sequence 57, Appl
35	642	92.0	124	8	US-08-450-842-55	Sequence 55, Appl
36	586	84.0	114	8	US-08-450-842-58	Sequence 58, Appl
37	571	81.8	105	8	US-08-450-842-31	Sequence 31, Appl
38	558	79.9	103	8	US-08-450-842-30	Sequence 30, Appl
39	540	77.4	142	8	US-08-450-842-52	Sequence 52, Appl
40	535.5	76.7	107	8	US-08-450-842-56	Sequence 56, Appl
41	535.5	76.7	132	8	US-08-450-842-51	Sequence 51, Appl
42	501.5	71.8	186	8	US-08-450-842-12	Sequence 12, Appl
43	494.5	70.8	216	8	US-08-450-842-8	Sequence 8, Appl
44	478.5	68.6	257	8	US-08-450-842-10	Sequence 10, Appl
45	468	67.0	92	8	US-08-450-842-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1
US-10-072-681-6
Sequence 6, Application US/10072681
Patent No. US20020137893A1
GENERAL INFORMATION:
APPLICANT: Burton, Louis E.
APPLICANT: Schmelzer, Charles H.
TITLE OF INVENTION: PURIFICATION OF NGF
FILE REFERENCE: GENENT.037C3
CURRENT APPLICATION NUMBER: US/10/072,681
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/030838
PRIOR FILING DATE: 1996-11-15
PRIOR APPLICATION NUMBER: 60/047855
PRIOR FILING DATE: 1997-05-29
PRIOR APPLICATION NUMBER: 08/970865
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: 09/363573
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: 09/675,503
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 130
TYPE: PRT
ORGANISM: Homo sapien

Query Match 100.0% Score 698 DB 12 Length 130:
Best Local Similarity 100.0% Pred. No. 7.7e-62
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVSTFAPASRGLAVCDVAVGVTTRRRAVYDLRGREVEYAGVPAAGSGFLROYFEETR 60
DB 1 GVSTFAPASRGLAVCDVAVGVTDRRAVYDLRGREVEYAGVPAAGSGFLROYFEETR 60
QY 61 CKADNAEEGGPGAGGCGGVDVRHNVSECKAKOSYVATLTAHAGRGVWRWIRIDYACV 120
DB 61 CKADNAEEGGPGAGGCGGVDVRHNVSECKAKOSYVATLTAHAGRGVWRWIRIDYACV 120